

From: Chan, Christina
Sent: Monday, March 29, 2004 11:10 AM
To: Yaen, Christopher; STIC-Biotech/ChemLib
Subject: RE: 09883848-RUSH

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Yaen, Christopher
Sent: Monday, March 29, 2004 11:01 AM
To: Chan, Christina
Subject: 09883848-RUSH

Hi Christina,

could you please rush the following search:

sequence search on seq id 15, include sequences that are at least 60% identical

thanks

Christopher Yaen
US Patent Office
Art Unit 1642
571-272-0838
REM 3A20
REM 3C18

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 3/30
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

or send an email to license@isb-sib.ch).

CC	RESULT 17	DHH2_XENLA	STANDARD;	PRT;	398 AA.
CC	ID DHH2_XENLA	AC Q91611;	PR		
DR	ENBL; U26349; AAIB5163; 1; -	DT 15-JUL-1999 (Rel. 38, Created)			
DR	HSSP; Q62226; 1VHFF.	DT 15-JUL-1999 (Rel. 38, Last sequence update)			
DR	MEROPS; C46_UPW; -.	DT 10-OCT-2003 (Rel. 42, Last annotation update)			
DR	InterPro; IPR009045; Hedgehog/DD_Pept.	DB Desert hedgehog protein precursor 2 (DHH-2) (X-			
DR	InterPro; IPR003557; Hedgehog_hint_N.	DB HH4.			
DR	InterPro; IPR003516; Hedgehog_hint_C.	GN Xenopus laevis (African clawed frog).			
DR	InterPro; IPR000320; HH signal.	OS Osteichthyes; Chondrichtyes; Gnathostomata; Vertebrata; Euteleostomi;			
DR	InterPro; IPR006141; InFein_S.	OC Eukaryota; Metazoa; Chordata; Craniata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;			
DR	InterPro; IPR001767; Pept_C6_hint.	OC Xenopodinae; Xenopus.			
DR	InterPro; IPR000167; Peptidase_C46.	OC NCBITaxID:8355; OX NCBI_TaxID:8355;			
PFAM	PF01085; HH signal; 1.	RN [1] -			
PFAM	PF01079; Hint; 1.	RN SEQUENCE FROM N.A.			
DR	ProDom; PDD00042; HH signal; 1.	RP TISSUE=Embryo;			
SMART	SM00305; HintC; 1.	RC MEDLINE=93401852; PubMed=7671800;			
DR	PROSITE; PS50017; INTEIN_N_TER; 1.	RA Moon R.T., Beachy P.A.;			
KW	Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; Lipoprotein; Palmitate.	RA "Distinct expression and shared activities of members of the hedgehog gene family of Xenopus laevis."			
KW	Signal; Lipoprotein; Palmitate.	RT Gene family of Xenopus laevis."			
FT	SIGNAL 1	RT Development 12:233-244 (1995).			
FT	CHAIN 23	RL -!- FUNCTION: SIGNAL INVOLVED IN THE EARLY INDUCTION AND PATTERNING OF ANTERIOR-POSTERIOR ECTODERM, NERVOUS SYSTEM AND SOMITES. INDUCES ECTOPIC CEMENT GLAND FORMATION IN EMBRYO.			
FT	CHAIN 23	CC -!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE SURFACE. HEDGEHOG PROTEIN IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).			
FT	DOMAIN 198	CC -!- PIM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity (By Similarity).			
FT	DOMAIN 276	CC -!- SIMILARITY: Belongs to the hedgehog family.			
FT	SITE 197	CC This SWISS-PROT entry is copyright of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
FT	SITE 267	CC DR EMBL; U26350; AA85164_1; -.			
FT	ACT_SITE 270	CC DR MBROPS; C46_UPW; -.			
FT	LIPID 23	CC DR InterPro; IPR00045; Hedgehog/DD_Pept.			
FT	LIPID 197	CC DR InterPro; IPR003587; Hedgehog_hint_N.			
FT	SEQUENCE 396 AA;	CC DR InterPro; IPR003586; Hedgehog_hint_C.			
FT	SEQUENCE 396 AA;	CC DR InterPro; IPR00320; HH signal.			
FT	SEQUENCE 396 AA;	CC DR InterPro; IPR001767; PepT_C46_hint.			
FT	SEQUENCE 396 AA;	CC DR InterPro; IPR001657; PepTase_C46.			
FT	SEQUENCE 396 AA;	CC DR PF01085; HH signal; 1.			
Db	Query Match 43.7%; Score 1079.5; DB 1; Length 396; Best Local Similarity 50.1%; Pred. No. 1.2e-70; Matches 222; Conservative 55; Mismatches 109; Indels 6;	CC DR PF01079; HH signal; 1.			
Qy	6 RCLLLVSSSLIVCGLACPGGRG-FGKRRHPKLTPLAKYQFIPVAEKTIGASGRVEG 64	CC DR PR00632; SONICHOG.			
Db	5 RIVILAIICCGHLIVPVRCGPGRGVGRSYMRKLIVLPIYKQFVNPKTIGASGRSEG 64	CC DR Prodrom; PD003042; SONICHOG.			
Qy	65 KISRSRNSERFLKELTPNNDTIPKDENTGADRMLTQRCDKLNALAISSMANQPGVKLRV 124	CC DR SMART; SM00305; HintN; 1.			
Db	65 KIHRGSEFIELVPPYNPDIIKFDEKTFGADRMLTQRCRVLNAIASTNMMPGVKLRV 124	CC DR Signal; Lipoprotein; Palmitate.			
Qy	125 TEGWDDEDGHSEBESLHYEGRAVDITTSDRSKYGMALARLAVEAGFDWVTTYESKAHIFCS 164	CC DR SIGNAL 1; POTENTIAL.			
Db	125 TEGWDDEDGHADSLHYEGRAVDITTSDRKNYGMALARLAVEAGFDWVTTYESKAHIFCS 184	CC DR SIGNAL 1; POTENTIAL.			
Qy	185 VKAENSYVAKSGGGPSATVLEQGTLYKVDLSFGDRLTAADQGRLLYSDLTFLR 244	CC DR DESERT_HEDGEHOG_PROTEIN_2.			
Db	185 VRADNSLJSVRSGCFPQTAMMGTCKERPLSSELKIGDTVYTDTETGQLITSVVLFLR 244	CC DR DESERT_HEDGEHOG_PROTEIN_2.			
Qy	245 DDGAKKVFYVETREPRLIUTAAHLYFAPHNDSATGEPEASSGGSPGSSGGALGPRL 304	CC DR DESERT_HEDGEHOG_PROTEIN_2.			
Db	245 NPYKTAFFVLIQAEIGFSLKLIVTPNLLFI-----OSSSAFLP-----T 285	CC DR DESERT_HEDGEHOG_PROTEIN_2.			
Qy	305 FASVRPGQRVYVVAERDGDRLPAAVHSVTLSEEAGAYAPLTAQGTLINRVLASY 364	CC DR DESERT_HEDGEHOG_PROTEIN_2.			
Db	286 FAERVQDGLYQIYV--NGTQVQSSKVRVSL-BEQTGYZAPMTEBHGTLVGVLTSSY 341	CC DR DESERT_HEDGEHOG_PROTEIN_2.			
Qy	365 AVIEERWAHRAFAPPRLAHALLAAPAR DRGGDSGGDRGGGRVALTQAADP 424	CC DR POLYSER.			
Db	342 ATVESHTLHYSLAPRLFOGIFTASWL-----P 368	CC DR DOMAIN 281			
Qy	425 GAGATAGIHWYSQLYQIGTML 447	CC DR DOMAIN 281			
Db	369 DIDMSDWHWCHILYVAKVYI 391	CC DR DOMAIN 281			

FT SITE	199	200	CLEAVAGE (AUTO-) (BY SIMILARITY).
FT SITE	269	269	INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
FT ACT_SITE	272	272	ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
FT LIPID	24	24	N-palmitoyl cysteine (BY similarity).
FT LIPID	199	199	Cholesteryl glycine ester (BY similarity).
SEQUENCE	398 AA:	44458 MN;	DBC23A85F69DD08 CRC64;
Qy	1	MLLARC--LLLVIITVSSLLIVCSGLACGPGRG--FGKRPBPKPLTPLAYKQFPVNVEKT	55
Db	6	LILIAACCWILLPPVR-----CCGPGRGPyGRRYMRRLVPLVLYKQFPVNPEKT	57
Qy	56	LGASGRYEGKLSRSNRFKELTPTNPYNPDIIFKDEENTGADRMLTQRCKDNLTKNLAISVMN	115
Db	58	LGASGKSEGKPRGSERFRIKLVNPYNPDIIFKDENTGADRMLTQRCKDNLTKNLAISVMN	117
Qy	116	QWPGYKLRLTVTEGWDEDGHHSSEBSLHYEGAVDITTSDRRSKYGMALARAVEAGFDWYY	175
Db	118	MWPGLKLRLTVTEGWDEDGHHSLETRGEALDITTSDRDENKTMGMLARAVEAGFDWYY	177
Qy	176	ESKAHTHCSKAENSAAKSGCGCPGSAVTHLEQGGTKLVKDKLSPGDRTLAADDGGRUY	235
Db	178	ESKAHTHVSNTDNSIGVRSGCFCPTAAYNMETRKPKPSLSELKGDTFTTDGTGLIHK	237
Qy	236	SDFLTFLDRDGAKKVYVIE TREPRERLLTAHHLYVAPHNDSATGGPPEASSGSGPPS	295
Db	238	SVVLFELHRDPYKTTATEVLEAEHPTKLLVTPNHLFI-----RS	278
Qy	296	GGALGPALFAFSRVRGQQ--RIVYTAERDGRRLPAATHSVTLSSEANGAYAPLTAGQ	353
Db	297	SSSTGFQPTFAYRVQGDLIQLIVNTQVQSSKVYRVSV-----DEQGTYVAMTENC	332
Qy	354	ILINRVLASCVAVEBHSWAIRAFAPRLAHALLAALAPARTDRGGDSSGGDRGGGRV	413
Db	333	LLVDGVLTSCATVESHTLAHASLPLRLFQGIASM-----	369
Qy	414	ALTAPGRADAPGAGATAGIHWYSQQLYQIGTWLL 447	
Db	370	-----PDLHTSDGVHWCYLVILVAKYL 393	
RESULT 18			
HH_DRONE		STANDARD;	PRT;
ID	007936	Q9VCQ4;	421 AA.
AC			
DT	01-FEB-1994	(Rel. 28, Created)	
DT	15-MAR-2004 (Rel. 43, Last sequence update)		
DE	Hedgehog protein precursor.		
GN	OR_CG4637.		
OS	Drosophila melanogaster (Pruit fly).		
OC	Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Ephydriidea; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydriidae; Drosophilidae; Drosophila.		
RN	NCBI_TAXID=227;		
SEQUENCE FROM N.A. (ISOFORM LONG), FUNCTION, DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.			
STRAIN=Canton-S; TISSUE=Embryo;			
MEDLINE=931185922; PubMed=816682;			
RA	Tashiro S., Michie T., Higashijima S.-I., Zenno S., Ishimaru S.,		
RA	Takahashi F., Orihara M., Kojima T., Saito K.;		
RT	"Structure and expression of hedgehog, a Drosophila segment-polarity gene required for cell-cell communication.";		
RL	Gene 124:183-189(1993).		
RN	[2]		
SEQUENCE FROM N.A. (ISOFORM LONG), FUNCTION, DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.			
STRAIN=Oregon-R; TISSUE=Embryo;			
MEDLINE=94040725; PubMed=1340474;			
RA	Tabata T., Bacon S., Kornberg T.B.;		
RT	"The Drosophila hedgehog gene is expressed specifically in posterior compartment cells and is a target of engrailed regulation.";		
RL	Genes Dev. 6:2635-2645(1992).		
RN	[15]		
SEQUENCE FROM N.A.			
STRAIN=Berkeley;			
MEDLINE=20596005; PubMed=107211132;			
RA	Adams M.D., Ceniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amanatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Gallo R.S.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		
RA	Brandon R.C., Rogers Y.H.C., Blazquez R.G., Champe M., Peiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,		
RA	Abrial J.P., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,		
RA	Baldew R.M., Basu A., Basden J., Bayraktaroglu L., Beasley E.M.,		
RA	Beeson K.Y., Benos P.V., Berman B., Bhanda D., Bolkhakov S.,		
RA	Borkova D., Botchan M.R., Bouck J., Brookstein P., Brottier P.,		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		
RA	De la Torre B., Delcher A., Deng Z., Mayes A.D., Dew I., Dietz S.M.,		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W.,		
RA	Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K.,		
RA	Glodk A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris N.L., Harvey D.A., Heiman T.J., Hernández J.R., Houck J.,		
RA	Hortin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,		
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		
RA	Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,		
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,		
RA	Merkulov G., Milashina N.V., Moharrir C., Morris J., Moehretti A.,		
RA	Mount S.M., Moy M., Murphy B., Murphy L., Murdy D.M., Nelson D.L.,		
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacie J.M.,		
RA	Palaizo M., Pittman G.S., Pan S.S., Pollard J., Puriv V., Reese M.G.,		
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,		
RA	Shieh B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,		
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang X.,		
RA	Svirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,		
RA	Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,		
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,		
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,		
RA	Zheng X.-H., Zhong W., Zhou X., Zhou S., Zhu X., Smith H.O.,		
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,		
RT	"The genome sequence of Drosophila melanogaster.";		
RT	Science 287:2185-2195 (2000).		
RN	[6]		
RT	AUTOPROTEOLYTIC CLEAVAGE;		
RA	POURER J.A., von KESSLER D.P., ECKER S.C., YOUNG K.E., LEE J.J.,		
RA	MOSSES K., BEACHY P.A.;		
RA	"The product of hedgehog autoproteolytic cleavage active in local and		

RT long-range signalling.";
 RN Nature 374:363-366(1995).
 RP FUNCTION AND MUTAGENESIS OF CYS-35.
 MEDLINE=21220785; PubMed=1131986;
 RX Lee J.D., Kraus P., Galano N., Nery S., Kohtz J., Fishell G.,
 RA Loomis C.A., Treisman J.E.;
 RT "An acylatable residue of Hedgehog is differentially required in
 Drosophila and mouse limb development";
 RL Dev. Biol. 233:122-136(2001).
 RP PALMITOYLATION, MASS SPECTROMETRY, AND MUTAGENESIS OF CYS-35.
 MEDLINE=21442023; PubMed=1186055;
 RA Chamoun Z., Mann R.K., Nellen D., von Kessler D.P., Bellotto M.,
 RA Beachy P.A., Basler K.;
 RT "Skinny hedgehog, an acyltransferase required for palmitoylation and
 activity of the hedgehog signal";
 RL Science 293:2080-2084(2001).
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 208-358, AND MUTAGENESIS.
 RX MEDLINE=97474313; PubMed=9315337;
 RA Hall T.M.T., Porter J.A., Young K.E., Beachy P.A.,
 RA Leatly D.J.;
 RT "Crystal structure of a Hedgehog autoprocessing domain: homology
 between Hedgehog and self-splicing proteins.";
 RT Cell 91:95-97(1997).
 RL 91:95-97(1997).
 -!- FUNCTION: Intercellular signal essential for a variety of
 patterning events during development. Establishes the anterior-
 posterior axis of the embryonic segments and patterns the larval
 imaginal disks. Binds to the patched (ptc) receptor, which
 functions in association with smoothened (smo) to activate the
 transcription of target genes wingless (wg), decapentaplegic (dpp)
 and ptc. In the absence of hh, ptc represses the constitutive
 signaling activity of smo through fused (fu).
 -!- SUBCELLULAR LOCATION: Nuclear up to embryonic stage 10 and then at
 stage 11 shifts to the cytoplasm. C-terminal peptide diffuses from
 the cell, the N-terminal peptide remains associated with the cell
 surface. Also secreted in either cleaved or uncleaved form to
 mediate signaling to other cells.
 -!- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=Q0936-1; Sequence=Displayed;

CC -!- TISSUE SPECIFICITY: In embryos, expression starts at stage 5 as a few stripes at the anterior and posterior ends, this expands to 17 stripes during stages 8-11. Expression is also seen in CNS and some PNS cells until stage 13-14, and in foregut, hindgut and salivary glands. In larvae, expression is seen in the posterior compartment of the wing imaginal disk.

CC -!- DEVELOPMENTAL STAGE: Expressed in embryos, larvae and pupae at high levels with maximum expression in 6-12 hour embryos and 0-24 hour pupae. Low levels of expression are seen in adults.

CC -!- PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length hedgehog protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated amino-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the hedgehog activity to the cell surface. Amino-terminal Palmitoylation of hedgehog N-product is required for the embryonic and larval patterning activities of the hedgehog signal. The N-product is the active species in both local and long-range signaling, whereas the C-terminal product has no signaling activity.

CC -!- PTM: Rasp acts within the secretary pathway to catalyze the N-terminal palmitoylation of Hh.

CC -!- MASS SPECTROMTRY: MW=20238.44; METHOD=MALDI; RANGE=35-207.

CC -!- SIMILARITY: Belongs to the hedgehog family.

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CC DR EMBL: L05404; PAA28604_1; ALT INIT.
 CC DR EMBL: L05405; ; NOT ANNOTATED CDS.
 CC DR EMBL: L02793; AA1145B_1; ALT INIT.
 CC DR EMBL: S66384; AAB28646_1; ALT INIT.
 CC DR EMBL: AE003742; AAES56102_1; ALT INIT.
 DR PIR; A46400; A46400.
 DR MEROPS; C46_001; ;
 DR PIRBase; FBgn004644; ;
 DR GO; GO_0005737; C:cytoplasm; IEP.
 DR GO; GO_0005576; C:extracellular; NAS.
 DR GO; GO_0005334; C:nucleus; IEP.
 DR GO; GO_0005886; C:plasma membrane; NAS.
 DR GO; GO_0005113; F:patched binding; NAS.
 DR GO; GO_0005119; F:smoothened binding; NAS.
 DR GO; GO_0007267; P:cell-cell signaling; NAS.
 DR GO; GO_0008959; P:determination of anterior/posterior axis; e. . . ; NAS.
 DR GO; GO_0009880; P:embryonic pattern specification; IEP.
 DR GO; GO_0008347; P:glia cell migration; IMP.
 DR GO; GO_0007442; P:imaginal disc pattern formation; NAS.
 DR GO; GO_0007447; P:progression of morphogenetic furrow (senseu . . . ; IEP.
 DR GO; GO_0016540; P:protein autoprocessing; IDA.
 DR GO; GO_0016540; P:protein autoprocessing; IDA.

Query Match 36.0%; Score 890; DB 1; Length 421;
 Best Local Similarity 44.8%; Pred. No. 5..9e-57;
 Matches 202; Conservative 65; Mismatches 137; Indels 52; Gaps 10;

QY 6 RCL-----LIVLVSSLLVCSGLACGPGRGFGRHRPKKLTPLAYKOFIPNVAEKTLLG 57
 QY 9 RCLSLRSLSVALLLTVLPWYFSPASWCGRPGRLGRH-ARNLYPLVKQTIPNLSEYTNS 67
 QY 58 ASGRYGRISRNSERKELTPNNDIIFDEENTGADRIMTOCKDKUNALAISVNNOV 117
 DB 68 ASGPIGLFVIRDSDPKEDSPKFDVNPYNDILFDEEGGADRUMSKRKEXKLNVLYAVMNNEW 127
 QY 118 PGVKLRVTEGMDGGHSEBSLHYGRADVTITSDRSXKGMLARLAVEAGFDIVVYYS 177
 DB 128 PGIRLLYTESDIDTHGQESLHYGRAVIATSDRDQSYGMALARLAVEAGFDIVVYS 187
 QY 178 KAHICGSKVKAENSAKSQGGCPFGSATVHLEQGGITKLVKDLSGPGRVLADDQGRILYSD 237
 DB 188 RHHYIYCSVKSDSISSHVHGCFPESTALLESVGKEPLGELSIGDRVLSTMANGAVYSE 247
 DB 238 PLTFUDRDGAKKKVFVIEPREPFLTAHHLFVAPINDSATGEPEASSGSGPSSGG 297
 DB 248 VILFMDNLQNQNFTQLHT-DGGAWLTVP AHL/SV-----WQEPAQQLT----- 292
 QY 298 ALGPRAFLASVRPGGVYVVAERGDDRLLPAAYTSVTLSEEAGGAYAPLTAQGTILIN 357
 DB 293 -----FVFADEEKKQVLYRVDVETGELR--PQRVTKVG-SVRSKVVABLRECTIVN 344
 QY 358 RVIASCYAVIEEHSHWAHAPFLNHALLAALARPTDGGDSGGGDRCGGGRVALTA 417
 DB 345 SYAACSYAVINSQSLAHWGLAPMRJLSTLEBWL-PAKEQ-----LHSS 386
 QY 418 PGADAPGAGATGIVWYQOLYQITGWWLDSEALH 453
 DB 397 PKVYSS-AQQQNGIHWYANLYKTDYVLPQSWRH 420

RESULT 19
 HH DROHY ID HH DROHY STANDARD; PRT; 422 AA.
 AC 25674; DT 15-JUL-1999 (Rel. 38, Created)

DT	15-MAR-2004 (Rel. 43, Last sequence update)	ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)	N-palmitoyl cysteine (By similarity).		
HN	Hedgehog protein precursor.	Cholesterol; glycine ester (By similarity).		
[1]	Drosophila hydei (Fruit fly)			
OC	Ephydriidae; Drosophilidae; Drosophila.			
OX	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
RN	Ephydriidae; Drosophilidae; Drosophila.			
RRP	SEQUENCE FROM N.A. MOLCODE: 95236997; PubMed=7720571; Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K., Zhao R., Selim M.F., Fallon J.F., Beachy P.A., "Products, genetic linkage and limb patterning activity of a murine hedgehog gene," Development 120:3339-3353 (1994).			
CC	-!- FUNCTION: Interacellular signal essential for a variety of patterning events during development. Establishes the anterior-posterior axis of the embryonic segments and patterns the larval imaginal disks. Binds to the patched (ptc) receptor, which functions in association with smoothed (smo), to activate the transcription of target genes wingless (wg), decapentaplegic (dpp) and ptc. In the absence of hh, ptc represses the constitutive signaling activity of smo through fused (fuf).			
CC	-!- SUBCELLULAR LOCATION: C-terminal peptide diffuses from the cell, the N-terminal peptide remains associated with the cell surface. Also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).			
CC	-!- PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length hedgehog protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated amino-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the hedgehog activity to the cell surface. Ami-ro-terminal palmitoylation of hedgehog N-product is required for the embryonic and larval patterning activities of the hedgehog signal. The N-product is the active species in both local and long-range signaling, whereas the C-terminal product has no signaling activity (By similarity).			
CC	-!- PTM: Rasp acts within the secretory pathway to catalyze the N-terminal palmitoylation of Hh (By similarity).			
DR	HSSP; Q02936; 1ATQ.			
MEROPS	FlyBase; FBgn0015616; Dhydhb.			
DR	InterPro; IPR09045; Hedgehog/DD_pept.			
DR	InterPro; IPR003587; Hedgehog_hntN.			
DR	InterPro; IPR003586; Hedgehog_hntC.			
DR	InterPro; IPR000320; HH_Signal.			
DR	InterPro; IPR001441; Intein_S.			
DR	InterPro; IPR001767; Pept_C46_hint.			
DR	InterPro; IPR001657; Pept_Iddae_C46.			
DR	Pfam; PF01085; HH_Signal_1.			
DR	Pfam; PF01079; Hint_1.			
DR	PRINTS; PR00612; SONICHHOG.			
DR	ProDom; PD003042; HH_Signal_1.			
SMART	SM00306; HintC_1.			
DR	SMART; SM00306; HintN_1.			
DR	PROSITE PS50017; INTEIN_N-TER; 1.			
KW	Hydrolease; Protease; Developmental Protein; Segmentation; Polarity Protein; Signal; Autocatalytic cleavage;			
KW	Lipoprotein; Palmitate.			
SIGNAL	1	POTENTIAL.		
FT	CHAIN	32	422	HEDGEHOG PROTEIN_N-PRODUCT.
FT	CHAIN	32	205	HEDGEHOG PROTEIN_C-PRODUCT.
FT	CHAIN	206	422	CLEAVAGE (AUTO-) (BY SIMILARITY).
FT	SITE	205	206	INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY).
FT	SITE	251	251	INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
FT	SITE	274	274	SEQUENCE FROM N.A.
SHH_RASEL	ID—SHH_RASEL STANDARD; PRT; 121 AA.			
AC	P79858; P79859;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Sonic hedgehog protein (SHH) (Fragments).			
GN	Rasbora elegans (Elegant rasbor).			
OS	Batiraja, Matsuzaki; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygi; Neopterygi; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasbora.			
OC	NCBI_TaxID=27712; [1]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=MUSCLE;			
RX	MEDLINE=97075114; PubMed=8917540;			
RA	Zarroya R., Abouheif E., Meyer A.; "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish," Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041 (1996).			
RT	-!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH,			

CC PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY SIMILARITY). The C-terminal peptide diffuses from the CC -!- SUBCELLULAR LOCATION: The C-terminal peptide remains associated with the cell, while the N-terminal peptide remains associated with the CC cell surface. It is also secreted in either cleaved or uncleaved form CC to mediate signaling to other cells (By similarity).

CC -!- PTM: The C-terminal domain displays an autoproteolysis activity CC and a cholesterol transfer activity. Both activities result in the cleavage of the full-length protein and covalent attachment of CC a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears CC to play an essential role in restricting the spatial distribution CC of the protein activity to the cell surface. The N-product is the CC active species in both local and long-range signaling, whereas the CC C-product has no signaling activity (By similarity).

CC -!- SIMILARITY: Belongs to the hedgehog family.

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DR EMBL; U51355; AAB38578.1; -
DR EMBL; U51374; AAB38597.1; -
DR ASSP; Q62226; 1VH.
DR InterPro; IPR00945; Hedgehog/DD_Pept.
DR InterPro; IPR000320; HH_Signal.
DR InterPro; IPR001657; Peptidase_C46.
PRINTS; PR00632; SONICHHOG.
ProDom; PD003042; HH_Signal_1.
KW Developmental_protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1
FT NON_TER 63 64
FT NON_CONS 121 121 AA; 13975 MW; 6C9334EA1C739B4F CRC64;
SQ SEQUENCE

Query Match 24.4%: Score 602; DB 1; Length 121;
Best Local Similarity 81.6%; Pred. No. 7.4e-37;
Matches 115; Conservative 4; Mismatches 20; Gaps 1;

Qy 30 FGKRRHPKLTPLAYKQFIPNVAEKLIGASRYEGKISSNSERKEELTPNYNPDIIFKDE 89
Db 1 YGKRRHPKLTPLAYKQFIPNVAEKLIGASRYEGKISSNSERKEELTPNYNPDIIFKDE 60
Qy 90 ENTGADRLLMTQRCKDLNAAISVNQWPGYKLRTVEGDEDGHSSESHYEGRAVDIT 149
Db 61 ENT-----VNQWPGYKLRTVEGDEDGHSSESHYEGRAVDIT 100
Qy 150 TSDRDRSKYGMMLAALAVEAGF 170
Db 101 TSDRDKSKYGMMLAALAVEAGF 121

RESULT 21
SHH_CARAU STANDARD; PRT; 121 AA.
ID SHH_CARAU
AC P79651; P79692;
DT 15-JUL-1995 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Sonic hedgehog protein (SHH) (Fragment(s)).
GN SHH.
OS Carassius auratus (Goldfish).
OC Actinopterygii; Chondrocephali; Craniata; Vertebrata; Buteleostomi;
OC Cyprinidae; Carassiini.
NCBI TaxID: 7957;
RN [1]
RP SEQUENCE FROM N.A.
TISSUE=Muscle;

RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R.; Abouheif E.; Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041 (1996).
CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR THE PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS FLOOR PLATE INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSIONS THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. It is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).
CC -!- PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transfer activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity).
CC -!- SIMILARITY: Belongs to the hedgehog family.

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DR EMBL; U51356; AAB38565.1; -
DR EMBL; U51375; AAB38583.1; -
DR HSSP; Q62226; 1VH.
DR InterPro; IPR009045; Hedgehog/DD_Pept.
DR InterPro; IPR000320; HH_Signal.
DR InterPro; IPR001657; Peptidase_C46.
PRINTS; PR00632; SONICHHOG.
DR PRODOM; PD003042; HH_Signal_1.
KW Developmental_protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1 1
FT NON_CONS 63 64
FT NON_TER 121 121 AA; 14003 MW; 559334E4057391C1 CRC64;
SQ SEQUENCE 121 AA; Conservatve 80.3%; P5; Mismatches 5; Indexes 2; Gaps 1;

Query Match 24.3%: Score 599; DB 1; Length 121;
Best Local Similarity 80.3%; Pred. No. 1.2e-16;
Matches 114; Conservative 80.3%; P5; Mismatches 5; Indexes 2; Gaps 1;

Qy 30 FGKRRHPKLTPLAYKQFIPNVAEKLIGASRYEGKISSNSERKEELTPNYNPDIIFKDE 89
Db 1 YGKRRHPKLTPLAYKQFIPNVAEKLIGASRYEGKISSNSERKEELTPNYNPDIIFKDE 60
Qy 90 ENTGADRLLMTQRCKDLNAAISVNQWPGYKLRTVEGDEDGHSSESHYEGRAVDIT 149
Db 61 ENT-----VNQWPGYKLRTVEGDEDGHSSESHYEGRAVDIT 100
Qy 150 TSDRDRSKYGMMLAALAVEAGF 170
Db 101 TSDRDKSKYGMMLAALAVEAGF 121

RESULT 22
SHH_PUNTE STANDARD; PRT; 121 AA.
ID SHH_PUNTE
AC P79550; P79851;
DT 15-JUL-1999 (Rel. 38, Created)
DE Sonic hedgehog protein (SHH) (Fragment(s)).
GN SHH.
OS Carassius auratus (Goldfish).
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassiini.
NCBI TaxID: 7957;
RN [1]
RP SEQUENCE FROM N.A.
TISSUE=Muscle;

RESULT 22
SHH_PUNTE STANDARD; PRT; 121 AA.
ID SHH_PUNTE
AC P79550; P79851;
DT 15-JUL-1999 (Rel. 38, Created)

DT	15-JUL-1999 (Rel. 38; Last sequence update)	61 ENT-----VNINQWPGVLRVTEGWDDEGHFEESSLHYEGRADIT 100
DE	Sonic hedgehog Protein (SHH) (Fragments).	
GN	SHH.	
OS	Puntius tetrazona (Tiger barb).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
OC	Cyprinidae; Puntius.	
OX	NCBI_TaxID=27709;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Muscle;	
RC	LINE=Muscle;	
RC	LINE=917540; PubMed=8917540;	
RA	Zardoya R., Abouheif E., Meyer A.;	
RA	"Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish,"	
RL	Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041 (1996).	
-!	PTM: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES SONITE PATTERNING, DORSO-VENTRAL PATTERNING OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, SIMILARITY. .	
CC	CC FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO) , TO CC REPRESSIONS THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, CC SIMILARITY. .	
CC	CC: SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. Is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity). .	
CC	-!- PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity). .	
CC	-!- SIMILARITY: Belongs to the hedgehog family.	
CC	CC: This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-bib.ch/announce/or send an email to license@isb-bib.ch). .	
CC	CC: DR EMBL: U51352; AAB38577.1; .	
CC	DR EMBL: U51371; AAB38596.1; .	
CC	DR HSSP: Q62226; 1VHF.	
DR	InterPro: IPR00945; Hedgehog/DD_Pept.	
DR	InterPro: IPR00320; HH_Signal.	
DR	InterPro: IPR01657; Peptidase_C46.	
DR	PRINTS: PRO0632; SONICHHOG.	
DR	ProDom: PD00304.5; HH_Signal.1.	
RW	Developmental protein; Autocatalytic.	
FT	NON_TER 1 1	
FT	NON_CONS 63 64	
FT	NON_TER 121 121	
SQ	SEQUENCE 121 AA; 14003 MW; 559334B4057391C1 CRC64;	
Query Match	24.3%; Score 599; DB 1; Length 121;	
Best Local Similarity	80.9%; Pred. No. 1.2e-16; Mismatches 5; Indels 20; Gaps 1;	
Matches	114; Conservative	
DR	30 FGRRHPPKLTPLAYQIPNAEKTLGASRYEGKTSNSRERFELTPNTNPDIKE 89	
DR	1 YGRRHPPKLTPLAYQIPNAEKTLGASRYEGKTRNSRERFELTPNTNPDIKE 60	
Db	90 ENGADRIMTQRCKDKLNALATSVNNQWPGLRVTTEGWDGGHSEESLHYEGRADIT 149	
Qy	90 ENGADRIMTQRCKDKLNALATSVNNQWPGLRVTTEGWDGGHSEESLHYEGRADIT 149	

active species in both local and long-range signaling, whereas the CC 1- SIMILARITY: Belongs to the hedgehog family.

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DR EMBL; U51349; AAB38581.1; -. DR HSSP; Q6226; 1VHH.
DR InterPro; IPR009045; Hedgehog/DD_Pept.
DR InterPro; IPR000320; HH_Signal.
DR InterPro; IPR001657; Peptidase_C46.
DR PRINTS; PRD00632; SONICHHOG.
DR ProDom; PDD003042; HH_Signal_1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1
FT NON_CONS 63 64
FT NON_TER 121 121 AA; 13988 MW; 232334B4057291C5 CRC64;
SQ SEQUENCE 121 AA; .

Query Match 24.2%; Score 597; DB 1; Length 121;
Best Local Similarity 80.9%; Pred. No. 1.7e-36;
Matches 114; Conservative 4; Mismatches 3; Indels 20; Gaps 1;
Db 30 FGKRRPKLTKLPLAYKQFIVNAEKLIGASRYEGKISSNSERFKELTNYNPDIFKDE 89
Db 90 ENTGADRMLTQRCKDKLNALAIISVNQWPGYKLRLTVEGNDGHHSE3ELHYEGRAVDIT 149
Db 61 ENT-----VNQWPGYKLRLTVEGNDGHHFEE3ELHYEGRAVDIT 100
Qy 150 TSDRDRSKYGMHLARLAVEAGF 170
Db 101 TSDRDRSKYGTLSRLAVEAGF 121

RESULT 26
SHH_AMBCH STANDARD; PRT; 121 AA.
TD SHH_AMBCH
AC P79682; P79683;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Sonic hedgehog protein (SHH) (Fragments).
GN SHH.
OS Amblypharyngodon chubabhorae.
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysii; Cypriniformes;
OC Cyprinidae; Amblypharyngodon.
OX NCBI_TaxID:38661;
RN SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;
RA Zardoya R., Abouheif E., Meyer A.;
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish." Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041 (1996).
RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish." Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041 (1996).
CC 1- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE NOTCHOID THAT INDUCES SONIC PATTERNING, DORSVENTRAL PATTERNING OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS FLOOR PLATE INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SMO (BY PTC) REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SHH. (1)

SIMILARITY. LOCATION: The C-terminal peptide diffuses from the cell surface, is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).
SIMILARITY: Belongs to the hedgehog family.
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SIMILARITY: Belongs to the hedgehog family.
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SIMILARITY: Belongs to the hedgehog family.
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DR EMBL; U51341; AAB38584.1; -. DR EMBL; U51360; AAB38582.1; -. DR HSSP; Q6226; 1VHH.
DR InterPro; IPR000045; Hedgehog/DD_Pept.
DR InterPro; IPR00320; HH_Signal.
DR InterPro; IPR01657; Peptidase_C46.
DR PRINTS; PRD00632; SONICHHOG.
DR ProDom; PDD003042; HH_Signal_1.
KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
FT NON_TER 1
FT NON_CONS 63 64
FT NON_TER 121 121 AA; 14033 MW; 0C9034B41C709B4E CRC64;
SQ SEQUENCE 121 AA; .
Query Match 24.1%; Score 595; DB 1; Length 121;
Best Local Similarity 80.9%; Pred. No. 2.4e-36;
Matches 114; Conservative 4; Mismatches 3; Indels 20; Gaps 1;
Qy 30 FGKRRPKLTKLPLAYKQFIPNVAEKLIGASRYEGKISSNSERFKELTNYNPDIFKDE 89
Db 1 YDKRRPKLTKLPLAYKQFIPNVAEKLIGASRYEGKISSNSERFKELTNYNPDIFKDE 60
Qy 90 ENTGADRMLTQRCKDKLNALAIISVNQWPGYKLRLTVEGNDGHHSE3ELHYEGRAVDIT 149
Db 61 ENT-----VNQWPGYKLRLTVEGNDGHHFEE3ELHYEGRAVDIT 100
Qy 150 TSDRDRSKYGMHLARLAVEAGF 170
Db 101 TSDRDRSKYGTLSRLAVEAGF 121
RESULT 27
SHH_DANAA STANDARD; PRT; 121 AA.
ID SHH_DANAA AC 013235; O13191; O13236;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Sonic hedgehog protein (SHH) (Fragments).
GN SHH.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eltteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysii; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID:46783;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=97075114; PubMed=8917540;

RA Zardoya R., Abouheif E., Meyer A.;
 RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
 closely related to the zebrafish.";
 RT Proc. Natl. Acad. Sci. U.S.A. 93:13016-13041 (1996).
 CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
 PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE
 NOTOCHORD THAT INDUCES SOMITE PATTERNING. DORSO-VENTRAL PATTERNING
 OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS
 FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC)
 RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
 ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH,
 PTC REPRESSIONS THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
 SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
 CC cell, while the N-terminal peptide remains associated with the
 CC cell surface. It is also secreted in either cleaved or uncleaved form
 CC to mediate signaling to other cells (By similarity).
 CC -!- PTM: The C-terminal domain displays an autoproteolysis activity
 CC and a cholesterol transferase activity. Both activities result in
 CC the cleavage of the full-length protein and covalent attachment of
 CC a cholesterol moiety to the C-terminal of the newly generated N-
 CC terminal fragment (N-product). This covalent modification appears
 CC to play an essential role in restricting the spatial distribution of
 CC the protein activity to the cell surface. The N-product is the
 CC active species in both local and long-range signaling, whereas the
 CC C-product has no signaling activity (By similarity).
 CC -!- SIMILARITY: Belongs to the hedgehog family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 DR EMBL; U51347; AAB30567.1; -;
 DR EMBL; U51366; AAB30584.1; -;
 DR HSSP; Q6226; 1VHH.
 DR InterPro; IPR009045; Hedgehog/DD_pept.
 DR InterPro; IPR000320; HH signal.
 DR InterPro; IPR001657; Peptidase_C46.
 DR PRINTS; PR00632; SONICHHOG.
 DR ProDom; PD003042; HH signal; 1.
 KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
 FT NON_TER 1
 FT NON_CONS 63 64
 FT NON_TER 121 121 AA; 14012 MW; A58A2DB40573825C CRC64;
 SQ SEQUENCE 121 AA; -
 Query Match 24.1%; Score 594; DB 1; Length 121;
 Best Local Similarity 80.1%; Pred. No. 2.8e-36;
 Matches 113; Conservative 5; Mismatches 3; Indels 20; Gaps 1;
 Qy 30 FGKRRHPKLTPLAYQFIPVAEKLIGASGRYEGKISNSERFELTPNYNPDLIFDE 89
 Db 1 YGRRRHPKLTPLAYQFIPVAEKLIGASGRYEGKISNSERFELTPNYNPDLIFDE 60
 Qy 90 ENTGADRLLMTQRCKDNLNALISVNQWPGKLRTEGDEDGHSEELHYGRAVDT 149
 Db 61 ENT-----VNWHWPGVKLRTVEGDEDGHFEELHYGRAVDT 100
 Qy 150 TSDRDKSKYGNMLARAVEAGF 170
 Db 101 TSDRDKSKYGNMLARAVEAGF 121

RESULT 28
 SHH_DANAE STANDARD 1013190; O13199; PRT; 121 AA.
 ID SHH_DANAE STANDARD 1013190; O13199; PRT; 121 AA.
 AC O13199; 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Sonic hedgehog protein (SHH) (Fragments).
 GN SHH.
 OS Danio aequipinnatus (Giant danio) (Brachydanio aequipinnatus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=46778;
 RN [1]
 RP SEQUENCE FROM N.A.
 TISSUE=MUSCLE;
 RX MEDLINE=97075114; PubMed=8917540;
 RX MEDLINE=9311036; 13041(1996).
 RA Zardoya R., Abouheif E., Meyer A.;
 RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
 closely related to the zebrafish";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041(1996).
 CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
 PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE
 CC NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING
 CC OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS
 CC FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC)
 CC RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO). TO
 CC ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH,
 CC PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
 CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
 CC cell, while the N-terminal peptide remains associated with the
 CC cell surface. It is also secreted in either cleaved or uncleaved form
 CC to mediate signaling to other cells (By similarity).
 CC -!- PTM: The C-terminal domain displays an autoproteolysis activity. Both activities result in
 CC and a cholesterol transferase activity. The cleavage of the full-length protein and covalent attachment of
 CC a cholesterol moiety to the C-terminal of the newly generated N-
 CC terminal fragment (N-product). This covalent modification appears
 CC to play an essential role in restricting the spatial distribution of
 CC the protein activity to the cell surface. The N-product is the
 CC active species in both local and long-range signaling, whereas the
 CC C-product has no signaling activity (By similarity).
 CC -!- SIMILARITY: Belongs to the hedgehog family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U51344; AAB30566.1; -;
 DR EMBL; U51363; AAB30585.1; -;
 DR HSSP; Q6226; 1VHH.
 DR InterPro; IPR000320; HH signal.
 DR InterPro; IPR001657; Peptidase_C46.
 DR PRINTS; PR00632; SONICHHOG.
 DR ProDom; PD003042; HH signal; 1.
 KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
 FT NON_TER 1
 FT NON_CONS 63 64
 FT NON_TER 121 121 AA; 14012 MW; A58A2DB40573825C CRC64;
 SQ SEQUENCE 121 AA; -
 Query Match 24.1%; Score 594; DB 1; Length 121;
 Best Local Similarity 80.1%; Pred. No. 2.8e-36;
 Matches 113; Conservative 5; Mismatches 3; Indels 20; Gaps 1;
 Qy 30 FGKRRHPKLTPLAYQFIPVAEKLIGASGRYEGKISNSERFELTPNYNPDLIFDE 89
 Db 1 YGRRRHPKLTPLAYQFIPVAEKLIGASGRYEGKISNSERFELTPNYNPDLIFDE 60
 Qy 90 ENTGADRLLMTQRCKDNLNALISVNQWPGKLRTEGDEDGHSEELHYGRAVDT 149
 Db 61 ENT-----VNWHWPGVKLRTVEGDEDGHFEELHYGRAVDT 100
 Qy 150 TSDRDKSKYGNMLARAVEAGF 170
 Db 101 TSDRDKSKYGNMLARAVEAGF 121

Query Match 24.1%; Score 594; DB 1; Length 121;
 Best Local Similarity 80.1%; Pred. No. 2.8e-36;
 Matches 113; Conservative 5; Mismatches 3; Indels 20; Gaps 1;
 Qy 30 FGKRRHPKLTPLAYQFIPVAEKLIGASGRYEGKISNSERFELTPNYNPDLIFDE 89
 Db 1 YGRRRHPKLTPLAYQFIPVAEKLIGASGRYEGKISNSERFELTPNYNPDLIFDE 60
 Qy 90 ENTGADRLLMTQRCKDNLNALISVNQWPGKLRTEGDEDGHSEELHYGRAVDT 149
 Db 61 ENT-----VNWHWPGVKLRTVEGDEDGHFEELHYGRAVDT 100

DR EMBL; U51357; AAB38588.1; .
 DR HSSP; Q62226; IVHH.
 DR InterPro; IPR00045; Hedgehog/DD_pept.
 DR InterPro; IPR00320; HH_signal.
 DR PRINTS; PRO0632; Peptidase_C46.
 DR PRINTS; PRO0632; SONIC_HHOG.
 DR ProDom; PDD003042; HH signal; 1.
 DR ProDom; PDD003042; HH signal; 1.
 DR Developmental_protein; Autocatalytic_cleavage; Hydrolase; Protease.
 KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
 FT NON_TER 1 1
 FT NON_TER 63 64
 FT NON_TER 121 AA; 14012 MW; A58A2DE40573825C CRC64;
 SQ SEQUENCE 121 AA; 14012 MW; A58A2DE40573825C CRC64;
 Query Match 24.1%; Score 594; DB 1; Length 121;
 Best Local Similarity 80.1%; Pred. No. 2.8e-36;
 Matches 113; Conservative 5; Mismatches 3; Indels 20; Gaps 1;
 Qy 30 FGKRRHPPKLTPLAYKQFIPVNAEKTIGASGRYEGKISRSNTERFKELTPNYPNPDIIFKDE 69
 Db 1 YGRRRHPKLTPLAYKQFIPVNAEKTIGASGRYEGKISRSNTERFKELTPNYPNPDIIFKDE 60
 Qy 90 ENTGADRLLMTQRCKDKNLALIAISWNHQPGVLRVTEGDDGHSEESTHYEGRADIT 149
 Db 61 ENT-----VMNHRPGVLRVTEGDDGHFFEEESTHYEGRADIT 100
 Qy 150 TSDRDRSKYGMMLARLAVEGF 170
 Db 101 TSDRDRSKYGMMLARLAVEGF 121
 Qy 150 TSDRDRSKYGMMLARLAVEGF 170
 Db 101 TSDRDRSKYGMMLARLAVEGF 121
 RESULT 32
 SHH_DANKE STANDARD; PRT; 121 AA.
 AC P79709; P79710;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Sonic hedgehog protein (SHH) (Fragments).
 OS Danio rerri (Kerr's danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=38750;
 RP SEQUENCE FROM N.A.
 RC TISSUE=muscle;
 RX MEDLINE=97075114; PubMed=8917540;
 RA Zardoya R., Abouheif E., Meyer A.;
 RT "Evolutionary analyses of sonic hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041 (1996).
 CC -!- FUNCTION: INTRACELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL, PRODUCED BY THE NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES, DISPLAYS FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSIONS THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (By SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell surface. Is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).
 CC -!- PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the

CC C-product has no signaling activity (By similarity).
 CC -!- SIMILARITY: Belongs to the hedgehog family.
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 CC CC EMBL; U51340; AAB38571.1; .
 DR DR HSSP; Q62226; IVHH.
 DR DR InterPro; IPR009045; Hedgehog/DD_pept.
 DR DR InterPro; IPR00320; HH_signal.
 DR DR InterPro; IPR01657; Peptidase_C46.
 PRINTER; PR00532; SONICHHOG.
 DR DR Problem: PD003042; HH signal; 1.
 KW KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
 FT FT NON_TER 1
 FT FT NON_TER 63 64
 FT FT NON_TER 121 AA; 14012 MW; A58A2DE40573825C CRC64;
 SQ SQ Query Match 24.1%; Score 594; DB 1; Length 121;
 Best Local Similarity 80.1%; Pred. No. 2.8e-36;
 Matches 113; Conservative 5; Mismatches 5; Indels 20; Gaps 1;
 Qy 30 FGKRRHPPKLTPLAYKQFIPVNAEKTIGASGRYEGKISRSNTERFKELTPNYPNPDIIFKDE 69
 Db 1 YGRRRHPKLTPLAYKQFIPVNAEKTIGASGRYEGKISRSNTERFKELTPNYPNPDIIFKDE 60
 Qy 90 ENTGADRLLMTQRCKDKNLALIAISWNHQPGVLRVTEGDDGHSEESTHYEGRADIT 149
 Db 61 ENT-----VMNHRPGVLRVTEGDDGHFFEEESTHYEGRADIT 100
 Qy 150 TSDRDRSKYGMMLARLAVEGF 170
 Db 101 TSDRDRSKYGMMLARLAVEGF 121
 RESULT 32
 SHH_DANPU STANDARD; PRT; 121 AA.
 AC P79709; P79710;
 AC P79717; P79718; STANDARD; PRT; 121 AA.
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE SHH.
 DE SHH.
 DE SHH.
 DE SHH.
 OS Danio rerri (Kerr's danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=38751;
 RN RN SEQUENCE FROM N.A.
 RC TISSUE=muscle; PMID=8917540;
 RA Zardoya R., Abouheif E., Meyer A.;
 RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041 (1996).
 CC -!- FUNCTION: INTRACELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL, PRODUCED BY THE NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES, DISPLAYS FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSIONS THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (By SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: The C-terminal peptide remains associated with the cell surface. Is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).
 CC -!- PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the

-> SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. It is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).

-!- PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity).

-> SIMILARITY: Belongs to the hedgehog family.

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ENB1; U51342; AAB38573.1 ; - .
 ENB2; U51361; AAB38591.1 ; - .
 HSSP1; Q62226; 1VH.
 InterPro; IPR009045; Hedgehog/DD_pept.
 InterPro; IPR00320; HH_signal.
 InterPro; IPR001657; Peptidase_C46.
 PRINTS; PR000632; SONICHHOG.
 Prodrom; PDD03042; HH_sig39a1.
 Developmental_Protein; Autocatalytic_cleavage; Hydrolase; Protease.

RT	"Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish,"
RL	Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041 (1996).
CC	- - FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES SOMITE PATTERNING, DORSO-VENTRAL PATTERNING OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SMO, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY SIMILARITY).
CC	- - SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. Is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).
CC	- - PTM: The C-terminal domain displays an autoproteolytic activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity).
CC	- - SIMILARITY: Belongs to the hedgehog family.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
CC	EMBL: US1350; AAB38569_1; - .
CC	EMBL: US1369; AAB38587_1; - .
DR	HSSP: Q62226; 1VHH.
DR	InterPro: IPR009045; Hedgehog/DD_pept.
DR	InterPro: IPR00320; HH_signal.
DR	InterPro: IPR001657; Peptidase_C46.
DR	PRINTS: PR00632; SONICHHOG.
DR	PRODOM: PD003042; HH_signal; 1.
RW	Developmental Protein; Autocatalytic cleavage; Hydrolase; Protease.
FT	NON-TER 1 1
FT	NON-CONS 63 64
FT	NON-TER 121 121
SEQUENCE	121 AA: 14012 MN; A58A2D2E40573825C CRC64;
Query Match	24.1%; Score 594; DB 1; Length 121;
Best Local Similarity	80.1%; Pred. No. 2.88-36;
Matches	113; Conservative 5; Mismatches 3; Indels 20; Gaps 1;
Oy	30 FGKRRPKKLTPLAKQFVNVAKTIGSAGRYEGKISRNNSERPEKLTPNYNNPDIIFPKDE 89
Db	1 YGRRPKKLTPLAKQFVNVAKTIGSAGRYEGKISRNNSERPEKLTPNYNNPDIIFPKDE 60
Qy	90 ENTGAADLMTORCKDNLNAISWNQWPKVKLRVTGMDDEGHSHSESSLHYGRAVDIT 149
Db	61 ENT-----VNHWPKVKLRVTGMDDEGHSHSESSLHYGRAVDIT 100
Qy	150 TSDRDRSKYKGMLARLAVEAGF 170
Db	101 TSDRDRSKYKGMLARLAVEAGF 121

CC	C-product has no signaling activity (By similarity).	CC	to mediate signaling to other cells (By similarity)
CC	-1- SIMILARITY: Belongs to the hedgehog family.	CC	-1- PTM: The C-terminal domain displays an autoprotolytic activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity).
CC	EMBL; US1388; AA38613.1; -.	CC	-1- SIMILARITY: Belongs to the hedgehog family.
DR	AFO71336; AAD1531.1; -.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
DR	US1388; AA38613.1; -.	CC	-1- SIMILARITY: Belongs to the hedgehog family.
DR	Q62226; 1VHH.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
DR	ZFPN; ZB-GENE-990714-5; dhh.	CC	-1- SIMILARITY: Belongs to the hedgehog family.
DR	InterPro; IPR009445; Hedgehog/DD_pept.	CC	DR InterPro; IPR00320; HH signal.
DR	InterPro; IPR000340; HH signal.	CC	DR InterPro; IPR0165; Peptidase_C46.
DR	InterPro; IPR001677; Peptidase_C46.	CC	PFam; PF01085; HH signal; 1.
DR	PFam; PF01085; HH signal; 1.	CC	PRINTS; PR00632; SONICHHOG.
DR	PRINTS; PR00632; SONICHHOG.	CC	PRODOM; PD003042; HH signal; 1.
DR	Developmental Protein; Autocatalytic cleavage; Hydrolase; Protease; KW Developmental Protein; Autocatalytic cleavage; Hydrolase; Protease.	CC	KW Developmental Protein; Autocatalytic cleavage; Hydrolase; Protease.
FT	NON_TER 1 1.	CC	FT NON_TER 1 1.
FT	CONFFLICT 17 17 Q -> M (IN REF. 2).	CC	FT CONFFLICT 17 17 Q -> M (IN REF. 2).
FT	CONFFLICT 22 22 R -> K (IN REF. 2).	CC	FT CONFFLICT 22 22 R -> K (IN REF. 2).
FT	CONFFLICT 28 28 A -> G (IN REF. 2).	CC	FT CONFFLICT 28 28 A -> G (IN REF. 2).
FT	CONFFLICT 34 38 HHPG -> NHED (IN REF. 2).	CC	FT CONFFLICT 34 38 HHPG -> NHED (IN REF. 2).
FT	CONFFLICT 56 57 TK -> R (IN REF. 2).	CC	FT CONFFLICT 56 57 TK -> R (IN REF. 2).
FT	CONFFLICT 61 61 L -> M (IN REF. 2).	CC	FT CONFFLICT 61 61 L -> M (IN REF. 2).
FT	CONFFLICT 64 64 Q -> R (IN REF. 2).	CC	FT CONFFLICT 64 64 Q -> R (IN REF. 2).
FT	NON_TER 88 88 MW: E3D34AA0036677FA6 CRC64;	CC	FT NON_TER 88 88 MW: E3D34AA0036677FA6 CRC64;
SQ	SEQUENCE 88 AA; 10069 MW;	CC	SQ SEQUENCE 88 AA; 10069 MW;
Query Match	16.0%; Score 336; DB 1; Length 88;	CC	Query Match 11.9%; Score 293; DB 1; Length 58;
Best Local Similarity	81.8%; Pred. No. 3.6e-22;	CC	Best Local Similarity 93.1%; Pred. No. 5.3e-15;
Matches	6; Mismatches 10; Indels 0; Gaps 0;	CC	Matches 54; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy	100 QRCRDKLNIAIISMVNQWGVKLRVTGMDDEGHHSSESSLHVEGRADTTSDRDRSKYKG 159	CC	Qy 113 VMNONQFQVKLRLRTGMDDEGHHSSESSLHVEGRADTTSDRDRSKYKG 170
Db	1 ORCDDCLYKIAIAYMNQWGVRLTEAMDEDGHPPGSLLHVEGRADTTSDRDTKYG 60	CC	Db 1 VVNLLWGPVRLRTGMDDEGHHSSESSLHVEGRADTTSDRDRSKYKG 58
RESULT 39		CC	RESULT 39
IHH_DANAT	ID IHH_DANAT STANDARD; PRT; 58 AA.	CC	IHH_DANAT ID IHH_DANAT STANDARD; PRT; 58 AA.
AC	O13244; O13200; O13200;	CC	AC O13244; O13200; O13200;
DT	15-JUL-1999 (Rel. 38. Created)	CC	DT 15-JUL-1999 (Rel. 38. Created)
DT	15-JUL-1999 (Rel. 38. Last sequence update)	CC	DT 15-JUL-1999 (Rel. 38. Last sequence update)
DT	15-JUL-1999 (Rel. 38. Last annotation update)	CC	DT 15-JUL-1999 (Rel. 38. Last annotation update)
DB	Indian hedgehog protein (IHH) (Fragment).	CC	DB Indian hedgehog protein (IHH) (Fragment).
GN	Danio ff. tweediei.	CC	GN Danio ff. tweediei.
OS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi; OC Actinopterygii; Neopterygii; Teleostei; Cypriniformes; OC Cyprinidae; Danio.	CC	OS Buccaria; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi; OC Actinopterygii; Neopterygii; Teleostei; Cypriniformes; OC Cyprinidae; Danio.
INH	[1] TAXID:46785;	CC	INH [1] TAXID:46785;
RN	SEQUENCE FROM N.A.	CC	RN SEQUENCE FROM N.A.
RC	SEQUENCE FROM N.A.	CC	RC SEQUENCE FROM N.A.
RX	TISSUE=Muscle;	CC	RX TISSUE=Muscle;
RA	"Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish."	CC	RA "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish."
RL	Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041 (1996).	CC	RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041 (1996).
RL	PATTERNING events during development (By similarity).	CC	RL PATTERNING events during development (By similarity).
CC	CC -1- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell surface. Is also secreted in either cleaved or uncleaved form	CC	CC -1- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell surface. Is also secreted in either cleaved or uncleaved form
CC	CC -1- SUBCELLULAR LOCATION: The C-terminal peptide remains associated with the cell surface. Is also secreted in either cleaved or uncleaved form	CC	CC -1- SUBCELLULAR LOCATION: The C-terminal domain displays an autoproteolytic activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of

CC a cholesterol moiety to the C-terminal of the newly generated N-
 CC terminal fragment (N-product). This covalent modification appears
 CC to play an essential role in restricting the spatial distribution
 CC of the protein activity to the cell surface. The N-product is the
 CC C-terminal fragment in both local and long-range signaling, whereas the
 CC C-product has no signaling activity (By similarity).
 -!- SIMILARITY: Belongs to the hedgehog family.

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 CC or send an email to license@isb-sib.ch).
 CC

CC active species in both local and long-range signaling, whereas the
 CC C-product has no signaling activity (By similarity).
 -!- SIMILARITY: Belongs to the hedgehog family.

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 CC or send an email to license@isb-sib.ch).
 CC

CC active species in both local and long-range signaling, whereas the
 CC C-product has no signaling activity (By similarity).
 -!- SIMILARITY: Belongs to the hedgehog family.

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 CC or send an email to license@isb-sib.ch).
 CC

DR EMBL; U51376; AAB38604.1; -.
 DR HSSP; Q62226; 1VHH.
 DR InterPro; IPR003045; Hedgehog/DD_pept.
 DR InterPro; IPR003045; HH_Signal.
 DR InterPro; IPR00320; HH_Signal.
 DR Pfam; PF01085; HH_Signal; 1.
 DR PRINTS; PRO0632; SONICHHOG.
 DR Prodrom; PD00304; HH_Signal; 1.
 DR Developmental_protein; Autocatalytic_cleavage; Hydrolase; Protease.
 DR FT PFM; PF01085; HH_Signal; 1.
 DR FT PRINTS; PRO0632; SONICHHOG.
 DR FT ProDom; P0003042; HH_Signal; 1.
 DR KW Developmental_protein; Autocatalytic_cleavage; Hydrolase; Protease.
 DR FT NON_TER 1 58 AA; 6658 MW; 2CC8FP53CEC04D809 CRC64;
 DR SQ SEQUENCE 58 AA; 6658 MW; 2CC8FP53CEC04D809 CRC64;
 DR YQ 113 VNNQWPGVKLRVTEGNGDEGHSEESLHYEGRADITTSDBRSKYGMLARLAVEAGF 170
 DR RESULT 41
 DR ID IHHDANFU
 DR AC P19719;
 DR DT 15-JUL-1999 (Rel. 38, Created)
 DR DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DR DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DR DB Indian hedgehog protein (IHHD) (Fragment).
 DR GN Danio pulcher.
 DR OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Buteleostomi; Osteolesteti; Cypriniformes; Cyprinidae; Danio.
 DR NCBI_TaxID=8751;
 DR RN [1]
 DR RP SEQUENCE FROM N.A.
 DR RC TISSUE=Muscle;
 DR RA Zardoya R., Abouheif E., Meyer A.;
 DR RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish.";
 DR RL Natl. Acad. Sci. U.S.A. 93:13036-13041 (1996).
 DR RN MEDLINE=97075114; PubMed=8917540;
 DR RX PROC. NATL. ACAD. SCI. U.S.A. 93:13036-13041 (1996).
 DR RA Zardoya R., Abouheif E., Meyer A.;
 DR RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish.";
 DR CC FUNCTION: Intercellular signal essential for a variety of patterning events during development (By similarity).
 DR CC SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the C-terminal peptide to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the C-product has no signaling activity (By similarity).
 DR CC -!- SIMILARITY: Belongs to the hedgehog family.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

RESULT	42			
IHH_DEVDE		PRT;	58 AA.	
O13243; O13205;	STANDARD;			
C				
T	15-JUL-1993 (Rel. 38, Created)			
T	15-JUL-1993 (Rel. 38, Last sequence update)			
T	15-JUL-1993 (Rel. 38, Last annotation update)			
N	Indian hedgehog protein (IHH) (Fragment).			
S	Devario devario (Danio devario).			
AC	P79832; (Rel. 38, Created)	DT	15-JUL-1993 (Rel. 38, Last sequence update)	
		DT	15-JUL-1993 (Rel. 38, Last annotation update)	
		DB	Indian hedgehog protein (IHH) (Fragment).	
		GN	IHH.	
		OS	Puntius tetrazona (Tiger barb).	
		OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
		OC	Cyprinidae; Puntius.	
		OX	NCBI_TaxID:27709;	
		PN		
		P11		

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DR InterPro; IPR001657; Peptidase_C46.
 DR Pfam; PF01085; HH signal/1.
 DR PRINTS; PR00632; SONICHHOG.
 DR Prodrom; PD003042; HH signal/1.
 DR Developmental Protein; Autocatalytic cleavage; Hydrolase; Protease.
 DR KW FT
 DR NON_TER 1
 DR FT
 DR NON_TER 58
 DR SEQUNCE 58 AA; 6658 MW; 2CC8F53CEC04DB809 CRC64;
 DR Developmental Protein; Autocatalytic cleavage; Hydrolase; Protease.
 FT NON_TER 1
 FT NON_TER 58 Score 293; DB 1; Length 58;
 SQ SEQUENCE 58 AA; 6658 MW; 2CC8F53CEC04DB809 CRC64;
 Qy 113 VMNONPGVLRVTEGWDDEGHSEESLHVEGRADITTSDRDKYMLARLAVEAGF 170
 Best Local Similarity 93.1%; Pred. No. 5.e-15;
 Matches 54; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Db 1 VMNLWPGVLRVTEGWDDEGHSEESLHVEGRADITTSDRDKYMLARLAVEAGF 58

RESULT 45
 SHH_PSEPR STANDARD PRT; 58 AA.
 ID SHH_PSEPR
 AC P79859;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 OS Pseudorasp. Parva
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 GN IHH
 RN [1] NCBI_TaxID:51549;
 RN RP
 RN SEQUENCE FROM N.A.
 RN TISSUE=Muscle;
 RN MEDLINE=9707514; PubMed=8917540;
 RN RA Zarzoya R., Abouheif E., Meyer A.;
 RN RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
 closely related to the zebrafish.";
 RN RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041 (1996).
 RN CC FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
 PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE
 NOTOCHORD THAT INDUCES SONITE PATTERNING, DORSO VENTRAL PATTERNING
 OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS
 FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC)
 RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
 ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SMO
 PTC REPRESSIONS THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
 SIMILARITY).
 RN CC -I- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
 cell, while the N-terminal remains associated with the
 cell surface. Is also secreted in either cleaved or uncleaved form
 to mediate signaling to other cells (By similarity).
 RN CC -I- PTM: The C-terminal domain displays an autoproteolysis activity
 and a cholesterol transferase activity. Both activities result in
 the cleavage of the full-length protein and covalent attachment of
 a cholesterol moiety to the C-terminal of the newly generated N-
 terminal fragment (N-product). This covalent modification appears
 to play an essential role in restricting the spatial distribution
 of the protein activity to the cell surface. The N-product is the
 active species in both local and long-range signaling, whereas the
 C-product has no signaling activity (By similarity).
 RN CC -I- SIMILARITY: Belongs to the hedgehog family.
 RN CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@isb-sib.ch).
 RN CC EMBL; U051389; AAB38609.1; -.
 DR HSSP; Q62226; 1WHA
 DR InterPro; IPR000345; Hedgehog/DD_pept.
 DR InterPro; IPR000320; HH_signal.
 DR EMBL; U51358; AAB38594.1; -.

DR DR InterPro; IPR001657; Peptidase_C46.
 DR DR Pfam; PF01085; HH signal/1.
 DR DR PRINTS; PR00632; SONICHHOG.
 DR DR Prodrom; PD003042; HH signal/1.
 DR DR Developmental Protein; Autocatalytic cleavage; Hydrolase; Protease.
 DR DR KW FT
 DR DR NON_TER 1
 DR DR FT
 DR DR NON_TER 58
 DR DR SEQUNCE 58 AA; 6658 MW; 2CC8F53CEC04DB809 CRC64;
 DR DR Query Match 11.9%; Score 293; DB 1; Length 58;
 DR DR Best Local Similarity 93.1%; Pred. No. 5.e-15;
 DR DR Matches 54; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 113 VMNONPGVLRVTEGWDDEGHSEESLHVEGRADITTSDRDKYMLARLAVEAGF 170
 Db 1 VMNLWPGVLRVTEGWDDEGHSEESLHVEGRADITTSDRDKYMLARLAVEAGF 58

RESULT 44
 IHH_RASEL STANDARD PRT; 58 AA.
 ID IHH_RASEL
 AC P79860;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Indian hedgehog protein (IHH) (Fragment).
 OS Rasbora elegans (Elegant rasbora).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cypriidae; Rasbora.
 RN [1] NCBI_TaxID:27712;
 RN RP
 RN SEQUENCE FROM N.A.
 RN TISSUE=Muscle;
 RN MEDLINE=9707514; PubMed=8917540;
 RN RA Zarzoya R., Abouheif E., Meyer A.;
 RN RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
 closely related to the zebrafish.";
 RN RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041 (1996).
 RN CC FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
 PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE
 NOTOCHORD THAT INDUCES SONITE PATTERNING, DORSO VENTRAL PATTERNING
 OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS
 FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC)
 RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
 ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SMO
 PTC REPRESSIONS THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
 SIMILARITY).
 RN CC -I- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
 cell, while the N-terminal remains associated with the
 cell surface. Is also secreted in either cleaved or uncleaved form
 to mediate signaling to other cells (By similarity).
 RN CC -I- PTM: The C-terminal domain displays an autoproteolysis activity
 and a cholesterol transferase activity. Both activities result in
 the cleavage of the full-length protein and covalent attachment of
 a cholesterol moiety to the C-terminal of the newly generated N-
 terminal fragment (N-product). This covalent modification appears
 to play an essential role in restricting the spatial distribution
 of the protein activity to the cell surface. The N-product is the
 active species in both local and long-range signaling, whereas the
 C-product has no signaling activity (By similarity).
 RN CC -I- SIMILARITY: Belongs to the hedgehog family.
 RN CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@isb-sib.ch).
 RN CC EMBL; U051389; AAB38609.1; -.
 DR HSSP; Q62226; 1WHA
 DR InterPro; IPR000345; Hedgehog/DD_pept.
 DR InterPro; IPR000320; HH_signal.

Qy 113 VNNQWPGYKLRLVTEGMDDEGHSEESLHYEGRADITTSDRSKYGMARLAVEAGF 170
 Db 1 VNNLWPGYKLRLVTEGMDDEGHSEESLHYEGRADITTSDRDKYAMARLAVEAGF 58

Search completed: March 29, 2004, 18:32:32
 Job time : 21 secs

RESULT 50
 IHH_RASPA STANDARD PRT; 58 AA.
 AC P75871;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Indian hedgehog protein (IHH) (Fragment).
 GN IHH.
 OS Rasbora paviei (Sidestripe rasbora).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Rasbora.
 NCBI TaxID=38659;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE;
 RX MEDLINE=97075114; PubMed=8917540;
 RA Zardoya R., Abouheif E., Meyer A.;
 RT "phylogenetic analyses of hedgehog and Hoxd-10 genes in fish species
 closely related to the zebrafish";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:13036-13041 (1996).
 CC -!- FUNCTION: Intercellular signal essential for a variety of
 patterning events during development (By similarity).
 CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
 cell, while the N-terminal peptide remains associated with the
 cell surface. Is also secreted in either cleaved or uncleaved form
 to mediate signalling to other cells (By similarity).
 CC -!- PTM: The C-terminal domain displays an autoproteolysis activity
 and a cholesterol transferase activity. Both activities result in
 the cleavage of the full-length protein and covalent attachment of
 a cholesterol moiety to the C-terminal of the newly generated N-
 terminal fragment (N-product). This covalent modification appears
 to play an essential role in restricting the spatial distribution
 of the protein activity to the cell surface. The N-product is the
 active species in both local and long-range signalling, whereas the
 C-product has no signalling activity (By similarity).
 CC -!- SIMILARITY: Belongs to the hedgehog family.

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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U51378; AAB3611.1; -.
 DR HSSP; Q6226; 1VHH.
 DR InterPro; IPR009045; Hedgehog/DD_pept.
 DR InterPro; IPR000320; HH signal.
 DR InterPro; IPR001657; Peptidase_C46.
 DR Pfam; PF01085; HH_signal; 1.
 DR PRINTS; PRO0632; SONICHHOG.
 DR Probdom; PDO03042; HH_signal; 1.
 KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease.
 FT 1
 NON TER 58 58
 SQ SEQUENCE 58 AA; 6688 MW; A43BF53CEC1A1735 CRC64;

Query Match 11.6%; Score 287; DB 1; Length 58;
 Best Local Similarity 91.4%; Pred. No. 1 56-14;
 Matches 53; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Gaps 0;
 Qy 113 VMNQWPGYKLRLVTEGMDDEGHSEESLHYEGRADITTSDRSKYGMARLAVEAGF 170
 Db 1 VNNLWPGYKLRLVTEGMDDEGHSEESLHYEGRADITTSDRDKYAMARLAVEAGF 58

Result No.	Score	Query	Match	Length	DB ID	Description
<hr/>						
1	2062	83.5	437	11	Q8CT765	Q8CT765 mus musculus
2	1545	62.6	43.9	5	Q57404	Q57404 pleurodiles
3	1466	59.5	41.3	13	Q8AXT0	Q8AXT0 fugu rubripinnis
4	1454	58.9	41.4	13	Q9W7Q9	Q9W7Q9 paralichthys
5	1398	53.0	40.6	13	Q57567	Q57567 nocophthalmus
6	1262	51.1	44.9	11	Q8OXT9	Q8OXT9 mus musculus
7	1094	44.3	41.5	5	Q9U526	Q9U526 branchiostoma
8	1084	43.9	41.5	5	Q17499	Q17499 branchiostoma
9	1049	42.5	44.2	13	Q73803	Q73803 fugu rubripinnis
10	1041	42.2	44.7	5	Q9GBA8	Q9GBA8 gryllus bimaculatus
11	1010	40.9	38.1	5	Q72264	Q72264 auscorpius
12	9195	40.3	42.1	5	Q72263	Q72263 artemia salina
13	938	38.0	41.6	5	Q8MNG6	Q8MNG6 patella vulgaris
14	916	37.1	41.0	5	Q61676	Q61676 lytechinus variolosus
15	850	34.4	16.1	11	Q9R119	Q9R119 rattus norvegicus
16	821	33.3	40.2	5	Q8MY56	Q8MY56 ciona intestinalis

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
<hr/>						
1	2062	83.5	437	11	Q8CT765	Q8CT765 mus musculus
2	1545	62.6	43.9	5	Q57404	Q57404 pleurodiles
3	1466	59.5	41.3	13	Q8AXT0	Q8AXT0 fugu rubripinnis
4	1454	58.9	41.4	13	Q9W7Q9	Q9W7Q9 paralichthys
5	1398	53.0	40.6	13	Q57567	Q57567 nocophthalmus
6	1262	51.1	44.9	11	Q8OXT9	Q8OXT9 mus musculus
7	1094	44.3	41.5	5	Q9U526	Q9U526 branchiostoma
8	1084	43.9	41.5	5	Q17499	Q17499 branchiostoma
9	1049	42.5	44.2	13	Q73803	Q73803 fugu rubripinnis
10	1041	42.2	44.7	5	Q9GBA8	Q9GBA8 gryllus bimaculatus
11	1010	40.9	38.1	5	Q72264	Q72264 auscorpius
12	9195	40.3	42.1	5	Q72263	Q72263 artemia salina
13	938	38.0	41.6	5	Q8MNG6	Q8MNG6 patella vulgaris
14	916	37.1	41.0	5	Q61676	Q61676 lytechinus variolosus
15	850	34.4	16.1	11	Q9R119	Q9R119 rattus norvegicus
16	821	33.3	40.2	5	Q8MY56	Q8MY56 ciona intestinalis

90	109	4.4	Q8TAT1	Q8tati1 homo sapien	DE Sonic hedgehog homolog.
91	109	4.4	Q8RBL0	Q8rbl0 brdyrinizob	GN SHH OR 933003001RIR.
92	109	4.4	Q8RBL5	Q8rbl5 drosophila	OS Mus musculus (Mouse).
93	108.5	4.4	Q8FB7	Q8fb7 oryza sativ	OC Bokuyoya; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
94	108.5	4.4	Q8FB7	Q8fb7 oryza sativ	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
95	108	4.4	Q7KF8	Q7kf8 oryza sativ	OC [1] _ TaxID=10090;
96	108	4.4	Q9JW20	Q9jw2 streptomyce	RN
97	108	4.4	Q81ZW2	Q9jw2 streptomyce	RP
98	108	4.4	Q9L0V2	Q84cg4 streptomyce	RC STRAN=C57BL/6J; TISSUE=Lung;
99	109	4.4	Q84CG4	Q84cg4 streptomyce	RX MEDLINE=2235483; PubMed=12466851;
100	109	4.4	Q8FB7	Q93NB8	RA The PANTOM Consortium,
101	107	4.3	Q8FB7	Q93NB8	RA the RIKEN Genome Exploration Research Group Phase I & II Team,
102	106.5	4.3	Q8KBT5	Q93TB9	RA "Analysis of the mouse transcriptome based on functional annotation of
103	106.5	4.3	Q9FB7	Q93TB9	RT 60-70% full-length cDNAs."
104	106.5	4.3	Q9FB7	Q93TB9	RL Nature 420:563-73 (2002).
105	106	4.3	Q9AST6	Q9AST6	DR EMBL; AK052441; BAC14996.1; -.
106	106	4.3	Q82H40	Q82H40 streptomyce	DR PIR; PT0645; PT0645.
107	106	4.3	Q7YU69	Q7yu69 drosophila	DR MGD; MGI:982977 Shh.
108	106	4.3	Q8FB7	Q7wtfs streptomyce	DR GO; GO:0001708; P:axon guidance; IDA.
109	106	4.3	Q93NB6	Q93nb6 streptomyce	DR GO; GO:00017417; P:cell fate specification; IMP.
110	105.5	4.3	Q93NB6	Q93nb6 streptomyce	DR GO; GO:0001654; P:eye morphogenesis (sensu Mammalia); IMP.
111	105.5	4.3	Q8FB7	Q94270 chlamydomon	DR GO; GO:00017417; P:eye morphogenesis (sensu Mammalia); IMP.
112	105.5	4.3	Q8FB7	Q8FB7 drosophila	DR GO; GO:0001654; P:eye morphogenesis (sensu Mammalia); IMP.
113	105.5	4.3	Q9ALEO	Q9aleo simian herpesvirus	DR GO; GO:0001654; P:eye morphogenesis (sensu Mammalia); IMP.
114	105.5	4.3	Q81Z20	Q9aleo caulobacter	DR GO; GO:0001654; P:eye morphogenesis (sensu Mammalia); IMP.
115	105.5	4.3	Q52048	Q92048 streptomyce	DR GO; GO:0007389; P:pattern specification; IMP.
116	105.5	4.3	Q9ZAX6	Q9zax6 streptomyce	DR GO; GO:0042127; P:regulation of cell proliferation; IDA.
117	105	4.3	Q8FB7	Q8FB7 streptomyce	DR InterPro; IPR09045; Hedgehog/DD pept.
118	105	4.3	Q7W347	Q7w347 bordetella	DR InterPro; IPR03586; Hedgehog/antennal.
119	105	4.3	Q7Y1N8	Q7y1n8 oryza sativ	DR InterPro; IPR03587; Hedgehog/hint_N.
120	105	4.3	Q9GF7	Q9gf7 caenorhabditis	DR InterPro; IPR03587; Hedgehog/hint_N.
121	105	4.3	Q5582	Q5582 streptomyce	DR InterPro; IPR01657; Peptidase_C46.
122	105	4.3	Q7VVC2	Q7vvC2 bordetella	DR InterPro; IPR01767; Peptidase_C46.
123	105	4.3	Q8GBA6	Q8gbA6 pseudomonas	DR Pfam; PF01085; HH signal; 1.
124	104.5	4.2	Q82L07	Q82l07 streptomyce	DR Pfam; PF01079; Hint; 1.
125	104	4.2	Q89XP1	Q89xp1 bradyrhizobium	DR PRINTS; PRO0163; SONICCHOCG.
126	104	4.2	Q84R72	Q84r72 oryza sativ	DR PRODOM; PDD0302; HH signal; 1.
127	104	4.2	Q519	Q13350 drosophila	DR SMART; SM00305; HintC; 1.
128	104	4.2	Q519	Q18526 drosophila	DR SMART; SM00306; HintC; 1.
129	104	4.2	Q8VPM9	Q8vpm9 micrococcus	DR PROSITE; PS50817; INTEIN_NT_ER; 1.
130	104	4.2	Q82L07	Q82l07 streptomyce	SQ SEQUENCE 437 AA: 47785 MW: 491503875BB4227 CRC64;
131	104	4.2	Q8GBX4	Q8gbx4 polyangium	Query Match 83.5%; Score 2062; DB 11; Length 437;
132	103.5	4.2	Q8VPM5	Q8vpm5 mycobacterium	Best Local Similarity 87.2%; Pred. No. 3.e-145;
133	103.5	4.2	Q9L4N4	Q9l4n4 streptomyce	Matches 403; Conservative 8; Mismatches 3; Indels 26; Gaps 3;
134	103	4.2	Q82IJK3	Q82ijk3 streptomyce	
135	103	4.2	Q9NEC7	Q9neC7 leishmania	
136	103	4.2	Q91012	Q91012 streptomyce	QY 1 MILLARLLIVSSILVCSLACGPGRGKGPKRKPKLPLAKQFIPVAEKTGLGAG 60
137	103	4.2	Q93H19	Q93h19 streptomyce	Db 2 LILLARCPVILASSILVCPVLACGPGRGKGPKRKPKLPLAKQFIPVAEKTGLGAG 61
138	103	4.2	Q90255	Q90255 mycobacterium	QY 61 RYEKGKSRNSRFKEITPNNPDIIIFKDENTGADRIMTORCKXNLALISVNWNQPGV 120
139	102.5	4.2	P95236	P95236 mycobacterium	Db 62 RYEKGKTRNSRFKEITPNNPDIIIFKDENTGADRIMTORCKXNLALISVNWNQPGV 121
140	102.5	4.2	Q7TYS4	Q7tys4 mycobacterium	QY 121 KLRVTEGWDEGHHSDESILYEGRAVDITTSDRDSKGMNLAVALAEFGDWVYTESKAH 180
141	102.5	4.2	C06292	C06292 mycobacterium	Db 122 KLRVTEGWDEGHHSBSLHTEGRAVDITTSDRDSKGMNLAVALAEFGDWVYTESKAH 181
142	102.5	4.2	Q7U2B0	Q7u2b0 mycobacterium	QY 181 IHCSPVKAENSYAAKSQGCCPQSATVHLQEQGTKLVQDGRVLAADDQGRLLYSDFLT 240
143	102.5	4.2	Q81ZX5	Q81zx5 streptomyce	Db 182 IHCSPVKAENSYAAKSQGCCPQSATVHLQEQGTKLVQDGRVLAADDQGRLLYSDFLT 241
144	102.5	4.2	Q9L1L1	Q9l1l1 streptomyce	QY 241 FUDRDQAKCYFYVITREPERLITAAHLLFVAPRHDNSATGEPEASSSGGPPSGGALG 300
145	102.5	4.2	Q8L640	Q8l640 arabidopsis	Db 242 FQDRDEGAKCYFYVITREPERLITAAHLLFVAPHND-----SGPTPG 286
146	102.5	4.2	Q8P377	Q8p377 xanthomonas	
147	102.5	4.2	Q9W2T1	Q9w2t1 drosophila	
148	102.5	4.2	Q7WTF1	Q7wtf1 streptomyce	
149	102	4.1	Q8WVVO	Q8wvvo homo sapien	
150	102	4.1	Q9APG7	Q9apg7 anaplasma m	
				QY	RESULTS 1
				QY	ID Q8C765 PRELIMINARY; PRT; 437 AA.
				Db	AC Q8C765; DT 01-MAR-2003 (T=EMBLrel. 23, Created) 360
				Db	DT 01-MAR-2003 (T=EMBLrel. 23, Last sequence update) 346
				QY	DT 01-OCT-2003 (T=EMBLrel. 25, Last annotation update) 420
				Db	DT 01-OCT-2003 (T=EMBLrel. 25, Last annotation update) 395

ALIGNMENTS

RESULTS 1
 ID Q8C765 PRELIMINARY;
 AC Q8C765;
 DT 01-MAR-2003 (T=EMBLrel. 23, Created) 360
 DT 01-MAR-2003 (T=EMBLrel. 23, Last sequence update) 346
 DT 01-OCT-2003 (T=EMBLrel. 25, Last annotation update) 420
 DT 01-OCT-2003 (T=EMBLrel. 25, Last annotation update) 395

Qy	421 ADAPGAGATAGIHWYSOLLYQIGTWLIDSEALHPLGMNKSS	462	301 PRALFAASVPGQRVYVAERDGRRLLPAAVHSVTSEEAGAYAALTAQGNTLIRNLV 360
Db	396 TEARGAEPTAGIHWYSQHLHYGTLWLDSETMHPLGMNKSS	437	299 FRSNFASSYRPGRV-LTEDREG-RGRREATDVRVY-EATGAYAATVTAHGVVIRVL 355
RESULT 2			361 ASCVAVIEPHSWAHRAFAPPRLAHALLALAPARTDRGDSGGDRGGGRVALTARGA 420
O57404	PRELIMINARY;	PRT;	395 ASCVAVIEPHSWAHRAFAPPRLVGFGILSFFSP--QDSSHS----- 394
ID O57404			421 ADAPGAGATAGIHWYSOLLYQIGTWLIDSEALHPLGMNKSS 462
AC 057404;			395 -PFAPSQAEGVHMYSELRYGTWVQADTHPLGMNKSS 434
DT 01-JUN-1998	(TREMBrel.	06, Created)	
DT 01-OCT-1998	(TREMBrel.	06, Last sequence update)	
DT 01-OCT-2003	(TREMBrel.	25, Last annotation update)	
DE Sonic hedgehog-related protein.			
GN PW-SHH.			
OS Pleurodiles waltlisi (Iberian ribbed newt).			
OC Eulampridae; Chordata; Craniata; Vertebrata; Euteleostomi;			
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;			
Pleurodiles.			
NCB_TaxID=8319;			
RN [1]			
RP Caubit X., Nicolas S., Le Parco Y.,			
"Pleurodiles sonic hedgehog"; Submitted (May-1997) to the EMBL/GenBank/DDBJ databases.			
DR EMBL; A003532; AB294412.1; -.			
DR HSSP; Q22261; 1VHH.			
DR MEBOPS; C46_002; -.			
DR GO; GO:0008233; Peptidase activity; IEA.			
DR GO; GO:0007267; Pe cell-cell signaling; IEA.			
DR GO; GO:001775; P development; IEA.			
DR GO; GO:0006508; Protein splicing; IEA.			
DR InterPro; IPR00905; Hedgehog/DD_Pept.			
DR InterPro; IPR003586; Hedgehog/hint_N.			
DR InterPro; IPR003587; Hedgehog/hint_N.			
DR InterPro; IPR000320; HH_Signal_I.			
DR InterPro; IPR006141; Intein_S.			
DR InterPro; IPR001657; Peptidase_C46.			
DR InterPro; IPR00177; Pept_C46_Hint.			
DR Pfam; PF01085; HH_signal_1.			
DR Pfam; PF01079; Hint_1.			
DR PRINTS; PR00632; SONICHHOG.			
DR PRODOM; PD03042; HH_signal_1.			
DR SMART; SM00305; HintC_1.			
DR PROSITE; PS550817; INTEIN_N_TER; 1.			
DR PROSITE; PS550817; INTEIN_N_TER; 1.			
SEQUENCE 434 AA; 4842 MW; A9495E267151AE74	CRC64;		
Query Match Score 1544.5; DB 13; Length 434;			
Best Local Similarity 67.7%; Pred. No. 1.1e-106; Mismatches 41; Indels 31; Gaps 6;			
Matches 313; Conservative 41; SMART; SM00305; HintC_1.			
Db	1 MILLARCLLIVLVSISLIVCGPGRGFKRHPKKTPLAKQFIPVNAEKTLGASG 60	61 RYEKGKISRNSERFRKLTPNPDIFKDENTGADRMTORCKDKLNALAISMNQPGV 120	62.6% Score 1466.5; DB 13; Length 413;
Qy	4 MILLRDLLLGCFISTLVLPLGLGCOPGRGIGQRERPKQTPLAKQFIPVNSXKTLGASG 63	61 RYEKGKISRNSERFRKLTPNPDIFKDENTGADRMTORCKDKLNALAISMNQPGV 123	Query Match Score 1466.5; DB 13; Length 413;
Db	1 MILLARCLLIVLVSISLIVCGPGRGFKRHPKKTPLAKQFIPVNAEKTLGASG 60	61 RYEKGKISRNSERFRKLTPNPDIFKDENTGADRMTORCKDKLNALAISMNQPGV 120	Best Local Similarity 63.1%; Pred. No. 6.5e-101; Mismatches 52; Indels 51; Gaps 8;
Qy	4 MILLRDLLLGCFISTLVLPLGLGCOPGRGIGQRERPKQTPLAKQFIPVNSXKTLGASG 63	61 RYEKGKISRNSERFRKLTPNPDIFKDENTGADRMTORCKDKLNALAISMNQPGV 123	Matches 292; Conservative 52; Mismatches 68; Indels 51; Gaps 8;
Db	1 KLRVTEGWDEGHSEESLHYEGRAVDITTSDRSKYGMALARAVEGFDWVYESKAH 180	61 RYEKGKISRNSERFRKLTPNPDIFKDENTGADRMTORCKDKLNALAISMNQPGV 120	
Qy	121 KLRVTEGWDEGHSEESLHYEGRAVDITTSDRSKYGMALARAVEGFDWVYESKAH 180	61 RYEKGKISRNSERFRKLTPNPDIFKDENTGADRMTORCKDKLNALAISMNQPGV 120	
Db	124 KLRVTEGWDEGHSEESLHYEGRAVDITTSDRSKYGMALARAVEGFDWVYESKAH 183	61 RYEKGKISRNSERFRKLTPNPDIFKDENTGADRMTORCKDKLNALAISMNQPGV 120	
Qy	181 IHCSYKAENSAVAKSGCFPSATVHLEGGTKLDSGRYTAADDQGRLLYSDLT 240	61 RYEKGKISRNSERFRKLTPNPDIFKDENTGADRMTORCKDKLNALAISMNQPGV 120	
Db	184 IHCSYKAENSAVAKSGCFPSATVHLEGGTKLDSGRYTAADDQGRLLYSDLT 243	61 RYEKGKISRNSERFRKLTPNPDIFKDENTGADRMTORCKDKLNALAISMNQPGV 120	
Qy	241 FLDRDGAKCYFYVIETREPERRLLTAHLLFVAPHNSATGEPEASSGSPPSGGALG 300	61 RYEKGKISRNSERFRKLTPNPDIFKDENTGADRMTORCKDKLNALAISMNQPGV 120	
Db	244 FMDEEBSTARVVFYVIETSLPRLRLLTAHLLFVAQEHB---NAGNFRSKFGR 298	61 RYEKGKISRNSERFRKLTPNPDIFKDENTGADRMTORCKDKLNALAISMNQPGV 120	
Qy	181 IHCSYKAENSAVAKSGCFPSATVHLEGGTKLDSGRYTAADDQGRLLYSDLT 240	61 RYEKGKISRNSERFRKLTPNPDIFKDENTGADRMTORCKDKLNALAISMNQPGV 120	

Db	181 IHCSYKAENSVAARKSGGCPGSSTVLTQDGTKLKVXHRLSGRVLAADDGNPTEDFIM 240	Db	1 MLLWTRIVLAGVICLUSVSSGMGGPGCGYGRRRHPKLTPLAYQFIPNVAEKTLLGASG 60
Qy	241 FLDRDDGAKRKYFYVETTRPRERILITAHHLLEVAPRHDNSATGEPEASSGSPSGALG 300	Qy	61 RYEGLKLSRNSERFKEUTPNTNPDTIIFKDDEENTGADRMTORCKDKLNLAISYMNONPGV 120
Db	241 FVDRDSTTRLYHYET-DSGQKITLTAAHLLYVA-RNGTESD-----G 282	Db	61 RYEGLKTRNSERFRKELTPNNTDILIFKDDEENTGADRMTQRCDDKLNLAIISYMNQNPGV 120
Qy	301 PRALIFASRYRPQGORYVYVVAERDGR-RULPAAYHSVSLSEAGAYAAYPLTAQSTILINRV 359	Qy	121 KLRVTEGMDDGHHSEESLHYEGRAVDITTSDRSKYMLARAVEAGFDWVYYESEKAH 180
Db	283 MSAYFASQRQRGKVIV--SDPERSRLPPVTERI-YTQEHGVSYAPFTVQGNVVDEI 338	Db	121 KLRVTEGMDDGHHSEESLHYEGRAVDITTSDRSKYGTLSRAVEAGFDWVYYESEKAH 180
Qy	360 LASCYAVIEBBSWAHRAAFFPLAHALIAALAPARTDRGDGDSGGDRGGGRVALTAGP 419	Qy	181 IHCSYKAENSVAAKSGGCPGSATSHLEQGGTKLVKDLSPGDRVIAADDGGRLLSDFLT 240
Db	339 LASCYAVIEEDHLAHWALAPVRLLAHPVSSLLSRQ-----PG 375	Db	181 IHCSYKAENSVAAKSGGCPGSSTVLLQDGKTYKEVKALGDRVIAADHGQPYTDIFM 240
Qy	420 AADAGAGATAGIHWYSONLYQISITWLSEACHPLGMVAKSS 462	Qy	241 FLDRDDGAKRKYFYVETTRPERPLLTAAHLLFVYAPHNDSATGEPEASSGSPSGALG 300
Db	376 ----GGQZDGVHRYVSRLLYQVGTMWLLDGHATHPLGMVSVPs 413	Db	241 FIDQSBSTRFLFYVET-DSGQKLTLTAAHLLFVYGSNSTERAH----RG 285
RESULT 4			
ID Q9W7Q9	PRELIMINARY;	PRT;	414 AA.
AC Q9W7Q9;			
DT 01-NOV-1999	(TREMBLrel. 12, Created)	DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)	374
DT 01-OCT-2003	(TREMBLrel. 25, Last annotation update)	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
DE Sonic hedgehog.			
GN SHH.			
OS Paralichthys olivaceus (Plounder).			
OC Actinopterygii; Neopterygii; Teleostei; Buteleostomi;			
OC Acanthomorpha; Acanthopercygii; Percomorphai; Pleuronectiformes;			
OC Pleuronectoidae; Paralichthyidae; Paralichthys.			
OX NCBI_TaxID:8255;			
RN [1]			
RP SEQUENCE FROM N.A.			
MEDLINE=99338236;	PubMed=10223710;	DR GO; GO-0008233; F:peptidase activity; IBA.	
RA Suzuki, T., Ichiro O., Kurokawa T.	RT "Retinoic acid given at late embryonic stage depresses sonic hedgehog and Hoxd-4 expression in the pharyngeal area and induces skeletal malformation in flounder (Paralichthys olivaceus) embryos"; Dev. Growth Differ. 41:143-152(1999).	RA "Notophthalmus viridescens (Eastern newt) (Triturus viridescens), Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae, Notophthalmus".	
DR EMBL; AB028748; BAA82360.1; -.		DR GO; GO-0008233; F:peptidase activity; IBA.	
DR HSSP; Q62226; 1VHS.		DR GO; GO-0008233; F:transferring glycosyl. . . ; IBA.	
DR MEROPS; C45_001; -.		DR GO; GO-0016757; F:transferring activity, transferring glycosyl. . . ; IBA.	
DR GO; GO-0002733; F:peptide activity; IBA.		DR GO; GO-0007275; F:cell-cell signaling; IBA.	
DR GO; GO-0007275; F:cell-cell signaling; IBA.		DR GO; GO-0007275; F:development; IBA.	
DR GO; GO-0007275; F:development; IBA.		DR GO; GO-0006508; F:protein/protein interaction; IBA.	
DR GO; GO-0015539; F:protein splicing; IBA.		DR GO; GO-0006508; F:protein analysis and peptidolysis; IBA.	
DR GO; GO-000508; F:protein splicing; IBA.		DR InterPro; IPR00945; Hedgehog/HD pept.	
DR InterPro; IPR00945; Hedgehog/HD pept.		DR InterPro; IPR00945; Hedgehog/HD pept.	
DR InterPro; IPR001586; Hedgehog hint_N.		DR InterPro; IPR003586; Hedgehog hint_C.	
DR InterPro; IPR003587; Hedgehog hint_N.		DR InterPro; IPR003587; Hedgehog hint_N.	
DR InterPro; IPR003587; Hedgehog hint_N.		DR InterPro; IPR003220; HH signal_I.	
DR InterPro; IPR003587; Hedgehog hint_N.		DR InterPro; IPR001657; Peptidase_C46.	
DR InterPro; IPR001657; Hedgehog/HD pept.		DR InterPro; IPR001767; Pept_C46 hint.	
DR InterPro; IPR001657; Pept_C46 hint.		DR InterPro; IPR002375; Pr/PYR_transf.	
DR Pfam; PF01085; HH signal; 1.		DR Pfam; PF01085; HH signal; 1.	
DR InterPro; IPR01079; Hint; 1.		DR Pfam; PF01079; Hint; 1.	
DR PRINTS; PRO0632; SONICHHOG.		DR PRINTS; PRO0632; SONICHHOG.	
DR Prodrom; PD003045; SONICHHOG.		DR Prodrom; PD003042; HH signal; 1.	
DR SMART; SM00305; HintC; 1.		DR SMART; SM00306; HintN; 1.	
DR SMART; SM00306; HintN; 1.		DR SMART; SM00306; HintN; 1.	
DR PROSITE; PS00817; INFEIN_N_TER; 1.		DR PROSITE; PS00103; PUR_PR_TRANSFER; 1.	
SQ SEQUENCE 414 AA; 45945 MW; 50607BF3DB7CODA3 CRC64;		DR Glycosyltransferase; Transferase.	
Query Match 58.9%; Score 1454; DB 13; Length 414;			
Best Local Similarity 62.4%; Prod. No. 5.6e-100;			
Matches 289; Conservative 55; Mismatches 69; Indels 50; Gaps 7;			
Qy 1 MULLARCIILVLYSSMVGCGIACGPGRGFGRHRPKKLTPLAYQFIPNVAEKTLLGASG 60			

Qy	422 DAPGAGATIGHWSQLLYQIGTWILDSSDALHP	454	RP SEQUENCE FROM N.A. MEDLINE=2126614; PubMed=12128232;
Db	384 -----RHWHTQGLYLGKTYM-SDRLFP	406	RX RA "Expression of hedgehog genes in Ciona intestinalis embryos.";
RESULT 15			
ID Q9R179	PRELIMINARY;	PRT;	161 AA.
AC O9R179;			
DT 01-MAY-2000 (TREMBLrel. 13, Created)			
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE Sonic hedgehog protein (Fragment).			
OS Rattus norvegicus (Rat).			
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;			
NCBI_TaxID=10116;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;			
RA Garges P.L., Meyer R.A. Jr., Brown C.A., Price D.K.;			
RT "Sonic hedgehog in the rat."			
RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.			
DR AF162915;			
HSSP; Q62226; 1VH.			
DR GO:0008233; F:peptidase activity; IEA.			
DR GO:000267; P:cell-cell signaling; IEA.			
DR GO:000275; P:development; IEA.			
DR GO:0006508; P:protein and peptidolysis; IEA.			
DR InterPro; IPR009045; Hedgehog/DD_Pept.			
DR InterPro; IPR000320; HH_Signal.			
DR InterPro; IPR001657; Peptidase_C46.			
DR InterPro; IPR001767; Pept_C46_Hint.			
DR Pfam; PF01085; HH_Signal_1.			
DR Pfam; PF01079; Hint_1.			
DR PRINTS; PRO0032; SONICHHOG.			
DR Prodrom; PDO03042; HH_Signal_1.			
FT NON_TER 161 161			
SQ SEQUENCE 161 AA; 17906 MW; DF06DB85FD45AE4DB	CRC64;		
Query Match	34.4%; Score 850;	DB 11;	Length 161;
Best Local Similarity	100.0%;	Pred. No. 1_46-55;	
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	84 IIKFDENTGADRMLTQCKDKLNALAISYMWNQWVTKRTEGDEGHSESLHYEG	143	Db 248 AKKVYVIETREPRLIITAAHLIFVAPHND----SATGEPEASGSGPSPGGALGPR
Db	1 IIKFDENTGADRMLTQCKDKLNALAISYMWNQWVTKRTEGDEGHSESLHYEG	60	Db 248 IGSY--IEIRSQLEITRLTANHMLIATQINCSNSFSAT-----KR 287
Qy	144 RAVDITTSDRSKYGMHLARLAVEAGFDWVYYYESKAHHSVKAENSVAAKSGCCFPGSA	203	Db 303 ALFASRYRPQGVV-YVAERGDGRRLPAAVSYTSEEAGAYAALTAQSTILINRVLIA 361
Db	61 RAVDITTSDRSKYGMHLARLAVEAGFDWVYYYESKAHHSVKAENSVAAKSGCCFPGSA	120	Db 288 AVFGADIFSGQVVTYTIQARD-EFQPSRVEVT-TVTEGFLGLYALFTGTVVVBDGIVIA 345
Qy	204 TVHLEQCGTKLVKDLSPGDRYLAADDQGRLLYSDFLTFLDR	244	Db 362 SCAVIEHSHWAHRAAPAPRFLNALLANAPARTDGDSGGCGRGGGRVALTAPGAA 421
Db	121 TVHLEQCGTKLVKDLSPGDRYLAADDQGRLLYSDFLTFLDR	161	Db 346 SCYGTIGSETLAHAMMPIRSFPYL-----RRTN ----- 374
RESULT 16			
Q8MY56	PRELIMINARY;	PRT;	402 AA.
ID Q8MY56	PRELIMINARY;	PRT;	557 AA.
AC Q8MY56;			
DT 01-OCT-2002 (TREMBLrel. 22, Created)			
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
GN Hedgehog homolog 2.			
OS Ciona intestinalis.			
OC Ciona intestinalis.			
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;			
OC Phleobranchia; Cionidae; Ciona.			
OC Ciona intestinalis.			
NCBI_TaxID=7719;			
RN [1]			

Db	1	IPNVAEKTLLGASGRYEGKITRANSERFKELTPYNNSDILPKBENTADRRMTQRCKDKLN	60	
Qy	108	ALAI\$VN\$NQPGV\$KLRVTEGDEGH\$SESHYEGRAVDITTS\$DRSKYGM\$ALARAVE	167	
Db	61	ALAI\$VN\$NQPGV\$KLRVTEGDEGH\$SESHYEGRAVDITTS\$DRSKYGM\$ALARAVE	120	
Qy	168	AGFDWVYYESKAHICSV	185	
Db	121	AGFDWVYYESKAHICSV	138	
		RESULT 22		
Q9WV29		PRELIMINARY;	PRT;	177 AA.
ID	Q9WV29			
AC	Q9WV29;			
DT	01-NOV-1999	(TREMBrel. 12, Created)		
DT	01-NOV-1999	(TREMBrel. 12, Last sequence update)		
DT	01-OCT-2003	(TREMBrel. 25, Last annotation update)		
		Indian hedgehog protein (Fragment).		
OS	Rattus norvegicus (Rat)			
OC	Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Rattus.			
NCBI_TaxID	10116;			
OX				
RN				
RP		SEQUENCE FROM N.A.		
RC	STRAIN=Prague-Dawley; TISSUE=Kidney;			
RA	Gargies P.L., Meyer R.A. Jr., Brown C.A., Price D.K.;			
RA	"Indian hedgehog in rat."			
RA	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF162914; ADD45372.1; -			
DR	HSSP; Q2266; 1VHH.			
DR	METOPS; C46_0.03; -			
DR	GO: GO:0008233; F: peptidase activity; IEA.			
DR	GO: GO:0007267; P: cell-cell signaling; IEA.			
DR	GO: GO:0007275; P: development; IEA.			
DR	GO: GO:0016539; P: protein splicing; IEA.			
DR	GO: GO:0006508; P: proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR00905; Hedgehog/DD_Pept.			
DR	InterPro; IPR00358; Hedgehog hint_N.			
DR	InterPro; IPR000320; HH signal_1.			
DR	InterPro; IPR00611; Inter_S.			
DR	InterPro; IPR001767; Pept_C16_Hint.			
DR	InterPro; IPR00165; Pept_1.			
PFam	PF01085; HH signal_1.			
PRINTS	PR00532; SONICHHOG.			
PRODom	PD00332; SONICHHOG.			
PROSITE	PS00304; HH signal_1.			
FT	NON_TER 177			
SQ	SEQUENCE 177 AA; 19739 MW; CA5871626A565F65 CRC64;			
Qy	97	LMTQCKDKLNALAT\$VNQPGV\$KLRVTEGDBDGHSSESHYEGRAVDITTS\$DRS	156	
Db	1	LMTQCKDKLNALAT\$VNQPGV\$KLRVTEGDBDGHSSESHYEGRAVDITTS\$DRB\$RN	60	
Qy	157	KYGM\$ALARAVEAGFDWVYYESKAHICSV\$AENSAAKGGCFPGSATVHLBQGGTKLVK	216	
Db	61	KYGM\$ALARAVEAGFDWVYYESKAHICSV\$AENSAAKGGCFPGAQVHLT\$GERTYALS	120	
Qy	217	DLSPGD\$RVTAADDGCRLLYSDFELTFLDRDGAKVFVYLTREPRLTAAHLLF	273	
Db	121	AVKPGD\$RVLA\$MGEDENPT\$SDVLFLDRPFRNLRAFOVIE\$TQDP\$RLLT\$PAHLLF	177	
		RESULT 23		
Q8M\$TV7		PRELIMINARY;	PRT;	121 AA.

AC	Q8M\$TV7;			
DT	01-OCT-2002	(TREMBrel. 22, Created)		
DT	01-OCT-2002	(TREMBrel. 22, Last sequence update)		
DT	01-OCT-2003	(TREMBrel. 25, Last annotation update)		
GN	Sonic hedgehog (Fragment).			
OS	Suncus murinus (House shrew)			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Insectivora; Soricidae; Crocidurinae; Suncus.			
NCBI_TaxID	9378;			
OX				
RN	[1] -			
RP		SEQUENCE FROM N.A.		
RA	Ogi H., Tabata M.J., Yamamoto A., Yasui K., Uemura M.;			
RT	"COMPARISON OF EXPRESSION PATTERNS OF FIBROBLAST GROWTH FACTOR 8, BONE MORPHOGENETIC PROTEIN 4 AND SONIC HEDGEHOG IN JAW DEVELOPMENT OF THE HOUSE SHREW, SUNCUS MURINUS";			
RT	Cell. Mol. Biol. 48:OL289-OL296 (2002).			
RL	EMBL: AB081406; BAC02893.1; -			
DR	GO: GO:0007267; P: cell-cell signaling; IEA.			
DR	GO: GO:0007275; P: development; IEA.			
DR	InterPro; IPR009045; Hedgehog/DD_Pept.			
DR	InterPro; IPR00320; HH signal.			
DR	InterPro; IPR00165; Peptide_C46.			
DR	PFam: PF01085; HH signal.			
DR	PRINTS; PR00632; SONICHHOG.			
DR	PRODom; PD003042; HH signal_1.			
FT	NON_TER 1			
FT	121 AA; 13919 MW; D159C45D5A8A16 CRC64;			
SQ	SEQUENCE 121 AA; 13919 MW; D159C45D5A8A16 CRC64;			
Query Match	Score 649; DB 6; Length 121;			
Best Local Similarity	99.2%; Pred. NC. 8.7E-41;			
Matches	120; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Qy	71 ERKFKEITPNYPNDIIFKD\$BENTGADR\$M\$OR\$KDLN\$AL\$AIS\$MNQ\$WP\$KLV\$T\$G\$NDE			
Db	1 ERKFKEITPNYPNDIIFKD\$BENTGADR\$M\$OR\$KDLN\$AL\$AIS\$MNQ\$WP\$KLV\$T\$G\$NDE			
Qy	131 DGHHSSE\$LSHYEGRAVDITTS\$DRSKYGM\$ALARAVEAGFDWVYYESKAHICSVKAENS			
Db	61 DGHHSSE\$LSHYEGRAVDITTS\$DRSKYGM\$ALARAVEAGFDWVYYESKAHICSVKAENS			
RESULT 24				
Q9WV29				
ID	Q9WV29			
AC	Q9WV29;			
DT	01-MAY-1999	(TREMBrel. 10, Created)		
DT	01-OCT-2003	(TREMBrel. 25, Last annotation update)		
DE	Hedgehog protein (Fragment).			
OS	Junonia coenia (Peacock butterfly)			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Diptaria; Papilionoidea; Nymphalidae; Nymphalinae; Junonia.			
NCBI_TaxID	3978;			
OX				
RP		SEQUENCE FROM N.A.		
RA	Keys D.N., Lewis D.L., Selegue J.B., Pearson B.J., Goodrich L.V., Johnson R.L., Gates J., Scott M.P., Carroll S.B., RA			
RT	"Recruitment of a hedgehog regulatory circuit in butterfly eyespot evolution";			
RT	Science 0-0-0(1999)			
DR	EMBL: AF11742; AAD08931.1; -			
DR	HSSP; Q62246; 1VHH.			
DR	GO: GO:0007267; P: cell-cell signaling; IEA.			
DR	GO: GO:0007275; P: development; IEA.			
DR	InterPro; IPR009045; Hedgehog/DD_Pept.			

RESULT 26

DR	InterPro; IPR000320; HH signal.	PRT;	202 AA.
DR	InterPro; IPR001657; Peptidase_C46.		
DR	Pfam; PF01085; HH signal.		
DR	PRINTS; PR00634; SONICHHOG.		
DR	ProDom; PD003042; HH signal.		
DT	NON-TER 1		
FT	NON-TER 185		
FT	SEQUENCE 185 AA;	Score 619; DB 5; Length 185;	
SQ	20745 MW;	E9B9F4CE2FAAE662 CRC64;	
Query Match	Best Local Similarity 68.2%; Pred. No. 2.7e-38;	Indels 2; Gaps 2;	
Matches 116;	Conservative 21;	Mismatches 31;	

Qy 58 ASGRYGGKISNSERKELTPNNDIFKDEENTGADRIMTORKDKLNALAIISVNQW 117
Db 3 ASGPPEGCRITDDEKTRDLYPNYNPDIKDDEGTGADRIMTORKCKEINTLAVSNQW 62
Qy 118 PGVKGRVTEGVMDDEGHHSSEELHYPERAVIDTTSDDRSKYGMLARLAVEAGFDWVYTES 177
Db 63 PGVRLRVIEGVDEENSHLDNSLHYEGRAVDLITTSRDHSRKGMLARLATEAGFDWVYFEN 122
Qy 178 KAHITHCSVKKAANSVAAKSGGGCPGSATVHLEQQGPKLVQDLSPGDRVLLA 227
Db 123 RSYIHCSCVKTESSVGT-GAGCFFPSGAVVHTENGPD-IASLUKKGKVKLLA 170

RESULT 27

DR	InterPro; IPR000320; HH signal.	PRT;	99 AA.
DR	InterPro; IPR00641; Intern_S.		
DR	InterPro; IPR01657; Peptidase_C46.		
DR	InterPro; IPR01767; Pept C46 Hint.		
DR	InterPro; IPR02375; Pr/Pt_rP_transf.		
DR	Pfam; PF01079; Hint_1.		
DR	PRINTS; PR00632; SONICHHOG.		
DR	ProDom; PD003042; HH_Signal;		
DR	SMART; SM00305; HintC_1.		
DR	SMART; SM00306; HintN_1.		
DR	PROSITE; PS50817; INTBIN_N_TER/1.		
DR	PROSITE; PS00103; FUR_PYR_PR_TRANSFER; 1.		
RN	Sequence from N.A.		
RX	Medline=11932743; PubMed=11932743;	Score 526.5; DB 6; Length 202;	
R2	Tanaka M., Munsterberg A., Anderson W.G., Prescott A.R., Hazon N.,		
R2	Tickle C.;		
RT	"Pin" development in a cartilaginous fish and the origin of vertebrate		
RT	limbs.".		
RL	Nature 416:527-531(2002).		
DR	EMBL; AF39335; PAM08228.1.		
DR	GO; GO-0007267; Pe:cell-cell signaling; IEA.		
DR	GO; GO-0007225; Pe:development; IEA.		
DR	InterPro; IPR00945; Hedgehog/DD_Pept.		
DR	InterPro; IPR000120; HH_Signal.		
DR	InterPro; IPR00105; HH_Signal.		
DR	PRINTS; PR00632; SONICHHOG.		
DR	ProDom; PD003042; HH_Signal.		
FT	NON-TER 1		
FT	SEQUENCE 99 AA;	Score 11468 MW;	
SQ	831864DB34A1A20 CRC64;		

Query Match

Best Local Similarity 98.0%;	Pred. No. 4e-32;	Length 99;	
Matches 97;	Conservative 2;	Mismatches 0;	

Qy 78 PNINPDIIFKDEENTGADRIMTORKDNALAINISVNQWPGKLRVTEGDEDGHSEE 137
Db 1 PNINPDIIFKDEENTGADRIMTORKDNALAINISVNQWPGKLRVTEGDEDGHSEE 60

Query Match

Best Local Similarity 98.0%;	Pred. No. 4e-32;	Length 99;	
Matches 97;	Conservative 2;	Mismatches 0;	

Qy 138 SLHYEGRAVDITTSRDRSKYGMMLARLAVEAGFDWVYEE 176
Db 61 SLHYEGRAVDITTSRDRSKYGMMLARLAVEAGFDWVYEE 99

RESULT 27

DR	InterPro; IPR000320; HH signal.	PRT;	119 AA.
DR	InterPro; IPR01998 (TREMBLrel. 05, Last sequence update)		
DR	InterPro; IPR01998 (TREMBLrel. 05, Last sequence update)		
DR	InterPro; IPR01998 (TREMBLrel. 25, Last annotation update)		
DR	Shh (Fragment).		

GN ME-SHH.	DR PROD; PD003042; HH_signal; 1.
OS Crystas latipes (Medaka fish) (Japanese ricefish).	FT NON_TER 1 129 MW; AB33505B3E751319 CRC64;
OC Cetaria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	FT NON_TER 129 AA; 14378 MW;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;	SEQUENCE 129
OC Acanthopterygii; Percomorpha; Atherinomorpha;	Query Match 20.7%; Score 511; DB 11; Length 129;
OC Beloniformes; Adrianichthyidae; Oryziinae; Oryziinae.	Best Local Similarity 71.4%; Pred. No. 1.8e-30;
OX NCBI_TaxID=8090;	Matches 90; Conservative 24; Mismatches 10; Indels 2; Gaps 2;
RN [1]	
SEQUENCE FROM N.A.	
STRAIN=DBRR; TISSUE=Embryo;	23 ACGPGRG-FKRRHFK-K-TPLAKTQFINVAEKTLLGAGRYERKISNSERFFELTPVY 80
RC Araki K.;	: : : : : : : : : : : : : : : : : : : : : :
RT "The analysis of medaka haploid development.";	: : : : : : : : : : : : : : : : : : : : : :
RL Submitted (SPP-1997) to the EMBL/GenBank/DBJ databases.	4 SCGPGRGPVGRRTVKQLYPLMXQFVPSMPERTLGASGPAGRVTGSRERDVNPY 63
DR EMBL; AB007129; BAA22368.1; -.	81 NPDIIFKDEENTGADRIMTORCKDXLNALAISVNWPGVKLRTYEGMDGHSEBSLH 140
HSSP; Q6226; 1VHH.	: : : : : : : : : : : : : : : : : : : : : :
DR MEROPS; C46_001; -.	64 NPDIIFKDEENSGADRIMTERCRERNALIAVNMWPSVRLRTYEGMDGHQAQDSLH 123
GO; GO:0008233; F: peptidase activity; IEA.	: : : : : : : : : : : : : : : : : : : : : :
DR GO; GO:000267; P: cell-cell signaling; IEA.	QY 141 YEGRAY 146
DR GO; GO:0007275; P: development; IEA.	Db 124 YEGRAL 129
DR GO; GO:0006508; P: proteolysis and peptidolysis; IEA.	
InterPro; IPR00905; Hedgehog/DD_Pept.	RESULT 29
InterPro; IPR000320; HH_signal.	O42234 PRELIMINARY; PRT; 137 AA.
InterPro; IPR001677; Peptidase_C46.	ID O42234; AC 042234; ID 042234; AC 042234; PRELIMINARY; PRT; 137 AA.
InterPro; IPR001767; Pept_C46_Hint.	DR 01-JAN-1998 (TRIMBurrel. 05, Created)
Pfam; PF01085; HH_signal_1.	DR 01-JAN-1995 (TRIMBurrel. 05, Last sequence update)
DR PRINTS; PR006512; SONICHHOG.	RA Borycki A.G.; Mendham L.; Emerson C.P. Jr.;
DR PROD; PD003042; HH_signal_1.	DR 01-OCT-2003 (TRIMBurrel. 25, Last annotation update)
NON_TER 1	DE Sonic hedgehog (Fragment).
PT NON_TER 119 AA; 119 MW; A4868AC2E475CB1B CRC64;	GN SH.
SQ SEQUENCE 119 AA; 13179 MW;	OS Coturnix coturnix (Common quail).
Query Match 21.2%; Score 521; DB 13; Length 119;	OC Archaea; Metazoa; Chordata; Craniata; Vertebrata; Butelostomii; OC Archaea; Ayres; Neogastropoda; Galloformes; Phasianidae; Phasianinae;
Best Local Similarity 82.4%; Pred. No. 2.1e-31; Indels 0; Gaps 0;	OC Coturnix.
Matches 98; Conservative 8; Mismatches 13; Indels 0; Gaps 0;	NCBI_TaxID=9091;
QY 123 RVTGEWDEGGHSSESSLHYEGRADITTSDRSKYGMARLAVEAGEFDWVYYESKAHH 182	OX
Db 1 RVTGEWDEGGHSSESSLHYEGRADITTSDRSKYGMARLAVEAGEFDWVYYESKAHH 60	RN [1] SEQUENCE FROM N.A.
PRINTS; PR006512; SONICHHOG.	RP PubMed=98167903; PubMed=9435297;
DR PROD; PD003042; HH_signal_1.	RX MEDLINE=98167903; PubMed=9435297;
NON_TER 1	RA Borycki A.G.; Mendham L.; Emerson C.P. Jr.;
PT NON_TER 119 AA; 119 MW; A4868AC2E475CB1B CRC64;	DR "Control of sonic patterning by sonic hedgehog and its downstream signal response genes."
SQ SEQUENCE 119 AA; 13179 MW;	RT Development 125.;77-79(1998).
Query Match 21.2%; Score 521; DB 13; Length 119;	RL DR AF022882; AAB0949_1; -.
Best Local Similarity 82.4%; Pred. No. 2.1e-31; Indels 0; Gaps 0;	DR MEROPS; C46_002; -.
Matches 98; Conservative 8; Mismatches 13; Indels 0; Gaps 0;	DR GO; GO:0008233; F: peptidase activity; IEA.
Q9WTP6 Q9WTP6 PRELIMINARY; PRT; 129 AA.	DR GO; GO:0007154; P: cell communication; IEA.
ID Q9WTP6; PRELIMINARY; PRT; 129 AA.	DR GO; GO:0007275; P: development; IEA.
AC Q9WTP6; PRELIMINARY; PRT; 129 AA.	DR GO; GO:000508; P: proteolysis and peptidolysis; IEA.
RT 01-NOV-1999 (TRIMBurrel. 12, Created)	DR InterPro; IPR001658; Hedgehog_hint.
DT 01-NOV-1999 (TRIMBurrel. 12, Last sequence update)	DR InterPro; IPR001657; Peptidase_C46.
DT 01-OCT-2003 (TRIMBurrel. 25, Last annotation update)	DR InterPro; IPR001767; Pept_C46_Hint.
DE Desert hedgehog protein (Fragment).	DR Pfam; PF01079; Hint_1.
GN DHH.	DR PRINTS; PR00632; SONICHHOG.
OS Rattus norvegicus (Rat).	DR SMART; SM00305; HintC_1.
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi;	FT NON_TER 1 14571 MW; 7FD9DF815AF1532 CRC64;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	SEQUENCE 137 AA; 14571 MW;
NCBI_TaxID=10116;	Query Match 19.3%; Score 476_5; DB 13; Length 137;
RN [1]	Best Local Similarity 60.2%; Pred. No. 7.3e-28;
SEQUENCE FROM N.A.	Matches 103; Conservative 12; Mismatches 21; Indels 35; Gaps 5;
RC Sprague-Dawley;	
RC Garges P.L.; Meyer R.A. Jr.; Brown C.A.; Price D. K.;	
RT "Desert hedgehog in the rat."	
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.	
EMBL; AF14826; ADD1927.1; -.	
HSSP; Q6226; 1VHH.	
DR GO; GO:0007267; P: cell-cell signaling; IEA.	
DR GO; GO:0007275; P: development; IEA.	
DR InterPro; IPR006945; Hedgehog_DD_Pept.	
DR InterPro; IPR000320; HH_signal.	
DR InterPro; IPR001657; Peptidase_C46.	
DR Pfam; PF01085; HH_signal_1.	
DR PRINTS; PR00632; SONICHHOG.	
Db 94 ----DGA----IPFA----TTGTTGHWYSSRLYHGSWVLDGDAHLPLGMVAPAS 137	

RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AU33288; CDB6201; 1;

DR InterPro; IPR009045; Hedgehog/DD_Pept.

FT NON-TER 1 74 ;

SQ SEQUENCE 74 AA; 7839 MW; C5A80F6C2A5F2B45 CRC64;

Query Match 9.9%; Score 245; DB 6; Length 74;

Best Local Similarity 60.8%; Pred. No. 5.3e-11;

Matches 45; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

Qy 169 GFDWVYYESEKAIHCSVKAENSAVAKSGCGFPGSATVHLBQGTTKLVKDLSPODRVLAA 228

Db 1 GFDWVYYESEKAIHCSVKSSEHSAAKTGGCFPAGAQVRLESVARVSLAVRSDRVLMG 60

Qy 229 DQGRLLYSDFDFFL 242

Db 61 EDGNPNTPSDVLIPL 74

RESULT 37

Q9TX33 PRELIMINARY; PRT; 49 AA.

AC Q9TX33; ID Q9TX33; PRELIMINARY; PRT; 54 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DB Hedgehog_HH protein homology (Fragment).

DE Hirudo medicinalis (Medicinal leech).

OS Arynchobdellida; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

OC Hirudinida; Hirudiniformes; Hirudinidae; Hirudo.

OX NCBI_TaxID=6421;

RN [1]

RP SEQUENCE FROM N.A. PRELIMINARY; PRT; 54 AA.

RX MEDLINE=93236997; PubMed=7720571;

RA Chang D.T., Lopez A., von Kesseler D.P., Chiang C., Simandi B.K., Zhao R., Seldin M.F., Beachy P.A.; Beachy P.A.; Simandi B.K., "Products, generic linkage and limb patterning activity of a murine hedgehog gene.", Development 120:3339-3353 (1994).

DR HSSP; Q62226; 1VHH.

DR GO; GO:0007267; P:cell-cell signaling; IEA.

DR GO; GO:0007275; P:development; IEA.

DR InterPro; IPR009045; Hedgehog/DD_Pept.

DR InterPro; IPR00320; HH_signal_1.

DR InterPro; IPR001657; Peptide_disease_C46.

DR Pfam; PF01085; HH_signal_1.

DR PRINTS; PRO00632; SONICHHOG.

DR ProdDom; PD003042; HH_signal_1.

FT NON-TER 49 ;

SQ SEQUENCE 49 AA; 5580 MW; 4A8ECF56DEC99013 CRC64;

RESULT 38

Q9TX31 PRELIMINARY; PRT; 49 AA.

AC Q9TX31; ID Q9TX31; PRELIMINARY; PRT; 54 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DB Tribolium castaneum (Red flour beetle).

DE Tribolium castaneum (Red flour beetle).

OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Coleoptera; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Q9ESH3

Query Match 9.6%; Score 237; DB 5; Length 49;

Best Local Similarity 89.8%; Pred. No. 1.2e-10;

Matches 44; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 119 GYKLRYTEGWDGHHSBESTHYEGRAVDITTSDRRSKYGMALARLAVE 167

Db 1 GYKLRYTEGWDGHHSBESTHYEGRAVDITTSDRRSKYGMALARLAVE 49

RESULT 39

Q9TX33 PRELIMINARY; PRT; 54 AA.

AC Q9TX33; ID Q9TX33; PRELIMINARY; PRT; 54 AA.

DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DB Sonic hedgehog (Fragment).

GN Coturnix coturnix (Common quail).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Coraciiformes; Coracinae.

OC NCBI_TaxID=9091;

RN [1]

RP SEQUENCE FROM N.A. PRELIMINARY; PRT; 54 AA.

RX MEDLINE=98167903; PubMed=9435297;

RA Bortzki A.G., Mendham L., Emerson C.P. Jr.; "Control of sonic patterning by sonic hedgehog and its downstream signal response genes.", Development 125:777-780 (1998).

DR BMBL; AF022881; AB80484; -;

DR GO; GO:0007257; P:cell-cell signaling; IEA.

DR InterPro; IPR000320; HH_signal_1.

DR Pfam; PF01085; HH_signal_1.

DR ProdDom; PD003042; HH_signal_1.

FT NON-TER 54 ;

SQ SEQUENCE 54 AA; 5993 MW; D359B0B9DD44E1E9 CRC64;

Query Match 7.6%; Score 188; DB 13; Length 54;

Best Local Similarity 68.6%; Pred. No. 6e-07;

Matches 35; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MILLARCHLVLYSSLLVCGLACGPGRGFGRHPKKLTPPLAYKQFIPNV 51

Db 4 MMMLTRILVGFCIALVSSGLTCGPGRGIGRKPRKLTPLAYRXPFLQL 54

RESULT 40

Q9E8H3	PRELIMINARY;	PRT;	125 AA.
Q9E8H3;			
AC GO:0007267; P:cell-cell signaling; IEA.	DR GO;		
DD GO:0007275; P:development; IEA.	DR GO;		
DT InterPro; IPR00945; Hedgehog_DD_pept.	DR InterPro; IPR000320; HH signal.		
DT InterPro; IPR001657; Peptidase_C46.	DR InterPro; IPR001657; HH_signal; 1.		
DT PRAM; PF01045; HH_signal; 1.	DR PRAM; PF01045; HH_signal; 1.		
DT PRINTS; PRO0632; SONICHHOG.	DR PRINTS; PRO0632; SONICHHOG.		
DE PRODOM; PDO03042; HH_signal; 1.	DR PRODOM; PDO03042; HH_signal; 1.		
DR NON_TER 1	FT NON_TER 1		
RN 48	ET RN 48		
SQ 5347 MW;	SQ 5347 MW;		
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.		
STRAIN-Sprague-Dawley;	STRAIN-Bristol N2;		
RA D.A., Hasserjian R.P., Robson H., van Noorden S., Siebler T.,	RA Wilson R., Ainscough R., Andersen K., Baynes C., Berks M., Baynes C., Berks M., Coulson A.,		
RA Shalev S.M., Williams G.R.; Hedging hint N.	RA Burron J., Connell M., Copsey T., Cooper J., Coulson A.,		
RA "Hypothyroidism causes growth retardation by disrupting chondrocyte differentiation, matrix deposition and endochondral ossification in epiphyseal growth plate cartilage";	RA Bonfield J., Burron J., Connell M., Copsey T., Cooper J., Coulson A.,		
RT submitted (AUG-1999) to the ENB/GenBank/DDJB databases.	RA Bonfield J., Burron J., Connell M., Copsey T., Cooper J., Coulson A.,		
EMBL; AF172209; AG09197.1; -.	RA Bonfield J., Burron J., Connell M., Copsey T., Cooper J., Coulson A.,		
MEROPS; C46_003; -.	RA Bonfield J., Burron J., Connell M., Copsey T., Cooper J., Coulson A.,		
GO; GO:0007154; P:cell communication; IEA.	RA Bonfield J., Burron J., Connell M., Copsey T., Cooper J., Coulson A.,		
DR GO; GO:0007275; P:development; IEA.	RA Bonfield J., Burron J., Connell M., Copsey T., Cooper J., Coulson A.,		
DR GO; GO:0006508; P:protein binding; IEA.	RA Bonfield J., Burron J., Connell M., Copsey T., Cooper J., Coulson A.,		
DR InterPro; IPR00587; Hedging hint N.	RA Bonfield J., Burron J., Connell M., Copsey T., Cooper J., Coulson A.,		
DR InterPro; IPR001657; Peptidase_C46.	RA Bonfield J., Burron J., Connell M., Copsey T., Cooper J., Coulson A.,		
DR InterPro; IPR001767; Pept_C46_Hint.	RA Bonfield J., Burron J., Connell M., Copsey T., Cooper J., Coulson A.,		
DR Pfam; PF01049; Hint; 1.	RA Bonfield J., Burron J., Connell M., Copsey T., Cooper J., Coulson A.,		
DR PRINTS; PRO0632; SONICHHOG.	RA Bonfield J., Burron J., Connell M., Copsey T., Cooper J., Coulson A.,		
SMART; SM00306; HintN; 1.	RA Bonfield J., Burron J., Connell M., Copsey T., Cooper J., Coulson A.,		
FT NON_TER 125	FT NON_TER 125		
SQ SEQUENCE 125 AA;	FT NON_TER 125 AA;		
SEQUENCE 125 AA;	FT NON_TER 125 AA;		
Query Match 7.6%; Score 187.5; DB 11; Length 125;	Query Match 7.6%; Score 187.5; DB 11; Length 125;		
Best Local Similarity 34.9%; Pred. No. 2.1e-06;	Best Local Similarity 34.9%; Pred. No. 2.1e-06;		
Matches 51; Conservative 18; Mismatches 42; Indels 35; Gaps 4;	Matches 51; Conservative 18; Mismatches 42; Indels 35; Gaps 4;		
Qy 21.8 LSPGDRVLAADDQGRLLYSDFELTFLDGDAKKFVYVTEPREPRLITAAHLILFVAPH 277	Qy 21.8 LSPGDRVLAADDQGRLLYSDFELTFLDGDAKKFVYVTEPREPRLITAAHLILFVAPH 277		
Db 7 VKEPGDRVLAAMDGEQNPFTSDVLFIDRPNLRAFOVTEQDPPRLATPAHLFIADN 66	Db 7 VKEPGDRVLAAMDGEQNPFTSDVLFIDRPNLRAFOVTEQDPPRLATPAHLFIADN 66		
DB 27.8 NDSATGEBEASSSGGGPSSGGALGPRAFLASRVRPGQBYVVAERDDRLPAAVHSVTI 337	DB 27.8 NDSATGEBEASSSGGGPSSGGALGPRAFLASRVRPGQBYVVAERDDRLPAAVHSVTI 337		
Qy 67 H----AEBAARF-----RATFANTHQPGQYLV-----AGYQASSL 98	Qy 67 H----AEBAARF-----RATFANTHQPGQYLV-----AGYQASSL 98		
DB 33.8 -----BEAAAGAYAPTAQGQHLL 356	DB 33.8 -----BEAAAGAYAPTAQGQHLL 356		
Qy 99 LGWQPSPTWPLGPMLPSRSMTLV 124	Qy 99 LGWQPSPTWPLGPMLPSRSMTLV 124		
DB	DB		
RESULT 41	RESULT 41		
Q9TX32	PRELIMINARY;	PRT;	48 AA.
ID Q9TX32;	SEQUENCE FROM N.A.		
AC GO:0007154; P:cell communication; IEA.	RC STRAIN-Bristol N2;		
DD GO:0007275; P:development; IEA.	RA Nhan, M. Hawkins J.;		
DT "The sequence of <i>C. elegans</i> cosmid ZK377;"	RT "The sequence of <i>C. elegans</i> cosmid ZK377;"		
DT Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.	RT Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.		
DT [3]	RT [3]		
DR	DR		
RP	RP		
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.		
RC STRAIN-Bristol N2;	RC STRAIN-Bristol N2;		
RA Nhan, M. Hawkins J.;	RA Nhan, M. Hawkins J.;		
RT "The sequence of <i>C. elegans</i> cosmid ZK377;"	RT "The sequence of <i>C. elegans</i> cosmid ZK377;"		
RT Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.	RT Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.		
RN	RN		
RP	RP		
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.		
RC STRAIN-Bristol N2;	RC STRAIN-Bristol N2;		
RA Waterston R.	RA Waterston R.		
RT	RT		
RL	RL		
DR	DR		
PIR; T29350; T29355;	PIR; T29350; T29355;		
DR	DR		
RP	RP		
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.		
RC STRAIN-Bristol N2;	RC STRAIN-Bristol N2;		
RA Chang D.T., Lopez A., von Kesseler D.P., Chiang C., Simandl B.K., Zhao R., Selain M.F., Fallon J.F., Beachy P.A.,	RA Chang D.T., Lopez A., von Kesseler D.P., Chiang C., Simandl B.K., Zhao R., Selain M.F., Fallon J.F., Beachy P.A.,		
RT "Products, genetic linkage and limb patterning activity of a murine hedgehog gene.".	RT "Products, genetic linkage and limb patterning activity of a murine hedgehog gene.".		
DR	DR		
TPR-Pro; IPR003586; Hedgehog_hinc.	TPR-Pro; IPR003586; Hedgehog_hinc.		
[1]	[1]		
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.		
MDLINE: 95236997; PubMed: 7720571;	MDLINE: 95236997; PubMed: 7720571;		
Chang D.T., Lopez A., von Kesseler D.P., Chiang C., Simandl B.K., Zhao R., Selain M.F., Fallon J.F., Beachy P.A.,	Chang D.T., Lopez A., von Kesseler D.P., Chiang C., Simandl B.K., Zhao R., Selain M.F., Fallon J.F., Beachy P.A.,		
RT "Products, genetic linkage and limb patterning activity of a murine hedgehog gene.".	RT "Products, genetic linkage and limb patterning activity of a murine hedgehog gene.".		

DR	InterPro; IPR03587; Hedgehog_hint_N.	Query Match 6.0%; Score 149; DB 5; Length 1207;
DR	InterPro; IPR00611; Intein_S.	Best Local Similarity 26.5%; Pred. No. 0.039.
DR	InterPro; IPR001657; Peptidase_C46.	Matches 37; Mismatches 82; Indels 36; Gaps 9;
DR	InterPro; IPR01767; Pept_C46_Hint.	Matches 56; Conservative 37; Mismatches 56; Indels 82; Indels 36; Gaps 9;
Pfam; PF01079; Hint_1.		
DR	PRINTS; PRO00332; SONICHHOG.	
DR	SMART; SM00305; HintC_1.	
DR	SMART; SM00306; HintN_1.	
DR	PROSITE; PS00517; INTEIN_N_TER; 1.	
SQ	SEQUENCE 615 AA; 68615 MW; CC023FF1700ED869	CRC64;
Query Match 6.5%; Score 159.5; DB 5; Length 615;		
Best Local Similarity 28.3%; Pred. No. 0.0025;		
Matches 52; Conservative 33; Mismatches 74; Indels 25; Gaps 7;		
Db	198 CFPGSATVHLEQGGTKVLVDLSPGDRVLAADDQGRLLYASDFTFLDRDGAKKVYVYIET 257	
Qy	416 CFSGMDEVETD-GIRKMDLKGDKVLSM-DEAFVTVSPIVFLHKRDEELIAEFLNLTE 473	
Qy	258 REPRERLLTAAHHLFVAPHNDSATGEPEASSGSGPPSGGALGPRAFLFASRVRFQGRVY 317	
Db	474 ANGHS-I-KLTDNHLLIV--SDCRTRRS-----DIRLVAKREVNDDC-HV 514	
Qy	318 VAERGDRLRILPAAVHSSVITSEEAGAYAPLTAQGTLINRVLASCYAWIEEHSAWAHF 377	
Db	515 TTD---SNVYTKKYSKISKVIE-TGIYSSPLITSTGDIIVNRVLASCHSNLALKSQQTFF 570	
Qy	378 APPR 381	
Db	571 SLYK 574	
RESULT 43		
Q21535	PRELIMINARY; PRT; 1207 AA.	
[1]	SEQUENCE FROM N.A.	
Q21535; Q22872; PRELIMINARY; PRT; 790 AA.		
DR	SEQUENCE FROM N.A.	
RC	STAINLINE=2;	
RC	MEDLINE=96291396; PubMed=86896684;	
RX		
DT	01-NOV-1996 (TREMBLrel. 01, Created)	
DT	01-OCT-2003 (TREMBLrel. 10, Last sequence update)	
RA	Porter J.A., Ekker S.C., Park W.-J., von Kesseler D.P., Young K.E., Chen C.-H., Ma Y., Woods A.S., Cotter R.J., Koornin E.V., Beachy P.A.; "Hedgehog patterning activity: role of a lipophilic modification mediated by the carboxy-terminal autoprocessing domain.", Call 86(21-34)(1998)	
RT		
RT	DR GO:000288; F:Peptide activity; IEA.	
RT	DR GO:0007154; P:Cell communication; IEA.	
RT	DR GO:0007275; P:Development; IEA.	
RT	DR GO:0016339; P:Protein splicing; IEA.	
RT	DR GO:0006508; P:Proteolysis and peptidolysis; IEA.	
RT	DR InterPro; IPK0784; DUP398; DUP398.	
RT	DR InterPro; IPK03586; Hedgehog_hint_N.	
RT	DR InterPro; IPK03587; Hedgehog_hint_N.	
RT	DR InterPro; IPK06141; IntIn_S.	
RT	DR InterPro; IPK01651; Peptidase_C46.	
FT	NON_TER 1 1	
SQ	SEQUENCE 790 AA; 84661 MW; 70278E71A65C89BB CRC64;	
DR	WormPeP; CE0236; Hint_1.	
DR	GO; GO:0008233; F:Peptidase activity; IEA.	
DR	GO; GO:0007154; P:cell communication; IEA.	
DR	GO; GO:0007275; P:development; IEA.	
DR	GO; GO:0016539; P:protein splicing; IEA.	
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.	
DR	InterPro; IPK03586; Hedgehog_hint_N.	
DR	InterPro; IPK03587; Hedgehog_hint_N.	
DR	InterPro; IPK06141; IntIn_S.	
DR	InterPro; IPK01651; Peptidase_C46.	
DR	Pfam; PF01079; Hint_1.	
PRINTS; PRO0032; SONICHHOG.		
SMART; SM00305; Hint_1.		
SMART; SM00306; HintN_1.		
PROSITE; PS05081; INTEIN_N_TER; 1.		
SEQUENCE 1207 AA; 12107 MW; E548E943202C37AA CRC64;		
SQ	189 NSVAAKSGGCCPGSATVHLEQGGTKVLSPGDRVIAADDQGRLLYSDFLTLDRDGA 248	
Query Match 5.6%; Score 138.5; DB 5; Length 790;		
Best Local Similarity 24.4%; Pred. No. 0.13;		
Matches 50; Conservative 38; Mismatches 68; Indels 49; Gaps 8;		
Db	576 SALVATGACFSLDTWV-TPTGKRMQIDGYVLTADLE-KTYFFPITLMIHREPEK 633	
Qy	249 KKVFYVIEREPBRLLTAAHHLF-----VAPHNDSATGPEASSGGPBS 295	

Db	634	VQEFLTIMT-EYGLTRITTSRHFMRNKCGKSYFQYIKMLPHD----GE-----	677	OC Rhabditida; Pelioderinae; Caenorhabditis.
Qy	296	GGALGPRLAFASRYPGQRGTYVVAERDGDRRLPAAVHSTVLSEAAAGAYAPLTAQGTIL	355	OX RN [1]
Db	678	-----AFASDLEVGDCVVLYKGKTYQQKIEITRSV-----RTGYSPLTNNGRI	725	RP SEQUENCE FROM N.A. STRAIN=Bristol N2; MEDLINE=99069613; PubMed=9851916;
Qy	356	INRVLASCYAIEEHS-----WAH 374	1	RA "Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology."; RT Science 282:2012-2018(1998).
Db	726	VNDMLASCYSEIQQNTLQTTFFWAY 750	1	RL SCIENCE 282:2012-2018(1998).
RESULT 45				
Q21835	PRELIMINARY;	PRT; 1137 AA.		RN SEQUENCE FROM N.A. RC STRAIN=Bristol N2;
ID Q21835;				RC White S; RA Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
AC 001-NOV-1996	(TREMBLrel. 01, Created)			RL DR EMBL; Z68008; CAD9166.1; -.
DT 01-OCT-2003	(TREMBLrel. 25, Last sequence update)			KW Homeobox.
DT 01-OCT-2003	(TREMBLrel. 25, Last annotation update)			SQ SEQUENCE 1160 AA; 125411 MW; 77894C7C7E4A4B11 CRC64;
DE C. elegans GRD-1 protein (Corresponding sequence R08B4.1a);				Query Match 5.6%; Score 138.5; DB 5; Length 1160;
GN GRD-1.				Best Local Similarity 24.4%; Pred. No. 0.22;
OS Caenorhabditis elegans.				Matches 50; Conservative 38; Mismatches 68; Indels 8; Gaps 8;
RA Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;				Qy 189 NSVAAKSGGCPGSAVTHLEQGGTKLVKDLSFGDRVLAADDQGRLLYSDFLTFRDDGA 248
Rhhabditidae; Pelioderinae; Caenorhabditis.				Db 946 SALVAATGACSLDTMV-TTPGKRMQDIDGYVLTADLE-KTYFTPTLWIRPEK 1003
NCBI_TAXID=6239;				Qy 249 KKVFFYVETREPRLTLLTAHLLF-----VAPHNDSATGEPEAASSGGPPS 295
SEQUENCE FROM N.A.				Db 1004 VQEFLTIMT-EYGKTRITSRHEMYNKKCGKSYFQYIKMLPHD----GB----- 1047
STRAIN=Bristol N2;				Qy 296 GGALGPALFAASRVPRGQRTYVVAERDGDRRLPAAVHSTVLSEAAAGAYAPLTAQGTIL 355
MEDLINE=99069613; PubMed=9851916;				Db 1048 -----AIFASDLEYGDCVVLYKGKTYQQKIEITRSV-----RTGYSPLTNNGRII 1095
none;				Qy 356 INRVLASCYAIEEHS-----WAH 374
"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology."; RT Science 282:2012-2018(1998).				Db 1056 VNDMLASCYSEIQQNTLQTTFFWAY 1120
RL SCIENCE 282:2012-2018(1998).				
Q21835	SEQUENCE FROM N.A.			
Q21835;	SEQUENCE FROM N.A.			
AC 001-NOV-1996	(TREMBLrel. 01, Created)			
DT 01-OCT-2003	(TREMBLrel. 25, Last sequence update)			
DT 01-OCT-2003	(TREMBLrel. 25, Last annotation update)			
DE C. elegans GRD-1 protein (Corresponding sequence R08B4.1a).				
GN GRD-1.				
OS Caenorhabditis elegans.				
RA Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;				
Rhhabditidae; Pelioderinae; Caenorhabditis.				
NCBI_TAXID=6239;				
SEQUENCE FROM N.A.				
STRAIN=Bristol N2;				
MEDLINE=99069613; PubMed=9851916;				
none;				
"Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology."; RT Science 282:2012-2018(1998).				
RL SCIENCE 282:2012-2018(1998).				
RESULT 46				
Q7YXCB	PRELIMINARY;	PRT; 1160 AA.		RN SEQUENCE FROM N.A. RC STRAIN=Bristol N2;
Q7YXCB;				RA Basham V.M.;
AC 001-OCT-2003	(TREMBLrel. 25, Created)			RL Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
DT 01-OCT-2003	(TREMBLrel. 25, Last sequence update)			DR EMBL; Z81142; CAB03502; -.
DT 01-OCT-2003	(TREMBLrel. 25, Last annotation update)			SQ SEQUENCE 481 AA; 54512 MW; 4CE81DB2D0A9A962 CRC64;
DE C. elegans GRD-1 protein (Corresponding sequence R08B4.1b).				Query Match 5.4%; Score 134.5; DB 5; Length 481;
GN Caenorhabditis elegans.				Best Local Similarity 24.3%; Pred. No. 0.13;
RA "Genome sequence of the nematode <i>C.elegans</i> : A platform for investigating biology."; RT Science 282:2012-2018(1998).				Matches 34; Conservative 34; Mismatches 67; Indels 39; Gaps 6;
RL SCIENCE 282:2012-2018(1998).				

RT malformation.";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY192802; AA024699.1; JOINED.
 DR EMBL; AY192798; AA024699.1; JOINED.
 DR EMBL; AY192799; AA024699.1; JOINED.
 DR EMBL; AY192800; AA024699.1; JOINED.
 DR EMBL; AY192801; AA024699.1; JOINED.
 GO; GO:0005634; Cnuckles; IEA.
 GO; GO:0003700; F transcription factor activity; IEA.
 DR GO:0006355; P regulation of transcription, DNA-dependent; IEA.
 InterPro; IPR008967; 253 lines.
 InterPro; IPR01699; TF_T-box.
 Pfam; PF00907; T_box; 1.
 SMART; SM00425; TBOX; 1.
 PROSITE; PS01283; TBOX; 1.
 DR PROSITE; PS01264; TBOX; 1.
 DR PROSITE; PS5052; TBOX; 1.
 SQ SEQUENCE 702 AA; 73951 MN; 66ADE7D5531D95A3 CRC64;

Query Match	Score	Length
Best Local Similarity	4.9%	702;
Matches 104; Conservative	21.2%;	Pred. No. 1.8;
36; Mismatches	119;	Indels 232;
Gaps	22;	

Qy 118 PGVKLRVTEGMDEDHHSSESSLHNGRAVDITTSDR-----DRSKYGMALAR 163
 Db 95 PKVTLREAKLWDQ-----FHKLGTENWVTKSGRMPPPEKVRVSGIDKRAKYIIL-- 144

Qy 164 LAVEAGFDWYYYESKAHHGCSVKAENS--VAAKSGGCOPGSATVHLBQGT---- 212
 Db 145 MDIVADD-----CRYKFINSRNNVAGADPENPKRMYTHPSPATGBQWAKP 193

Qy 213 -----KLVKDSL-----PGDRVLAADDGCRLLYSDFELFL----- 242
 Db 194 VAFHKLKLTNNNISDGHGFITLNSMKYQPFHIVANDIKLPYSTRTVVPETDFAV 253

Qy 243 -----DRDGAKVVFYVITERPRERLIITAHLI--FVAPIND 279
 Db 254 TAYQNDKITQLKIDNNPFAKGFRDNGR-----REKKQLTLPSLRYEEHCKPBD 306

Qy 280 SATG-----EPEASSGGGP-----SGGALG 300
 Db 307 GAESDASSCDPAPRPPASPGSAPPPLHRTRADEKCAADSDEPEPLSEBAGPAG 366

Qy 301 -----PRALFASRV--RPGQRVYVAERGD-----RR----- 326
 Db 367 RSPGLDGSPLRTEPERARRSRSPRGKEPAESGDPGLRSHEKEAEARKDDGRK 426

Qy 327 -----LIPAAVHSVTLSBEAG-----AYAPLTAGTQSTILLNRVLAS 362
 Db 427 EAGEGKEPGLAPLVVQTDSASPLGAGLHPGLAFSGSHLHGQQFFGLGACQPLFLHP--- 482

Qy 363 CYAVIEPHSWAHRAPFRLLAHALLAALAPARTDREGDSGGDRGGGGRKVALTAPGA-- 421
 Db 483 -----GQFAMPGFASGAMGMGH-LLASVA-----GGGGGGGG-----PGTAT 520

Qy 422 --DAPGAGATA 430
 Db 521 GJDAGGGLGPA 531

Search completed: March 29, 2004, 18:33:34
 Job time : 53 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 29, 2004, 18:16:03 ; Search time 59 Seconds

Perfect score: 2469 US-09-883-848A-15

Sequence: 1 MILLARCHLVLVSSLVVCS.....GMAVKSSXSRGAGGGAREGA 475

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

Minimum DB Seq length: 0
Maximum DB Seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 150 summaries

Database : A_Geneseq_29Jan04:*

1: GeneseqP1980s:*

2: GeneseqP1990s:*

3: GeneseqP2000s:*

4: GeneseqP2001s:*

5: GeneseqP2002s:*

6: GeneseqP2003as:*

7: GeneseqP2003bs:*

8: GeneseqP2004s:*

Aae021266 Partial h

Aab85738 Human son

Aab85736 Human mut

Aaw48736 Human mut

Aab85086 Mouse son

Aab85084 Mouse son

Aab85082 Mouse son

Aab85080 Mouse son

Aab85078 Mouse son

Aab85076 Mouse son

Aab85074 Mouse son

Aab85072 Mouse son

Aab85070 Mouse son

Aab85068 Mouse son

Aab85066 Mouse son

Aab85064 Mouse son

Aab85062 Mouse son

Aab85060 Mouse son

Aab85058 Mouse son

Aab85056 Mouse son

Aab85054 Mouse son

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Aab85050 Mouse son

Aab85048 Mouse son

Aab85046 Mouse son

Aab85044 Mouse son

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Aab85040 Mouse son

Aab85038 Mouse son

Aab85036 Mouse son

Aab85034 Mouse son

Aab85032 Mouse son

Aab85030 Mouse son

Aab85028 Mouse son

Aab85026 Mouse son

Aab85024 Mouse son

Aab85022 Mouse son

Aab85020 Mouse son

Aab85018 Mouse son

Aab85016 Mouse son

Aab85014 Mouse son

Aab85012 Mouse son

Aab85010 Mouse son

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Aab85002 Mouse son

Aab85000 Mouse son

Aab85018 Mouse son

Aab85016 Mouse son

Aab85014 Mouse son

Aab85012 Mouse son

Aab85010 Mouse son

Aab85008 Mouse son

Aab85006 Mouse son

Aab85004 Mouse son

Aab85002 Mouse son

Aab85000 Mouse son

Aab85018 Mouse son

Aab85016 Mouse son

Aab85014 Mouse son

Aab85012 Mouse son

Aab85010 Mouse son

Aab85008 Mouse son

Aab85006 Mouse son

Aab85004 Mouse son

Aab85002 Mouse son

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Aab85012 Mouse son

Aab85010 Mouse son

Aab85008 Mouse son

Aab85006 Mouse son

Aab85004 Mouse son

Aab85002 Mouse son

Aab85000 Mouse son

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Aab85016 Mouse son

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Aab85012 Mouse son

Aab85010 Mouse son

Aab85008 Mouse son

Aab85006 Mouse son

Aab85004 Mouse son

Aab85002 Mouse son

Aab85000 Mouse son

Aab85018 Mouse son

Aab85016 Mouse son

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Aab85012 Mouse son

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Aab85012 Mouse son

Aab85010 Mouse son

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Aab85006 Mouse son

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Aab85016 Mouse son

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Aab85002 Mouse son

Aab85000 Mouse son

Aab85018 Mouse son

Aab85016 Mouse son

Aab85014 Mouse son

Aab85012 Mouse son

Aab85010 Mouse son

Aab85008 Mouse son

Aab85006 Mouse son

Aab85004 Mouse son

Aab85002 Mouse son

Aab85000 Mouse son

Aab85018 Mouse son

Aab85016 Mouse son

Aab85014 Mouse son

Aab85012 Mouse son

Aab85010 Mouse son

Aab85008 Mouse son

Aab85006 Mouse son

Aab85004 Mouse son

Aab85002 Mouse son

Aab85000 Mouse son

Aab85018 Mouse son

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Aab85008 Mouse son

Aab85006 Mouse son

Aab85004 Mouse son

Aab85002 Mouse son

Aab85000 Mouse son

Aab85018 Mouse son

Aab85016 Mouse son

Aab85014 Mouse son

Aab85012 Mouse son

Aab85010 Mouse son

Aab85008 Mouse son

Aab85006 Mouse son

Aab85004 Mouse son

Aab85002 Mouse son

Aab85000 Mouse son

Aab85018 Mouse son

Aab85016 Mouse son

Aab85014 Mouse son

Aab85012 Mouse son

Aab85010 Mouse son

Aab85008 Mouse son

Aab85006 Mouse son

Aab85004 Mouse son

Aab85002 Mouse son

Aab85000 Mouse son

Aab85018 Mouse son

Aab85016 Mouse son

Aab85014 Mouse son

Aab85012 Mouse son

Aab85010 Mouse son

Aab85008 Mouse son

Aab85006 Mouse son

Aab85004 Mouse son

Aab85002 Mouse son

Aab85000 Mouse son

Aab85018 Mouse son

Aab85016 Mouse son

Aab85014 Mouse son

Aab85012 Mouse son

Aab85010 Mouse son

Aab85008 Mouse son

Aab85006 Mouse son

Aab85004 Mouse son

Aab85002 Mouse son

Aab85000 Mouse son

Aab85018 Mouse son

Aab85016 Mouse son

Aab85014 Mouse son

Aab85012 Mouse son

Aab85010 Mouse son

Aab85008 Mouse son

Aab85006 Mouse son

Aab85004 Mouse son

Aab85002 Mouse son

Aab85000 Mouse son

Aab85018 Mouse son

Aab85016 Mouse son

Aab85014 Mouse son

Aab85012 Mouse son

Aab85010 Mouse son

Aab85008 Mouse son

Aab85006 Mouse son

Aab85004 Mouse son

Aab85002 Mouse son

Aab85000 Mouse son

Aab85018 Mouse son

Aab85016 Mouse son

Aab85014 Mouse son

Aab85012 Mouse son

Aab85010 Mouse son

Aab85008 Mouse son

Aab85006 Mouse son

Aab85004 Mouse son

Aab85002 Mouse son

Aab85000 Mouse son

Aab85018 Mouse son

Aab85016 Mouse son

Aab85014 Mouse son

Aab85012 Mouse son

Aab85010 Mouse son

Aab85008 Mouse son

ATTACHMENT

QY	241	FLDRDGAKKVYVIETREPERRLILTAHILFVAPHNDSATGEPEAASSGSPGGALG	300	SU LT 1
Db	241	FLDRDGAKKVYVIETREPERRLILTAHILFVAPHNDSATGEPEAASSGSPGGALG	300	R773A1
QY	301	PRALFAASRVPGQRVYVAERGDGRLLPAVHSVYLSEAAAGAYAALPAAQGTILINRVL	360	AAR773A1 standard; protein; 475 AA.
Db	301	PRALFAASRVPGQRVYVAERGDGRLLPAVHSVYLSEAAAGAYAALPAAQGTILINRVL	360	14-MAR-1996 (first entry)
QY	361	ASCYAVTEEHSAWAHRAAPFRLAHALLAALAPARTRGCGSGCDRGCGGGRVLTAPGA	420	Human sonic hedgehog protein.
Db	361	ASCYAVTEEHSAWAHRAAPFRLAHALLAALAPARTRGCGSGCDRGCGGGRVLTAPGA	420	Human; sonic hedgehog Protein; probe; primer; diagnostic; nervous system disorder; gene therapy; antibody.
QY	421	ADAPGAGATAGTHWYSOLIYQIGTWLIDSEAHPLGMAYKSSXSRGAGGAREGA	475	Homo sapiens.
Db	421	ADAPGAGATAGTHWYSOLIYQIGTWLIDSEAHPLGMAYKSSXSRGAGGAREGA	475	Key

XX The present sequence represents human Sonic hedgehog protein Shh. The invention relates to a method for modulating the growth state of an epithelial cell by ectopically contacting the epithelial cell, in vitro or in vivo, with a hedgehog therapeutic (i.e. a hedgehog polypeptide or gene therapy construct) or ptc therapeutic (i.e. a small organic molecule that mimics the effect of hedgehog proteins on patched signalling, or activates or potentiates patched signalling) in an amount effective to alter the rate of proliferation of the epithelial cell. The hedgehog therapeutic preferably comprises at least a bioactive extracellular portion of a hedgehog protein (see AAY0584-62), encoded by a vertebrate hedgehog gene (see AAY25617-25), especially a human hedgehog gene.

CC Promotion of proliferation of epithelial cells can be used to control a wound healing process in e.g. burn treatment, skin regeneration, skin grafting, pressure sore treatment, dermal ulcer treatment, post surgery scar reduction or treatment of ulcerative colitis (claimed). It can also be used to induce hair growth for the treatment of alopecia (claimed).

CC Inhibition of the growth of epithelial tissue can be used to treat or prevent hyperplastic or neoplastic conditions, e.g. psoriasis, keratosis, acne, comedogenic lesions, folliculitis and pseudofolliculitis keratoacanthoma, callosities, Darier's disease, keloids, hypertrophic scars, or autoimmune disorders, e.g. aphthous ulcers, pemphigus vulgaris, pemphigus foliaceus, pemphigus vegetans, pemphigus erythematosus, epidermolysis, lupus lesions, desquamative lesions or carcinomas. The methods can also be used to counteract the effects of ageing on skin

XX Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 2_1e-217; Indels 0; Gaps 0;
Matches 475; Conservative 0; Mismatches 0;

Qy 1 MIILARCCLLIVSSLLIVSGLACGPGRGFGKRRHPKKLTPLAYKOFIPNVAEKTIGASG 60
Db 1 MIILARCCLLIVSSLLIVSGLACGPGRGFGKRRHPKKLTPLAYKOFIPNVAEKTIGASG 60
Qy 61 RYEGRKISRSNERFKELTIPYNPDPDIFKDENTGADRINTQRCKDKNLALAISVMNQPGV 120
Db 61 RYEGRKISRSNERFKELTIPYNPDPDIFKDENTGADRINTQRCKDKNLALAISVMNQPGV 120
Qy 121 KLRVTEGMDGHSESHYEGRAVDTTSDRSKYGMMLARAVAEAGFDVYVYESKAH 180
Db 121 KLRVTEGMDGHSESHYEGRAVDTTSDRSKYGMMLARAVAEAGFDVYVYESKAH 180
Qy 181 IHCSYKAENSVAAKSGGGCPGSATVHLEGGTILVKDLSPGDRVLADDQGRLLYSDFL 240
Db 181 IHCSYKAENSVAASGGCCPGSATVHLEGGTILVKDLSPGDRVLADDQGRLLYSDFL 240
Qy 241 FLDRDDGAKKVVYVETTRPRERILLTAHLLVAPHDNSATGEPEASSGSPPSGCALG 300
Db 241 FLDRDDGAKKVVYVETTRPRERILLTAHLLVAPHDNSATGEPEASSGSPPSGCALG 300
Qy 301 PRAFASRTRPQGTYVVERGDGRRLIIPAVHSVTSEAAAYAPATQAQGTILNRL 360
Db 301 PRAFASRTRPQGTYVVERGDGRRLIIPAVHSVTSEAAAYAPATQAQGTILNRL 360
Qy 361 ASCYAVIEEHSAWAHRAFAFRLLAHTAALAPARTDRCGDGGDGRGCGGGRVALAPGA 420
Db 361 ASCYAVIEEHSAWAHRAFAFRLLAHTAALAPARTDRCGDGGDGRGCGGGRVALAPGA 420
Qy 421 ADAPGAGATAGIHWYSQLIQIGTMWLDSEALHPLGMWKSXSRGAGGAREGA 475
Db 421 ADAPGAGATAGIHWYSQLIQIGTMWLDSEALHPLGMWKSXSRGAGGAREGA 475

Qy 421 ADAPGAGATAGIHWYSQLIQIGTMWLDSEALHPLGMWKSXSRGAGGAREGA 475
Db 421 ADAPGAGATAGIHWYSQLIQIGTMWLDSEALHPLGMWKSXSRGAGGAREGA 475
Qy 121 KLRVTEGMDGHSESHYEGRAVDTTSDRSKYGMMLARAVAEAGFDVYVYESKAH 180
Db 121 KLRVTEGMDGHSESHYEGRAVDTTSDRSKYGMMLARAVAEAGFDVYVYESKAH 180

RESULT 4
AAW97770 ID AAW97770 standard; Protein: 475 AA.
AC AAW97770; XX 21-MAY-1999 (first entry)

DE Human Sonic hedgehog (Shh) protein.
XX Sonic hedgehog; Shh protein; human; dopaminergic; GABA-nergic;
KW ptc therapeutic; patched; signal transduction; Parkinson's disease;
KW Huntington's disease; amyotrophic lateral sclerosis; cerebral ischaemia;
KW hypoxia; neuroprotective; therapy.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 463 /note= "encoded by NNN"
XX PN WO9904775-A2.
XX PD 04-FEB-1999.
XX PP 24-JUL-1998; 98WO-US015419.
XX PR 24-JUL-1997; 97US-00900220.
XX PA (ONTO-) ONTOGENY INC.
XX PI Miao N, Wang M, Mahanthappa NK, Pang K;
XX DR WPI; 1999-142578/12.
XX DR N-PSDB; AAX0276.
XX Disclosure; Page 93-95; 138pp; English.
XX PT Increasing the survival of neuronal, dopaminergic and GABA-nergic cells -
PT by using a ptc therapeutic such as a protein kinase inhibitor, or an
PT agent derived from hedgehog polypeptides, useful in the treatment of
PT Parkinson's disease.
XX PS Disclosure; Page 93-95; 138pp; English.
XX CC This polypeptide is human Shh. Sonic hedgehog protein. The invention is based on the finding that hedgehog proteins are useful as protective agents in the treatment and prophylaxis of neurodegenerative disorders resulting from the loss of dopaminergic and/or GABA-nergic neurons, or the general loss of tissue from the substantia nigra. Exemplary disorders include Parkinson's disease, Huntington's disease (both claimed), amyotrophic lateral sclerosis and cerebral ischaemia. The invention relates to hedgehog therapeutics (i.e. hedgehog polypeptides and gene therapy constructs e.g. constructs encoding recombinant hedgehog polypeptides and trans-activation constructs for altering hedgehog gene regulatory sequences) and ptc therapeutics (i.e. agents which mimic the effect of naturally occurring hedgehog proteins on patched signalling) that are effective in both human and animal subjects. Human Ihh and Dhh polypeptides (see AAW97763-64) are preferred. The products can also be used for the maintenance of differentiated neurons in cultures, and to enhance the implantation of such neuronal cells in an animal. They can be used to prevent or treat neurodegenerative conditions arising from the use of certain drugs, and/or treatment of hypoxia, e.g. as a neuroprotective agent.
XX SQ Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 2_1e-217; Mismatches 0; Indels 0; Gaps 0;
Matches 475; Conservative 0; Mismatches 0;

Qy 1 MILLARCCLLIVSSLLIVSGLACGPGRGFGKRRHPKKLTPLAYKOFIPNVAEKTIGASG 60
Db 1 MILLARCCLLIVSSLLIVSGLACGPGRGFGKRRHPKKLTPLAYKOFIPNVAEKTIGASG 60
Qy 61 RYEGRKISRSNERFKELTIPYNPDPDIFKDENTGADRINTQRCKDKNLALAISVMNQPGV 120
Db 61 RYEGRKISRSNERFKELTIPYNPDPDIFKDENTGADRINTQRCKDKNLALAISVMNQPGV 120
Qy 121 KLRVTEGMDGHSESHYEGRAVDTTSDRSKYGMMLARAVAEAGFDVYVYESKAH 180
Db 121 KLRVTEGMDGHSESHYEGRAVDTTSDRSKYGMMLARAVAEAGFDVYVYESKAH 180
Qy 181 IHCSYKAENSVAAKSGGGCPGSATVHLEGGTILVKDLSPGDRVLADDQGRLLYSDFL 240
Db 181 IHCSYKAENSVAASGGCCPGSATVHLEGGTILVKDLSPGDRVLADDQGRLLYSDFL 240
Qy 241 FLDRDDGAKKVVYVETTRPRERILLTAHLLVAPHDNSATGEPEASSGSPPSGCALG 300
Db 241 FLDRDDGAKKVVYVETTRPRERILLTAHLLVAPHDNSATGEPEASSGSPPSGCALG 300
Qy 301 PRAFASRTRPQGTYVVERGDGRRLIIPAVHSVTSEAAAYAPATQAQGTILNRL 360
Db 301 PRAFASRTRPQGTYVVERGDGRRLIIPAVHSVTSEAAAYAPATQAQGTILNRL 360
Qy 361 ASCYAVIEEHSAWAHRAFAFRLLAHTAALAPARTDRCGDGGDGRGCGGGRVALAPGA 420
Db 361 ASCYAVIEEHSAWAHRAFAFRLLAHTAALAPARTDRCGDGGDGRGCGGGRVALAPGA 420
Qy 421 ADAPGAGATAGIHWYSQLIQIGTMWLDSEALHPLGMWKSXSRGAGGAREGA 475
Db 421 ADAPGAGATAGIHWYSQLIQIGTMWLDSEALHPLGMWKSXSRGAGGAREGA 475
Qy 121 KLRVTEGMDGHSESHYEGRAVDTTSDRSKYGMMLARAVAEAGFDVYVYESKAH 180
Db 121 KLRVTEGMDGHSESHYEGRAVDTTSDRSKYGMMLARAVAEAGFDVYVYESKAH 180

Qy	181	IHC SYKAENSYA AKSGGCFPGS ATVHLE QGAT KLVK DLS PGDR VLA ADD QGRLL YSDPLT	240	CC hedgehog polypeptide or ptc therapeutic can inhibit growth of myoblastic- CC derived tissue to provide treatment of 'hyperplastic or neoplastic growth CC of muscle tissue such as in myoblastic sarcoma (also claimed). The CC hedgehog therapeutic preferably comprises at least a bioactive CC extracellular portion of a hedgehog protein (see AAY0510-19) encoded by CC a vertebrate hedgehog gene (see AAX25098-107), especially a human CC hedgehog gene XX
Db	181	IHC SYKAENSYA AKSGGCFPGS ATVHLE QGAT KLVK DLS PGDR VLA ADD QGRLL YSDPLT	240	
Db	241	FLDR DGA KKVY FVY TETR PERL LTA HLL FVAP NHD SAT GE PEASS GSP GSG GAG	300	
Db	241	FLDR DGA KKVY FVY TETR PERL LTA HLL FVAP NHD SAT GE PEASS GSP GSG GAG	300	
Qy	301	PRL AFAS RVR PG QRY VVA ERD GDR LL PAV HST LSE PAAG AYAP LTA OG TL LIN RVL	360	Sequence 475 AA;
Db	301	PRL AFAS RVR PG QRY VVA ERD GDR LL PAV HST LSE PAAG AYAP LTA OG TL LIN RVL	360	Query Match 99.9%; Score 2467; DB 2; Length 475;
Db	361	ASCY ATE EHS WAH RAFA PPLA HLL A ALA PAR TDR GGS DGG DR GGG GRV ALTA QGA	420	Best Local Similarity 100.0%; Pred. No. 2.1e-217; Indels 0; Gaps 0;
Db	361	ASCY ATE EHS WAH RAFA PPLA HLL A ALA PAR TDR GGS DGG DR GGG GRV ALTA QGA	420	Matches 475; Conservative 0; Mismatches 0;
Qy	421	ADAP GAG ATAG IHW YSQL QIG TWIL DSE AL HPL GMAT KSS X SRG AGG GARE GA	475	
Db	421	ADAP GAG ATAG IHW YSQL QIG TWIL DSE AL HPL GMAT KSS X SRG AGG GARE GA	475	
RESULT 5				
AC	AY05515	standard; protein; 475 AA.		
AC	AY05515;			
XX	05-JUL-1999	(first entry)		
DE	Human Sonic hedgehog protein Shh.			
XX	Sonic hedgehog; Shh protein; human hedgehog therapeutic;			
XX	ptc therapeutic; patched; signal transduction; muscle atrophy; cachexia;			
KW	muscular myopathy; myoblastic sarcoma; therapy.			
XX	Misc-difference 463	Location/Qualifiers		
FT	/note= "encoded by NMN"			
XX	W09910004-A2.			
XX	04-MAR-1999.			
XX	28-AUG-1998;	98WO-US017922.		
XX	29-AUG-1997;	97US-0057394P.		
PA	(ONTO-) ONTOGENY INC.			
XX	Bladgen CS, Currie PD, Ingham PW, Hughes SM,			
XX	WPI; 1999-243557/20.			
DR	N-PSDB; AAX25103.			
XX	PT	A new method to regulate muscle growth.		
XX	Disclosure; Page 118-120; 130pp; English.			
XX	The present sequence is human Sonic hedgehog protein Shh. The invention CC relates to a method for modulating the formation and/or maintenance of CC muscle tissue by ecotopically contacting muscle cells, especially muscle CC stem/progenitor cells, in vitro or in vivo, with a hedgehog therapeutic CC (i.e. hedgehog polypeptides and gene therapy constructs) or ptc CC therapeutic (i.e. a small organic molecule that mimics the effect of CC hedgehog proteins on patched signalling, or activates or potentiates or CC patched signalling) in an amount effective to alter the growth state of CC the treated cells. Also claimed is a method for treatment or prevention CC of disorders of, or surgical or cosmetic repair of, such muscle tissues, CC by administering a hedgehog polypeptide or ptc therapeutic. The disorder CC may be muscle atrophy, in particular skeletal muscle atrophy or cardiac CC muscle atrophy, or muscular myopathy (all claimed). The			
PS	XX Human; sonic hedgehog; Shh; neuromuscular disorder; neuropathy; KW Guillain-Barre syndrome; peripheral neuropathy; diabetes; alcoholism; KW chronic inflammatory demyelinating polyneuropathy; CIPD; gene therapy; KW infection; inflammation; hereditary neuropathy; tumour; KW Charcot-Marie-Tooth disease; vacuolitis; lung cancer; kidney disease; KW multiple myeloma; nutritional imbalance; Refsum's disease; Abetalipoproteinemia; KW hypothyroid neuropathy; trauma; Refsum's disease; Metachromatic leukodystrophy; KW Tangier disease; Krabbe's disease; Fabry's disease; CMT; GBS; Dejerine-Sottas syndrome; acute neuropathy; KW Amyotrophic lateral sclerosis; AIS; Miller-Fisher syndrome; amyloidosis; KW Hereditary sensory neuropathy Type II; HSN II; B-cell lymphoma; KW Wallenstrom's Macroglobulinaemia; Chronic Lymphocytic Leukaemia; KW neuroprotective; cytoprotective; patch-mediated signal transduction. XX Homo sapiens.			
OS	XX			

FH	Key	Location/Qualifiers
PT	Misc-difference	453
PT		/label= unknown
PT		/note= "Encoded by NNN"
XX	WO200027422-A2.	
XX	18-MAY-2000.	
XX	08-NOV-1998;	99WO-US026334.
XX	06-NOV-1998;	98US-00187387.
XX	(BIOJ)	BIOPEN INC.
PA	(ONTO-)	ONTOGENY INC.
XX	Galdes A,	Mahanthappa N;
PI		
XX	WPI:	2000-387341/33.
DR		DR-PSDB; AAA30279.
XX	Novel method of preventing deterioration of peripheral nerves, useful for treating or preventing neuropathy, e.g. where associated with diabetes or viral infection, by administering hedgehog or patched agent.	
PS	Page 134-135;	152pp; English.
XX	The present sequence is the partial human sonic hedgehog protein, Shh. This sequence inhibits expression of the patched gene which has been implicated in neuromuscular disorders (neuropathies). This sequence may therefore be used for treating neuromuscular disorders i.e. preventing degradation in function of motor or sensory nerves and protecting peripheral nerve cells under conditions that normally cause neuropathy. A variety of neuromuscular disorders may be treated: Guillain-Barre syndrome, GBS; peripheral neuropathy; diabetic neuropathy; alcohol-induced neuropathy; chronic inflammatory demyelinating polyneuropathy, CIDP; infection-induced neuropathy, including HIV infection; inflammation-induced neuropathy; hereditary neuropathy e.g. Charcot-Marie-Tooth disease (CMT), Familial Amyloidotic neuropathy, Refsum's disease, abetalipoproteinemia, Tangier disease, Krabbe's disease, Metachromatic leukodystrophy, Fabry's disease, Dejerine-Sottas syndrome, Hereditary sensory neuropathy Type II (HSN II) and Amyotrophic lateral sclerosis (ALS); acute neuropathy e.g. Miller-Fisher syndrome; neuropathy caused by vasculitis; neuropathy associated with tumours e.g. lung cancer, multiple myeloma, B-cell lymphoma, Waldenstrom's Macroglobulinaemia, Chronic Lymphocytic Leukemia; neuropathy associated with: amyloidosis, nutritional imbalance, kidney disease, trauma, and hypothyroid, neuropathy. The coding sequence may be used in gene therapy of the above disorders.	
SQ	Sequence 475 AA;	
Query Match	99.9%	Score 2467; DB 3; Length 475;
Best Local Similarity	100.0%	Prod. No. 2.1e-21; Indels 0; Gaps 0;
Matches	475;	Conservative 0; Mismatches 0;
Db	1 MLLARCLIVLSSLLVSGLAAQPGRGPKRHPKLTPLAKQFIPVAEKTIGASG	60
Db	1 MLLARCLIVLSSLLVSGLAAQPGRGPKRHPKLTPLAKQFIPVAEKTIGASG	60
Qy	1 RYEGRKISRSERFKELTPNYPDIFKDENTGADRMTQRCKDNALAIYSMNQPGV	120
Qy	1 RYEGRKISRSERFKELTPNYPDIFKDENTGADRMTQRCKDNALAIYSMNQPGV	120
Db	121 KLRVTEGWDGHSEESLHYEGRADITTSDRSKYGMALAVAEQFDWYESKAH	180
Db	121 KLRVTEGWDGHSEESLHYEGRADITTSDRSKYGMALAVAEQFDWYESKAH	180
Qy	181 IHCSYKAENSAVAKSGCFPGSATVHLEGGTKLVDGPDRVLAADDQGRLLYSFLT	240
Db	181 IHCSYKAENSAVAKSGCFPGSATVHLEGGTKLVDGPDRVLAADDQGRLLYSFLT	240
Qy	241 FLDRDDGAKRKYFYVETTRERERLLTA AHLLVAPHNDSATGPEASSGSFP SGGALG	300
Db	241 FLDRDDGAKRKYFYVETTRERERLLTA AHLLVAPHNDSATGPEASSGSFP SGGALG	300
Qy	301 PRALFA SRTGPQRYVVAERDGDRLPAVHSVTLSSEAAGA YAPLTAQGTILINRVL	360
Db	301 PRALFA SRTGPQRYVVAERDGDRLPAVHSVTLSSEAAGA YAPLTAQGTILINRVL	360
Qy	361 ASCVIA TEEH SWA HRA FAFRLLA LAPARTDRGD SGGDRGGGRV ALTA VGA	420
Db	361 ASCVIA TEEH SWA HRA FAFRLLA LAPARTDRGD SGGDRGGGRV ALTA VGA	420
Qy	421 ADAPGAGATAGIHWYSQQLYQIGTWLDS EALHPLGM AVKSSXSRGAGGAREGA	475
Db	421 ADAPGAGATAGIHWYSQQLYQIGTWLDS EALHPLGM AVKSSXSRGAGGAREGA	475

CC syndrome, allergic rhinitis, asthma, pulmonary fibrosis and primary
 CC pulmonary hypertension. It is also used to control wound healing or other
 CC reparation processes in the lung and augment lung transplantation. The
 CC present sequence is the human sonic hedgehog (Shh) protein, essential for
 CC development of the respiratory system. Hedgehog polypeptides can be used
 CC to control the formation and/or maintenance of the lung tissue
 XX Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 3; Length 475;
 Best Local Similarity 100.0%; Pred. No. 2.1e-21; Indels 0; Gaps 0;

Matches 475; Conservative 0; Mismatches 0; PT Treating disorders involving exotoxicity, e.g. trauma, hypoglycemia,
 PT senile dementia and Korsakoff's disease, by using lipophilic modified
 PT hedgehog polypeptide.

XX Disclosure; Page 157-159; 17app; English.

Db 1 MILLARCLLIVLVSLLIVCSGLACGPGRGFGRKPKKLTPLAYQFIPNVAEKTIGASG 60

Db 1 MILLARCLLIVLVSLLIVCSGLACGPGRGFGRKPKKLTPLAYQFIPNVAEKTIGASG 60

Qy 61 RYEKGTSRNSERFKELTPNPDIFKDENTGADRIMTORCKDKLNALAISYMNNQPGV 120

Db 61 RYEKGTSRNSERFKELTPNPDIFKDENTGADRIMTORCKDKLNALAISYMNNQPGV 120

Qy 121 KLRVTEGMDWEIGHREBESLVEYEGRAVDITTSDRDKTMLAVEGDFDWTYYESKAH 180

Db 121 KLRVTEGMDWEIGHREBESLVEYEGRAVDITTSDRDKTMLAVEGDFDWTYYESKAH 180

Qy 181 IHCSYKAENSYAAKSGCFPSOSATVHLDQGRLLYSDELT 240

Db 181 IHCSYKAENSYAAKSGCFPSOSATVHLDQGRLLYSDELT 240

Qy 241 FLDRDGAKKVFYVIEPRELLTAHILLFVAPHNSATGEPEASSGSPPSGGALG 300

Db 241 FLDRDGAKKVFYVIEPRELLTAHILLFVAPHNSATGEPEASSGSPPSGGALG 300

Qy 301 PRAIFASRVRPGQRIVYVAFRDGDRLPILPAVHSVTLSEEAGAYAPLAQGTLLINRVL 360

Db 301 PRAIFASRVRPGQRIVYVAFRDGDRLPILPAVHSVTLSEEAGAYAPLAQGTLLINRVL 360

Qy 361 ASCYAVIEEHSAWAHRAFAFPFLAHALLAALAPARTDRCGSDGGDRGGGRVYALTAGA 420

Db 361 ASCYAVIEEHSAWAHRAFAFPFLAHALLAALAPARTDRCGSDGGDRGGGRVYALTAGA 420

Qy 421 ADAPGAGATAGIHWSQLQLQIGTWILDSEALHPGMAYKSSXSRGAGGCCREGA 475

Db 421 ADAPGAGATAGIHWSQLQLQIGTWILDSEALHPGMAYKSSXSRGAGGCCREGA 475

RESULT 8
 AAY95286 standard; protein: 475 AA.

AC AAY95286; XX Human Sonic hedgehog Shh protein.

XX Sonic hedgehog; Shh; human; excitotoxicity; Parkinson's disease; Huntington's disease; neuronal degeneration; neuroprotective; dopamnergic; GABAergic; substantia nigra; therapy.

XX Homo sapiens.

FH Key-Misc-difference 463
 FT /note= "Encoded by NMN"

FT DT 12-SEP-2000 (first entry)

XX DE Human Sonic hedgehog Shh protein.

XX KW Sonic hedgehog; Shh; human; excitotoxicity; Parkinson's disease; Huntington's disease; neuronal degeneration; neuroprotective; dopamnergic; GABAergic; substantia nigra; therapy.

XX OS Homo sapiens.

XX FH Location/Qualifiers

PR 27-JAN-1999; 99US-00238243.
 PR 03-JUN-1999; 99US-00325602.
 XX PA (BIOGEN INC.
 XX PA (ONTO-) ONTOGEN INC.

XX PI Galde A, Mahanthappa N;

XX DR WPI; 2000-431510/37.
 DR N-PSDB; AIA27881.

XX PT Treating disorders involving exotoxicity, e.g. trauma, hypoglycemia, senile dementia and Korsakoff's disease, by using lipophilic modified hedgehog polypeptide.

XX Disclosure; Page 157-159; 17app; English.

Db 1 MILLARCLLIVLVSLLIVCSGLACGPGRGFGRKPKKLTPLAYQFIPNVAEKTIGASG 60

Db 1 MILLARCLLIVLVSLLIVCSGLACGPGRGFGRKPKKLTPLAYQFIPNVAEKTIGASG 60

Qy 61 RYEKGTSRNSERFKELTPNPDIFKDENTGADRIMTORCKDKLNALAISYMNNQPGV 120

Db 61 RYEKGTSRNSERFKELTPNPDIFKDENTGADRIMTORCKDKLNALAISYMNNQPGV 120

Qy 121 KLRVTEGMDWEIGHREBESLVEYEGRAVDITTSDRDKTMLAVEGDFDWTYYESKAH 180

Db 121 KLRVTEGMDWEIGHREBESLVEYEGRAVDITTSDRDKTMLAVEGDFDWTYYESKAH 180

Qy 181 IHCSYKAENSYAAKSGCFPSOSATVHLDQGRLLYSDELT 240

Db 181 IHCSYKAENSYAAKSGCFPSOSATVHLDQGRLLYSDELT 240

Qy 241 FLDRDGAKKVFYVIEPRELLTAHILLFVAPHNSATGEPEASSGSPPSGGALG 300

Db 241 FLDRDGAKKVFYVIEPRELLTAHILLFVAPHNSATGEPEASSGSPPSGGALG 300

Qy 301 PRAIFASRVRPGQRIVYVAFRDGDRLPILPAVHSVTLSEEAGAYAPLAQGTLLINRVL 360

Db 301 PRAIFASRVRPGQRIVYVAFRDGDRLPILPAVHSVTLSEEAGAYAPLAQGTLLINRVL 360

Qy 361 ASCYAVIEEHSAWAHRAFAFPFLAHALLAALAPARTDRCGSDGGDRGGGRVYALTAGA 420

Db 361 ASCYAVIEEHSAWAHRAFAFPFLAHALLAALAPARTDRCGSDGGDRGGGRVYALTAGA 420

Qy 421 ADIFGAGATAGIHWSQLQLQIGTWILDSEALHPGMAYKSSXSRGAGGCCREGA 475

Db 421 PRMFAVIEEHSAWAHRAFAFPFLAHALLAALAPARTDRCGSDGGDRGGGRVYALTAGA 475

Db 421. ADAFGAGATAGIHWYSQIYQITWILDEALHPLGNAVKSXSRGAGGGAREGA 475
RESULT 9
 ID AAY95977 standard protein; 475 AA.
 AC AAY95977;
 XX 05-DEC-2000 (first entry)
 DE Human Sonic hedgehog Shh protein.
 XX Sonic hedgehog; Shh; human; agonist; antagonist; lipid modulator;
 vacuole; cholesterol disorder; lipid disorder; lipid metabolism;
 lipid storage; lipid transport; apolipoprotein; triglyceride;
 hypercholesterolemia; abetalipoproteinemia; hypobetaalipoproteinemia;
 chylomicron retention; Anderson's disease; fat absorption;
 atherosclerosis; Obesity; weight loss; vitamin A disorder;
 vitamin E disorder; anorectal; arteriosclerotic;
 gene therapy; diagnosis;
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Misc-difference 463 /note= "encoded by NNN"
 FT PN WO200051628-A2.
 PD 08-SEP-2000.
 XX 03-MAR-2000; 2000WO-US005662.
 PF PR 03-MAR-1999; 99US-0122640P.
 PR 15-MAR-1999; 99US-0124446P.
 XX (BIOJ) BIOPEN INC.
 PA Burkly L, Wang LC;
 PI WPI: 2000-611340-58.
 DR N-PSDB; AAA95977.
 XX Use of lipid modulators (e.g. hedgehog agonists or antagonists) for
 PT modulating lipid metabolism and storage, especially useful for treating
 PT lipid metabolism or cholesterol disorders, e.g. obesity or
 PT hypercholesterolemia.
 XX Disclosure; Page 118-120; 136pp; English.
 CC The present sequence of that of human Sonic hedgehog (Shh) protein. The
 invention provides claimed methods for modulating lipid metabolism, for
 modulating vacuole formation in intestinal epithelial cells, for
 modulating the accumulation of fat in intestinal epithelial cells, for
 treating a cholesterol disorder and for treating a lipid metabolism
 disorder in an animal (especially human) by administering a lipid
 modulator selected from a hedgehog antagonist or hedgehog agonist. In
 particular, the lipid metabolism disorder is a lipid storage disorder, a
 triglyceride disorder, an apolipoprotein disorder, a triglyceride
 disorder, e.g. a triglyceride metabolism disorder, a triglyceride
 transport disorder or a triglyceride storage disorder; a diet-induced
 hypercholesterolemia, hypercholesterolemia, a triglyceride disorder;
 hypobetalipoproteinemia, a chylomicron-retention disorder; Anderson's
 disease, a fat absorption disorder, e.g. obesity or associated with
 weight loss, normotriglyceridemic abetalipoproteinemia, an apolipoprotein
 -B100 deficiency, a fat soluble vitamin disorder, where the fat soluble
 vitamin A or E, or atherosclerosis (all claimed). The hedgehog
 antagonist binds to the hedgehog receptor, but does not elicit a
 response. It is preferably a hedgehog mimetic, a modified hedgehog
 protein, e.g. an injective hedgehog variant, or an anti-hedgehog
 homologue, especially a human, chimeric or humanised antibody. The
 methods are useful in preventing these disorders or protecting a subject

CC from these disorders. The hedgehog antagonist and agonist are also useful
 CC in diagnosis and research associated with these disorders. The lipid
 CC modulators may also be used as a part of a gene therapy protocol to
 CC deliver polynucleotides encoding these lipid modulators
 XX SQ Sequence 475 AA;
 Query Match 99.9%; Score 2467; DB 3; Length 475;
 Best Local Similarity 100.0%; Pred. No. 2.1e-217;
 Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLLARCLLVLVSSLYCSGLACGPGRGFGRKRHPKLTPLAKOPTPNVAEKTIGASG 60
 Db 1 MLLARCLLVLVSSLYCSGLACGPGRGFGRKRHPKLTPLAKOPTPNVAEKTIGASG 60
 Qy 61 RYEKGISRSRSERFELTPHYNPDLIFKQEENTCAADRMTQRCKDKUNALAISSVMNQPGV 120
 Db 61 RYEKGISRSRSERFELTPHYNPDLIFKQEENTCAADRMTQRCKDKUNALAISSVMNQPGV 120
 Qy 121 KLRVTEGMDEDGHSESHYEGRAVIDITSDRSKYGMMLARLAVBAGEDFWVYYSKAH 180
 Db 121 KLRVTEGMDEDGHSESHYEGRAVIDITSDRSKYGMMLARLAVBAGEDFWVYYSKAH 180
 Qy 181 IHCSTKAENSAVAKSGGCCPGSATVHLEGGTFLKYLQDLSPGDRVLAADDQGRLLYSPLFT 240
 Db 181 IHCSTKAENSAVAKSGGCCPGSATVHLEGGTFLKYLQDLSPGDRVLAADDQGRLLYSPLFT 240
 Qy 241 FLDRDGAKKVYYTEPRERILLTAHLLVAPRNDSDATEPEASSGSPGSGALG 300
 Db 241 FLDRDGAKKVYYTEPRERILLTAHLLVAPRNDSDATEPEASSGSPGSGALG 300
 Qy 301 PRALFAASRVPGQTYVVAERDGRRLPAAVHSVTSEAAAGAYPLTAQGTILIRNL 360
 Db 301 PRALFAASRVPGQTYVVAERDGRRLPAAVHSVTSEAAAGAYPLTAQGTILIRNL 360
 Qy 361 ASCYAVIEEWSWAHAFAPRLAHLLAALAPARTDRGDSGGDRGGGGRVALTAGA 420
 Db 361 ASCYAVIEEWSWAHAFAPRLAHLLAALAPARTDRGDSGGDRGGGGRVALTAGA 420
 Qy 421 ADAPGAGATAGIHWYSQIYQIGTWLIDSEALHPLGMAVKSXSRGAGGGAREGA 475
 Db 421 ADAPGAGATAGIHWYSQIYQIGTWLIDSEALHPLGMAVKSXSRGAGGGAREGA 475
RESULT 10
 ID AAB84674 standard; protein; 475 AA.
 AC AAB84674;
 XX DT 17-SEP-2001 (first entry)
 XX DE Amino acid sequence of a human hedgehog (Shh) polypeptide.
 XX KW Shh gene; hedgehog gene; T lymphocyte; patched gene; infection; diabetes;
 XX KW nutritional deficiency; graft rejection; hyperacute response;
 XX KW cornea transplant; autoimmune disorder; multiple sclerosis; psoriasis;
 XX KW atopic dermatitis; inflammatory disease; eczematous dermatitis; urticaria; vasculitis;
 XX KW hyperproliferative disease; scleroderma.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Misc-difference 463
 FT /note= "unspecified residue encoded by NNN"
 XX PN WO200140438-A2.
 XX PD 07-JUN-2001.
 XX PP 30-NOV-2000; 2000WO-US032590.

Query Match Score 2467; DB 4; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217; -

Qy	1	MILLARCLLIVLVSLLVSGLACGPGRGKRRHPKKLTPLAYKOFIPNVAEKTIGASG	60	DR	N-PSDB; AAD09034.
Db	1	MLLARCLLIVLVSLLVSGLACGPGRGKRRHPKKLTPLAYKOFIPNVAEKTIGASG	60	PT	Novel isolated hedgehog fusion polypeptide useful for treating
Qy	61	RYEGKISRNSERFKELTPTPNPDIKFDENTGADRIMTORCKDKLNALAISSYMNQPGV	120	PT	neurological conditions such as Alzheimer's disease, Parkinson's disease,
Db	61	RYEGKISRNSERFKELTPTPNPDIKFDENTGADRIMTORCKDKLNALAISSYMNQPGV	120	PT	Huntington's chorea, amyotrophic lateral sclerosis, and multiple
Db	61	RYEGKISRNSERFKELTPTPNPDIKFDENTGADRIMTORCKDKLNALAISSYMNQPGV	120	XX	sclerosis.
Db	61	RYEGKISRNSERFKELTPTPNPDIKFDENTGADRIMTORCKDKLNALAISSYMNQPGV	120	XX	Disclosure: Page 117-118; 178pp; English.
Qy	121	KLRTEGWWDDGHISSESHYEGRAVDITTSDRSKYGMNLARLAVEAGFDVYYEYSAH	180	CC	The present invention relates to hedgehog fusion proteins. Hedgehog
Db	121	KLRTEGWWDDGHISSESHYEGRAVDITTSDRSKYGMNLARLAVEAGFDVYYEYSAH	180	CC	proteins are a family of extracellular signalling proteins that regulate
Qy	181	IHCSYKAENSVAAKGGCFGSATHLBEGGTGKLVKDLSPGDRVLAADDQGRLLYSFLT	240	CC	various aspects of embryonic development both in vertebrates and in
Db	181	IHCSYKAENSVAAKGGCFGSATHLBEGGTGKLVKDLSPGDRVLAADDQGRLLYSFLT	240	CC	invertebrates. Hedgehog fusion protein is useful for the prophylaxis or
Qy	241	FLDRDGAKKVYVLIBTREPRLILTAHLLFVAPHDNSATGEPEASSGSPPSGALG	300	CC	treatment of any condition or disease state for which a hedgehog or
Db	241	FLDRDGAKKVYVLIBTREPRLILTAHLLFVAPHDNSATGEPEASSGSPPSGALG	300	CC	patched protein constituent is efficacious and in the diagnosis of
Qy	301	PRALFASRVRPGQRTYVVAIRDGRDLRLLPAVHTVLSEAAAYAPTAQGTILNRL	360	CC	CC constituents or conditions of disease states in biological systems or
Db	301	PRALFASRVRPGQRTYVVAIRDGRDLRLLPAVHTVLSEAAAYAPTAQGTILNRL	360	CC	CC specimens and for diagnostic purposes in non-physiological systems.
Qy	361	ASCYAVIEHSWAHAFAPFLRLLAALAPARTDGGDSGGDRGGGRVALTAGA	420	CC	Hedgehog fusion protein is useful for treating neurological conditions
Db	361	ASCYAVIEHSWAHAFAPFLRLLAALAPARTDGGDSGGDRGGGRVALTAGA	420	CC	due to injury, aging of nervous system, including Alzheimer's disease,
Qy	421	ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA	475	CC	CC chronic neurodegenerative diseases of the nervous system, including
Db	421	ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA	475	CC	CC Parkinsoin's disease, Huntington's chorea, amyotropic lateral sclerosis
RESULT 12				CC	CC and chronic immunological diseases of nervous system, including multiple
AAE04687				CC	CC sclerosis and malignant gliomas, medulloblastomas, neuroectodermal
ID	AAE04687	standard; protein; 475 AA.		CC	CC tumours and to specifically target medical therapies against cancers and
XX				CC	CC tumours which express the receptor for the protein. The present sequence
AC	AAE04687;			CC	CC is human sonic hedgehog (Shh) protein
XX				XX	Sequence 475 AA;
DT	04-SEP-2001	(first entry)		Qy	Query Match 99.9%; Score 2467; DB 4; Length 475;
AAE04687				Db	Best Local Similarity 100.0%; Pred. No. 2.1e-217; Mismatches 0; Indels 0; Gaps 0;
Db	421	ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA	475	Qy	1 MLLACLLIVLVSLLVSGLACGPGRGKRRHPKLUPLPLAYKOFIPNVAEKTIGASG
Db	421	ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA	475	Db	1 MLLACLLIVLVSLLVSGLACGPGRGKRRHPKLUPLPLAYKOFIPNVAEKTIGASG
Db	421	ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA	475	Qy	61 RYEKGISRNSERFKELTPTPNPDIKFDENTGADRIMTORCKDKLNALAISSYMNQPGV
Db	421	ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA	475	Db	61 RYEKGISRNSERFKELTPTPNPDIKFDENTGADRIMTORCKDKLNALAISSYMNQPGV
Db	421	ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA	475	Qy	121 KLRVTEGWDDEGHISSESHYEGRAVDITTSDRSKYGMNLARLAVEAGFDWYYEYSAH
Db	421	ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA	475	Db	121 KLRVTEGWDDEGHISSESHYEGRAVDITTSDRSKYGMNLARLAVEAGFDWYYEYSAH
Db	421	ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA	475	Qy	181 IHCSYTAENSVAAKGGCFPOSATVHLEQGKTIVKLDSPGDRVLAADDQGRLLYSDFLT
Db	421	ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA	475	Db	181 IHCSYTAENSVAAKGGCFPOSATVHLEQGKTIVKLDSPGDRVLAADDQGRLLYSDFLT
Db	421	ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA	475	Qy	241 FLDRDGAKKVYVLIBTREPRLILTAHLLFVAPHDNSATGEPEASSGSPPSGALG
Db	421	ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA	475	Db	241 FLDRDGAKKVYVLIBTREPRLILTAHLLFVAPHDNSATGEPEASSGSPPSGALG
Db	421	ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA	475	Qy	301 PRALFASRVRPGQRTYVVAIRDGRDLRLLPAVHTVLSEAAAYAPTAQGTILNRL
Db	421	ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA	475	Db	301 PRALFASRVRPGQRTYVVAIRDGRDLRLLPAVHTVLSEAAAYAPTAQGTILNRL
Db	421	ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA	475	Qy	361 ASCYATEEHSHWAHAFAPFLRLLAALAPARTDGGDSGGDRGGGRGVLTAPGA
Db	421	ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA	475	Db	361 ASCYATEEHSHWAHAFAPFLRLLAALAPARTDGGDSGGDRGGGRGVLTAPGA
RESULTS 13				Qy	421 ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA
AAE05317				Db	421 ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA
ID	AAE05377	standard; protein; 475 AA.		XX	421 ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA
XX				AC	421 ADAPGAGATAGIHNYSQLIQIGTMLDSEALHPLGMWAKSSXSRGAGGAREGA
XX				DT	12-SEP-2001 (first entry)

XX	Human Sonic hedgehog protein.	QY	1 MLLARCLLIVSSLLIVCSGLACGGGRGFKRHPKCLPPLAYCFIPNVAEKTIGASG 60
DB		Db	1 MLLARCLLIVSSLLIVCSGLACGGGRGFKRHPKCLPPLAYCFIPNVAEKTIGASG 60
XX	Human; Sonic hedgehog; Shh; morphogenic signal; neuron; chromosome 7q; embryonic patterning; cell culture; cell differentiation; ischaemia; Q;	QY	61 RYEKGIISRNSERFKEITPNYNPDIIIFKDENTGADLMTORCKDNALAIISVWNQWPGV 120
KW	cell proliferative disorder; intracerebral grafting; Huntington's chorea; neurological disorder; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; ALS; multiple sclerosis.	Db	61 RYEKGIISRNSERFKEITPNYNPDIIIFKDENTGADLMTORCKDNALAIISVWNQWPGV 120
KW		QY	121 KLRVTEGWDEDGHHSSEESLHYEGRADITTSDRDRSKYGMALARLAVEAGEDFWVYTESKAH 180
XX	Homo sapiens.	Db	121 KLRVTEGWDEDGHHSSEESLHYEGRADITTSDRDRSKYGMALARLAVEAGEDFWVYTESKAH 180
XX		QY	121 KLRVTEGWDEDGHHSSEESLHYEGRADITTSDRDRSKYGMALARLAVEAGEDFWVYTESKAH 180
PH	Location/Qualifiers	QY	181 IHCSVRAENSYAASKGCCFPGSATVLEOGGTKLVDLSPGDRVLADDQGRLLYSDFLT 240
FT	Misc-difference 463 /label= "Unknown" /note= "Encoded by NNN"	Db	181 IHCSVRAENSYAASKGCCFPGSATVLEOGGTKLVDLSPGDRVLADDQGRLLYSDFLT 240
FT		QY	241 FLDRDGAKKYFYVITREPRLILITAAHLLFVAPHNDSATGEPEASSGSPSGSAGLG 300
FT		Db	241 FLDRDGAKKYFYVITREPRLILITAAHLLFVAPHNDSATGEPEASSGSPSGSAGLG 300
PF	02-JUL-1996; 96US-00674509.	QY	301 PRALFASRVRPGQVTVAAERGDDRILLPAVHSTLSEEEAGAYPLTAQCTILINRVL 360
XX		Db	301 PRALFASRVRPGQVTVAAERGDDRILLPAVHSTLSEEEAGAYPLTAQCTILINRVL 360
PN	US6261786-B1.	QY	361 ASCYAVIEEHSAWAHRAAPFRIAHALLAALPARTDRGGDGGGGCRVALTAPGA 420
XX		Db	361 ASCYAVIEEHSAWAHRAAPFRIAHALLAALPARTDRGGDGGGGCRVALTAPGA 420
PD	17-JUL-2001.	QY	421 ADAPGAGATAGIHWYSQOLYQIGTWILDEALHPGMATKSSXSRAGGGAREGA 475
XX		Db	421 ADAPGAGATAGIHWYSQOLYQIGTWILDEALHPGMATKSSXSRAGGGAREGA 475
XX		RESULT 14	
XX		XX	AAC65748 standard; protein: 475 AA.
XX		XX	AAC65748;
XX		AC	
XX		DT	07-JAN-2002 (first entry)
XX		XX	Human sonic hedgehog (shh) polypeptide.
XX		XX	Adiocyte; hedgehog polypeptide; desert hedgehog; indian hedgehog; Dhh; Ihh; sonic hedgehog; shh; therapeutic; cytostatic; tumor.
XX		XX	Homo sapiens.
XX		FH	Key Location/Qualifiers
XX		FT	Misc-difference 463 /note= "encoded by NNN"
XX		FT	W020164238-A2.
XX		PR	29-FEB-2000; 2000US-0186058P.
PS	Claim 2 ; Col 163-166; 127PP; English.	XX	07-SEP-2001.
XX	Screening compounds that potentiate or inhibit binding of hedgehog polypeptide to naturally occurring patched receptor, comprises contacting polypeptide with receptor and test compound, and detecting change in binding.	XX	28-FEB-2001; 2001WO-US006450.
PT	The present invention relates to assay for screening compounds that occurring, patch receptor. The hedgehog proteins comprise morphogenic signals produced by embryonic patterning centres, and are involved in the formation and maintenance of ordered spatial arrangements of differentiated tissues in vertebrates, both adult and embryonic. The proteins can be used to generate and/or maintain an array of different vertebrate tissues both in vitro and in vivo. The invention also relates to a method for modulating growth, differentiation or survival of a mammalian cell (e.g. neuron, testicular cell) responsive to hedgehog induction. Hedgehog agonists and antagonists can be used in cell culture techniques to enhance survival and maintenance of neurons and various vertebrate organogenic pathways. The hedgehog gene is useful in determining whether a patient is at the risk of disorder characterised by unwanted cell proliferation or aberrant control of differentiation. The hedgehog proteins or mimetics can be used to induce foetal neurons especially neuronal stem cells in intracerebral grafting. The protein or its mimetic can be used in the treatment of neurological conditions e.g. injury to nervous system, ischaemia resulting from stroke, Alzheimer's disease, Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis (ALS) and multiple sclerosis. The present sequence is human sonic hedgehog (shh) protein. The Shh gene is located on human chromosome 7q	XX	WPI; 2001-607352/69.
XX	Sequence 475 AA;	XX	N-PDB; AAI6676.
PS	Query Match 99.9%; Score 2467; DB 4; Length 475;	XX	Method for regulating formation and/or maintenance of adipocyte tissue by contacting pre-adipocyte or adipocyte cells with a hedgehog polypeptide or Btc therapeutic.
PS	Best Local Similarity 100.0%; Conservative Matches 475; Mismatches 0; Indels 0; Gaps 0;	XX	Disclosure; Page 102-104; 132pp; English.
PS	Sequence 475 AA;	XX	

Db 301 PRALFASRVRPGQRYVVAERDGRRLPAAVHSTLSSBEAGAYAPLTAQGTILINRVL 360
 Qy 361 ASCYAVIEEWSWAHRAAPPLAHALLAALAPARTDRGGDSGGDRGGGRVALTAGA 420
 Db 361 ASCYAVIEEWSWAHRAAPPLAHALLAALAPARTDRGGDSGGDRGGGRVALTAGA 420
 Db 421 ADAPGAGATAGIHWTSQQLQIGTWILDSEALHPJGMATKSSXSRGAGGAREGA 475
 Qy 421 ADAPGAGATAGIHWTSQQLQIGTWILDSEALHPJGMATKSSXSRGAGGAREGA 475
 Db 421 ADAPGAGATAGIHWTSQQLQIGTWILDSEALHPJGMATKSSXSRGAGGAREGA 475

RESULT 16

ID ABB79137 standard; protein; 475 AA.
 XX AC ABB79137;
 XX DT 06-AUG-2002 (first entry)
 XX DE Human sonic hedgehog (Shh) protein SEQ ID NO:13.
 KW Sonic hedgehog; Shhh; desert hedgehog; Dhh; Indian hedgehog; Ihh;
 KW anticarsonian; antiarhythmic; neuroprotective; anticonvulsant;
 KW cytosolic; nootropic; spermatogenesis; peripheral nervous system;
 KW central nervous system; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; arrhythmia; nerve degeneration; multiple sclerosis;
 KW immunological disorder; neoplastic; hyperplastic.
 XX OS Homo sapiens.
 XX FH Location/Qualifiers
 FT Misc-difference 463
 FT /label= "unknown"
 FT /not= "encoded by NNN"
 XX PN US6384192-B1.
 PD 07-MAY-2002.
 XX PP 20-OCT-1997; 97US-00957874.
 XX PR 30-DEC-1993; 93US-00176427.
 PR 14-DEC-1994; 94US-00358060.
 PR 04-MAY-1995; 95US-00435193.
 PR 05-JUN-1995; 95US-004623186.
 XX PA (HARD) HARVARD COLLEGE.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 PI Ingham PW, McMahon AP, Tabin CJ;
 XX DR WPI: 2002-442817/47.
 DR N-PSDB; ABN87544.
 XX PT New vertebrate hedgehog-related proteins, useful e.g. for promoting
 PT differentiation, survival and proliferation of cells, e.g. for treating
 PT neurodegeneration.
 XX PS Claim 2; Col 149-152; 116PP; English.
 XX CC The present invention describes an isolated and/or recombinant
 CC polypeptide (I) comprising a hedgehog (hh) amino acid (aa) sequence
 CC encoded by a nucleic acid (II) that hybridizes under stringent conditions
 CC to 1 of 6 sequences (see ABN87544, and ABN87546 to ABN87550). (I) binds
 CC to a natural patched receptor. Specifically claimed example of (I) are
 CC given in ABB79122 and ABB79134 to ABB79138. (I) has antiparkinsonian,
 CC nootropic, neuroprotective, anticonvulsant, antiarhythmic and cytotoxic
 CC activities. (I) induces the differentiation of the BMP-2 and -4 genes, and of
 CC the Hoxd gene. (I) can be used: (i) to promote differentiation of
 CC neuronal cells and survival of the differentiated cells, specifically
 CC dopaminergic or motor neurons, proliferation of chondrocytes, and
 CC proliferation, differentiation and/or survival of mesodermal or
 CC ectodermal cells, either in cell cultures (particularly for preparation

CC of transplants) or therapeutically; (ii) for detecting loss of response,
 CC in tissues or cells, to hh protein; (iii) in drug screening (to identify
 CC (ant)agonists, useful e.g. for inhibition of spermatogenesis); and (iv)
 CC for isolation of cognate receptors. (I) may be used therapeutically to
 CC treat e.g. injuries/defects in the central or peripheral nervous systems,
 CC including Alzheimer's, Parkinson's and Huntington's diseases, or
 CC arrhythmias caused by nerve degeneration; immunological disorders of the
 CC nervous system, e.g. multiple sclerosis; neoplastic and hyperplastic
 CC alterations in the central nervous system, also to promote attachment of
 CC prostheses. The present sequence represents the human sonic hedgehog
 CC (Shh) protein given in the present invention
 XX Sequence 475 AA;
 Query Match Score 99.9%; Score 2467; DB 5; Length 475;
 Best Local Similarity 100.0%; Pred No. 2.1e-217;
 Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MILLARCILLYVLSLLVCSGLACGPGRGFGRHPKLTPLAYKOFIPNVAEKTIGASG 60
 Db 1 MILLARCILLYVLSLLVCSGLACGPGRGFGRHPKLTPLAYKOFIPNVAEKTIGASG 60
 Qy 61 RYEGKISRNSENSEKFELTPNNDIIFKDEENTGADLMTCRDKINNALAISVMQWPGV 120
 Db 61 RYEGKISRNSENSEKFELTPNNDIIFKDEENTGADLMTCRDKINNALAISVMQWPGV 120
 Qy 121 KLRVTEGMDDEGHSSERSHSSESHHHVEGRADITTSQRDRSKYGMHLARLAVAGEFDWVYYSKAH 180
 Db 121 KLRVTEGMDDEGHSSERSHSSESHHHVEGRADITTSQRDRSKYGMHLARLAVAGEFDWVYYSKAH 180
 Qy 181 IHSSVKAEENSAVAKSGGCOPPSATVHLEQGTTKLVDLSPGDRVLAADDQGRLLYSDFLT 240
 Db 181 IHSSVKAEENSAVAKSGGCOPPSATVHLEQGTTKLVDLSPGDRVLAADDQGRLLYSDFLT 240
 Qy 241 FLDRDGAKKVYVIEPREPLLTAAHLLFVAHNSATGEPAASSGGGPSCSALG 300
 Db 241 FLDRDGAKKVYVIEPREPLLTAAHLLFVAHNSATGEPAASSGGGPSCSALG 300
 Qy 301 PRALFAASVRPGQRYVVAERDGRILLPAAVHSVTLSSEAGAYAPLTAQTLINRVL 360
 Db 301 PRALFAASVRPGQRYVVAERDGRILLPAAVHSVTLSSEAGAYAPLTAQTLINRVL 360
 Qy 361 ASCYAVIEEWSWAHRAAPPLAHALLAALAPARTDRGGDSGGDRGGGRVALTAGA 420
 Db 361 ASCYAVIEEWSWAHRAAPPLAHALLAALAPARTDRGGDSGGDRGGGRVALTAGA 420
 Qy 421 ADAPGAGATAGIHWTSQQLQIGTWILDSEALHPJGMATKSSXSRGAGGAREGA 475
 Db 421 ADAPGAGATAGIHWTSQQLQIGTWILDSEALHPJGMATKSSXSRGAGGAREGA 475

RESULT 17

ID ABB14297 standard; protein; 475 AA.
 XX AC ABB14297;
 XX DT 07-MAR-2002 (first entry)
 XX DE Human sonic hedgehog (Shh) protein.

XX KW Neuronal degeneration; hedgehog therapeutic; neurotrophic factor;
 KW therapy; amelioration; Alzheimer's disease; Parkinson's disease;
 KW Huntington's chorea; amyotrophic lateral sclerosis; schizophrenia;
 KW neurological disorder; hypoglycemia; senile dementia; depression;
 KW Korsakoff's disease; acquired immune deficiency syndrome; hypoxia;
 KW AIDS dementia; epileptic seizure; Tourette's syndrome; ischemia;
 KW suffocation; neurotoxic injury; cerebrovascular accident; anoxia; trauma;
 KW myocardial infarct; drowning; perinatal asphyxia; surgery;
 KW drug addiction; stroke; human; Sonic hedgehog; Shh protein; ALS.
 XX OS Homo sapiens.

PH	Key	Location/Qualifiers	Qy	301 PRALFASRVPRPGQRVYVVAERGDERRLLPAAVHSVTLSERAGAYAPITAQGTLINRVL 360
FT	Region	24 . 197 /note= "N-terminal fragment; This region is specifically referred in Claim 3"	Db	301 PRALFASRVPRPGQRVYVVAERGDERRLLPAAVHSVTLSERAGAYAPITAQGTLINRVL 360
FT	Misc-difference	463 /note= "Encoded by NNN"	Qy	361 ASCVAVIEEHSSWAHRAFAFRLLAALAPARTDGSGGDRGGGRVALTARGA 420
FT	XX	WO200182946-A2.	Db	361 ASCVAVIEEHSSWAHRAFAFRLLAALAPARTDGSGGDRGGGRVALTARGA 420
XX	XX	PD 08-NOV-2001.	Qy	421 ADAPAGATAGIHWYSQLLYQIGTWLDSBEAHPLGMAVKSSXSRGAGGARGA 475
PP	XX	PP 27-APR-2001; 2001WO-US013854.	Db	421 ADAPAGATAGIHWYSQLLYQIGTWLDSBEAHPLGMAVKSSXSRGAGGARGA 475
PR	XX	PR 28-APR-2000; 2000US-02007652.		
XX	PA	PA (CURI-) CURIS INC.		
XX	PI	PI Reilly JO;		
DR	XX	DR WPI: 2002-034488/04.		
DR	XX	DR N-PSDB; AAD23804.		
PS	XX	XX		
PT	PT	Ameliorating neuronal degeneration such as Huntington's Chorea, Alzheimer's or Parkinson's disease in a subject, by administering to the subject a composition comprising hedgehog therapeutic and neurotrophic factor.		
PT	PT	Subject a Composition comprising hedgehog therapeutic and neurotrophic factor.		
XX	PS	PS 3; Page 127-128; 139pp; English.		
CC	CC	The invention relates to a method of ameliorating neuronal degeneration in a subject. The method involves administering to the subject a composition comprising hedgehog therapeutic and neurotrophic factor.		
CC	CC	The method is useful for the treatment, amelioration or prevention of Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis (ALS) and Huntington's chorea. It is useful for promoting the survival and/or differentiation of cholinergic neurons. The method is also useful for treating or preventing neurological disorders such as hypoglycaemia, senile dementia, Korsakoff's disease, schizophrenia, acquired immune deficiency syndrome (AIDS) dementia, depression, epileptic seizures, Tourette's syndrome, drug addiction, for reducing neurotoxic injury, associated with conditions of hypoxia, anoxia or ischaemia which typically follows stroke, cerebrovascular accident, brain or spinal cord trauma, myocardial infarct, physical trauma, drowning, suffocation, perinatal asphyxia, hypoglycaemic events, and for treating or preventing the adverse neurological consequences of surgery. The present sequence is human Sonic hedgehog (Shh) protein		
CC	XX	XX		
SQ	XX	SQ Sequence 475 AA;		
Query Match	99.9%	Score 2467; DB 5; Length 475;		
Best Local Similarity	100.0%	Pred. No. 2.1e-21;		
Matches	475;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db	1	MLLARCLLIVLVLSSILVCSGLACGPGRFGKRPKCLTPLAYKQFIPVAEKTIGASG 60		
Db	1	MLLARCLLIVLVLSSILVCSGLACGPGRFGKRPKCLTPLAYKQFIPVAEKTIGASG 60		
Qy	61	RYEGKISRSNSRFKLTPTNPIDIKDEENTGADRLLMQRCKDKLNAIASTYNMOWGV 120		
Db	61	RYEGKISRSNSRFKETPNNPDIIFKDENTGADRLLMQRCKDKLNAIASTMNQNGV 120		
Qy	121	KLRVTEGWDEDGHSESHLYEGRADITTSDRSKYGMRLAIVEAGFDWYYYESKAH 180		
Db	121	KLRVTEGWDEDGHSESHLYEGRADITTSDRSKYGMRLAIVEAGFDWYYYESKAH 180		
Qy	181	IHCYKAENSAAKGGCFPSGATSHLEQGTKLKYDLSPGDRVLAADQGRILYSDFT 240		
Db	181	IHCYKAENSAAKGGCFPSGATSHLEQGTKLKYDLSPGDRVLAADQGRILYSDFT 240		
Qy	241	FLDRDGAKCYFYVETREPERLLTAAHLLFAPHNSATGPEASSGSPSGGALG 300		
Db	241	FLDRDGAKCYFYVETREPERLLTAAHLLFAPHNSATGPEASSGSPSGGALG 300		

XX	Sequence 475 AA;	DR N-PSDB; ABK88636.
SQ	Query Match 99.9%; Score 2467; DB 5; Length 475; Best Local Similarity 100.0%; Pred. No. 2.1e-217; Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	PT Preparing basal cell carcinoma culture useful for identifying BCC therapeutics by contacting non cancerous skin sample having dermis and epidermis, with culture medium having hedgehog protein.
Qy	1 MILLARCLLTVSSLAUCSGLAAGPGRGFKRKRIPKKPLAKQFIPNVAEKTIGAGC 60	PT PT PT PT XX
Db	1 MILLARCLLTVSSLAUCSGLAAGPGRGFKRKRIPKKPLAKQFIPNVAEKTIGAGC 60	XX
Qy	61 RYEGKISRSNTERFKELTPNYPDIIFKDEENTGADRMLTRCKDKLNAIASVNNQPGV 120	XX
Db	61 RYEGKISRSNTERFKELTPNYPDIIFKDEENTGADRMLTRCKDKLNAIASVNNQPGV 120	XX
Qy	121 KURVTEGWDEDHHSSELSLHTEGRAVDITTSDRDKYGMARLAVEADWDWTTYESKAKH 180	XX
Db	121 KURVTEGWDEDHHSSELSLHTEGRAVDITTSDRDKYGMARLAVEADWDWTTYESKAKH 180	CC
Qy	181 IHCYSVKAEANSYAAKSGGCFCPSATAVHLEQGTTKLVDLSGDRVIAADDGRLYLSDFT 240	CC
Db	181 IHCYSVKAEANSYAAKSGGCFCPSATAVHLEQGTTKLVDLSGDRVIAADDGRLYLSDFT 240	CC
Qy	241 FLDRDDGAKKYVIETREPERILITAHHILVAPHNDSATGEPASSGGPPSGGALG 300	CC
Db	241 FLDRDDGAKKYVIETREPERILITAHHILVAPHNDSATGEPASSGGPPSGGALG 300	CC
Qy	301 PRALFAASRVRPQRVIVAAERGDRLLPAHVSTLSEEAGAYAPLTAQGTLLINRYL 360	CC
Db	301 PRALFAASRVRPQRVIVAAERGDRLLPAHVSTLSEEAGAYAPLTAQGTLLINRYL 360	CC
Qy	361 ASCYAVIEHSHWAHRAAPFLAHALLAALAPARTDRGDSGGDGGGGRVALTAPGA 420	CC
Db	361 ASCYAVIEHSHWAHRAAPFLAHALLAALAPARTDRGDSGGDGGGGRVALTAPGA 420	CC
Qy	421 ADAPGAGATAGIHWYQSLQYQIGTMLIDSEALHPLGMVAKSXSRAGGSAREGA 475	CC
Db	421 ADAPGAGATAGIHWYQSLQYQIGTMLIDSEALHPLGMVAKSXSRAGGSAREGA 475	CC
RESULT 19		XX
AAU99483		XX
ID AAU99483	standard; protein; 475 AA.	XX
XX		AC AAU99483;
XX	07-OCT-2002 (first entry)	XX
XX	Human sonic hedgehog (Shh) protein.	XX
XX	Basal cell carcinoma; BCC; non cancerous skin sample; dermis; epidermis; culture medium; hedgehog signalling Pathway; growth; development; abnormality; cancer; cytosatic; human; Shh; sonic hedgehog.	XX
OS Homo sapiens.		OS
Key WO200214344-A2.	Location/Qualifiers	Key
FT Misc-difference 463	/label= Unknown	FT
XX		FT
FN		XX
XX		FN
PD 06-JUN-2002.		XX
XX	28-NOV-2001; 2001WO-US044457.	PD
PR 28-NOV-2000; 2000US-0253660P.		PR
XX (CURIS INC.		XX
XX Berg AP, Pepicelli C, Wang F,		PI
XX WPI: 2002-557537/59.		DR
RESULT 20		XX
ADA26256		ID ADA26256 standard; protein; 475 AA.
XX		XX
AC ADA26256;		AC
XX		XX

SQ	Sequence 475 AA;
DT	(first entry)
XX	XX
DB	Human Sonic hedgehog (Shh) polypeptide.
XX	XX
KW	Human; Sonic hedgehog; Shh; neuronal cell; skeletogenesis; chondrogenesis; osteogenesis; degenerative disorder; nervous system; neuronal cell death; neural cell; neuromuscular disorder; autonomic disorder; central nervous system disorder; anoxia; ischaemia; peripheral nervous system disorder; tachycardia; atrial cardiac arrhythmia; striated heart; stem cell development; digestive tract; liver; multiple sclerosis.
OS	OS
XX	XX
XX	Key Location/Qualifiers
FT	Mis-difference 463 /label= unknown
FT	FT
XX	XX
US2003054437-A1.	QY
PD	20-MAR-2003.
XX	XX
PR	20-OCT-1997; 97US-00954771.
XX	XX
PR	30-DEC-1993; 93US-00176427.
PR	14-DBC-1994; 94US-0035060.
PR	04-MAY-1995; 95US-00435093.
PR	05-JUN-1995; 95US-00462385.
PA	(INGH/) INGHAM P W.
PA	(MCMAHON A P.
PA	(TABIN C J.
XX	XX
PI	Ingham PW, McMahon AP, Tabin CJ;
WPI	WPI: 2003-555377/52.
N-PSDB:	ADA26295.
XX	XX
PT	Modulating growth, differentiation or survival of a cell, useful for treating a degenerative disorder of the nervous system characterized by neuronal cell death, comprising contacting the cell with a hedgehog polypeptide.
PT	PT
PT	PT
PT	PT
XX	XX
XX	Claim 5; Page 81-82; 121pp; English.
XX	The invention relates to a method for modulating growth, differentiation or survival of a cell, comprising contacting the cell with a hedgehog polypeptide. The invention also relates to methods for inducing a cell to differentiate to a neuronal cell phenotype comprising contacting the cell with a hedgehog polypeptide, modulating skeletogenesis by contacting a target tissue of a hedgehog polypeptide to cause chondrogenesis and/or osteogenesis in the target tissue and treating a degenerative disorder of the nervous system characterised by neuronal cell death, comprising administering a hedgehog polypeptide causing prolonged survival of neural cells in the patient, relating to the absence of hedgehog treatment. The hedgehog polypeptides are useful for treating a degenerative disorder of the nervous system characterised by neuronal cell death, including neuromuscular, autonomic or central nervous system disorders, specifically Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, Pick's disease, Huntington's disease, multiple sclerosis, neuronal damage resulting from anoxia, ischaemia or trauma and neuronal degeneration associated with a natural aging process. The polypeptides may also be used for treating peripheral nervous system disorders including disorders affecting innervation of smooth muscle and endocrine tissue, such as tachycardia or atrial cardiac arrhythmias which may arise from a degenerative condition whereby the nerves innervate the striated muscle of the heart, in nerve prostheses for repairing central and peripheral nerve damage, for treating neoplastic or hyperplastic transformations and in controlling the development of stem cells responsible for the formation of the digestive tract, liver and other organs. This sequence represents the human Sonic hedgehog (Shh) polypeptide.
XX	XX
SQ	Query Match 99.9%; Score 2467; DB 6; Length 475;
DB	Best Local Similarity 100.0%; Pred. No. 2.1e-21;
XX	Mismatches 0; Indels 0; Gaps 0;
XX	XX
Matches 475; Conservative 0;	XX
XX	XX
QY	1 MILLARCLLVLVSSLIVCCSLACCPGRGKGKRPKKLTPLAYKFIFPINAETKLGASS 60
Db	1 MILLARCLLVLVSSLIVCCSLACCPGRGKGKRPKKLTPLAYKFIFPINAETKLGASS 60
61	RYEGKRSNSRERKEITPTNPNPDI1FKEENTGADRMLTORCKDKNALAIISVNQWPGV 120
61	RYEGKRSNSRERKEITPTNPNPDI1FKEENTGADRMLTORCKDKNALAIISVNQWPGV 120
QY	121 KLRVTGWDDEGHSSBESLHYEGRADITTSDRSKYGMALARVAEAGDWPVVYESKAH 180
Db	121 KLRVTGWDDEGHSSBESLHYEGRADITTSDRSKYGMALARVAEAGDWPVVYESKAH 180
QY	181 IHCSVTAENSYAAKSQQCPEQSATVLEQGQTKLVDLSPEDRVLAADDQCRLLSDFLT 240
Db	181 IHCSVTAENSYAAKSQQCPEQSATVLEQGQTKLVDLSPEDRVLAADDQCRLLSDFLT 240
QY	241 FLDRDGAKKYYVIETPREPRLITAAHILFVARPHNDSATGEPEASSGSPGPPSGGALG 300
Db	241 FLDRDGAKKYYVIETPREPRLITAAHILFVARPHNDSATGEPEASSGSPGPPSGGALG 300
QY	301 PRALFAASRVRPQRQTVVAEFDGDRILLPAAVHSVTLSEEEAGAAYPLTAQGTILINRVL 360
Db	301 PRALFAASRVRPQRQTVVAEFDGDRILLPAAVHSVTLSEEEAGAAYPLTAQGTILINRVL 360
QY	361 ASCYATEEHSFAHRAFAPPRLAHLAAALAPARTRGGSQGGDRGGGRVALTAPGA 420
Db	361 ASCYATEEHSFAHRAFAPPRLAHLAAALAPARTRGGSQGGDRGGGRVALTAPGA 420
QY	421 ADAPGAGATAGIHWYSOLLYQIGTMLDSEALHPGMAVKSXRAGGGAREGA 475
Db	421 ADAPGAGATAGIHWYSOLLYQIGTMLDSEALHPGMAVKSXRAGGGAREGA 475
XX	XX
RESULT 21 ADD25260 standard; protein: 475 AA.	XX
ID	ADD25260
XX	XX
AC	AC
XX	XX
DT	15-JAN-2004 (first entry)
XX	XX
DE	Human Sonic hedgehog (SHH) polypeptide.
XX	XX
KW	human; Sonic hedgehog; SHH; patched receptor; spermatogenesis inhibition; ovary function inhibition; embryogenesis; differential tissue maintenance.
KW	KW
XX	Homo sapiens.
OS	OS
XX	XX
PN	US576227-B1.
XX	XX
PD	10-JUN-2003.
XX	XX
PP	16-AUG-2000; 2000US-00639695.
XX	XX
PR	30-DEC-1993; 93US-00176427.
PR	14-DEC-1994; 94US-00356060.
PR	04-MAY-1995; 95US-00435033.
PR	05-JUN-1995; 95US-00460900.
PA	(HARD) HARVARD COLLEGE.
PA	(IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
PA	Ingham PW, McMahon AP, Tabin CJ, Bumcrot DA, Marti-Gorostiza E;
PI	XX
XX	XX
DR	WPI: 2003-799823/75.
DR	N-PSDB; ADD252615.

XX Novel isolated antibody which is immunoreactive with a vertebrate hedgehog protein sequence that binds with a patched receptor, useful for blocking action of naturally occurring hedgehog protein, and for inhibiting spermatogenesis.

PS Claim 6; SEQ ID NO 13; 120pp; English.

XX Homo sapiens.

CC The invention relates to an isolated antibody (I) which is immunoreactive with a hedgehog polypeptide (II) that binds to a patched receptor, where (II) is encoded by nucleic acid which hybridise to a fully defined vertebrate hedgehog (hh) protein. (II) is useful as a hedgehog antagonist by blocking action of naturally occurring hedgehog protein, and therefore for inhibiting spermatogenesis. (II) is also useful for inhibiting normal ovarian function. (II) is useful for blocking the action of one or more hedgehog proteins and allows the study of the role of these proteins e.g., embryogenesis and/or maintenance of differential tissue. (II) is also useful in immunohistochemical staining of tissue samples in order to evaluate the abundance and pattern of expression of the hedgehog polypeptides. (II) is also useful for diagnostic immunoprecipitation and immunoblotting to detect and evaluate hedgehog protein levels as a part of clinical testing procedure. The present sequence represents the CC amino acid sequence of a hedgehog polypeptide.

XX Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 7; Length 475;

Best Local Similarity 100.0%; Pred. No. 2.1e-217; Mismatches 0; Indels 0; Gaps 0;

Matches 475; Conservative 0; CC 1 MILLARCLLVVSSLLVVCSSGLACGPRGFGRPKKLTPLAKQFVNVAEKTGLGAG 60
Db 1 MILLARCLLVVSSLLVVCSSGLACGPRGFGRPKKLTPLAKQFVNVAEKTGLGAG 60
Cc 61 RYEKGKISRNSRFKELTPNPDIFKDENTGADRMLTORCKDKLNALAIISVNKNOWPVE 120
Db 61 RYEKGKISRNSRFKELTPNPDIFKDENTGADRMLTORCKDKLNALAIISVNKNOWPVE 120
Cc 121 KLRVTEGWDDEGHHSSESLHVEGRADITTSDRSKYGMRLAVALAEAGFDWVYESKAH 180
Db 121 KLRVTEGWDDEGHHSSESLHVEGRADITTSDRSKYGMRLAVALAEAGFDWVYESKAH 180
Cc 181 IHCSVKTAENSYAAKSGCCFPSSATVHLEQGTTKLVDLSPGDRVLAADDQGRLLSDPFT 240
Db 181 IHCSVKTAENSYAAKSGCCFPSSATVHLEQGTTKLVDLSPGDRVLAADDQGRLLSDPFT 240
Cc 241 FLDRDGAKKYYVIETREPERRLLTAAHILFVAHNDSATGEBEAASSSGPPGGAG 300
Db 241 FLDRDGAKKYYVIETREPERRLLTAAHILFVAHNDSATGEBEAASSSGPPGGAG 300
Cc 301 PRALFAASVRPQQRVVVAERDGRILLPAVAVSTVLSEZAGAYAPLTAQGTILINRVL 360
Db 301 PRALFAASVRPQQRVVVAERDGRILLPAVAVSTVLSEZAGAYAPLTAQGTILINRVL 360
Cc 361 ASCYAVIEEHSAHRAFAPRIAHALLAALAPARTDGRILLPAVAVSTVLSEZAGAYAPLTAQGTILINRVL 420
Db 361 ASCYAVIEEHSAHRAFAPRIAHALLAALAPARTDGRILLPAVAVSTVLSEZAGAYAPLTAQGTILINRVL 420
Cc 421 ADAPGAGATAGIHWYSQQLYQIGTWLIDSEALHPLGMVAKSSXSRAGGAGREGA 475
Db 421 ADAPGAGATAGIHWYSQQLYQIGTWLIDSEALHPLGMVAKSSXSRAGGAGREGA 475

CC The present invention relates to a novel method for modulating growth, differentiation or survival of a cell. The method involves contacting the cell with a hedgehog polypeptide such as Desert hedgehog (Dhh), Sonic hedgehog (Shh) and Indian hedgehog (Ihh). The method is used to induce a cell to differentiate to a neuronal cell phenotype. It is used to modulate skeletogenesis. The method is used to treat a degenerative disorder of the nervous system such as neuro muscular, autonomic or central nervous system disorders (e.g., Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's disease, multiple sclerosis, Pick's disease, neuronal degeneration associated with a natural aging process and neuronal damage resulting from trauma and neuronal damage resulting from anoxia-ischaemia. The invention is also used for antisense gene therapy. The present sequence is human Shh protein

XX Sequence 475 AA;

Query Match 99.9%; Score 2467; DB 7; Length 475;

Best Local Similarity 100.0%; Pred. No. 2.1e-217; Mismatches 0; Indels 0; Gaps 0;

Matches 475; Conservative 0; CC 1 MILLARCLLVVSSLLVVCSSGLACGPRGFGRPKKLTPLAKQFVNVAEKTGLGAG 60
Db 1 MILLARCLLVVSSLLVVCSSGLACGPRGFGRPKKLTPLAKQFVNVAEKTGLGAG 60
Cc 61 RYEKGKISRNSRFKELTPNPDIFKDENTGADRMLTORCKDKLNALAIISVNKNOWPVE 120
Db 61 RYEKGKISRNSRFKELTPNPDIFKDENTGADRMLTORCKDKLNALAIISVNKNOWPVE 120
Cc 121 KLRVTEGWDDEGHHSSESLHVEGRADITTSDRSKYGMRLAVALAEAGFDWVYESKAH 180
Db 121 KLRVTEGWDDEGHHSSESLHVEGRADITTSDRSKYGMRLAVALAEAGFDWVYESKAH 180
Cc 181 IHCSVKTAENSYAAKSGCCFPSSATVHLEQGTTKLVDLSPGDRVLAADDQGRLLSDPFT 240
Db 181 IHCSVKTAENSYAAKSGCCFPSSATVHLEQGTTKLVDLSPGDRVLAADDQGRLLSDPFT 240
Cc 241 FLDRDGAKKYYVIETREPERRLLTAAHILFVAHNDSATGEBEAASSSGPPGGAG 300
Db 241 FLDRDGAKKYYVIETREPERRLLTAAHILFVAHNDSATGEBEAASSSGPPGGAG 300
Cc 301 PRALFAASVRPQQRVVVAERDGRILLPAVAVSTVLSEZAGAYAPLTAQGTILINRVL 360
Db 301 PRALFAASVRPQQRVVVAERDGRILLPAVAVSTVLSEZAGAYAPLTAQGTILINRVL 360
Cc 361 ASCYAVIEEHSAHRAFAPRIAHALLAALAPARTDGRILLPAVAVSTVLSEZAGAYAPLTAQGTILINRVL 420
Db 361 ASCYAVIEEHSAHRAFAPRIAHALLAALAPARTDGRILLPAVAVSTVLSEZAGAYAPLTAQGTILINRVL 420
Cc 421 ADAPGAGATAGIHWYSQQLYQIGTWLIDSEALHPLGMVAKSSXSRAGGAGREGA 475
Db 421 ADAPGAGATAGIHWYSQQLYQIGTWLIDSEALHPLGMVAKSSXSRAGGAGREGA 475

RESULT 22
ABW00868 ABW00868 Standard; protein: 475 AA.
XX AC ABW00868;
XX DT 15-JAN-2004 (first entry)
XX DE Human sonic hedgehog protein.
XX SQ Sequence 475 AA;
Query Match 99.9%; Score 2467; DB 7; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-217; Mismatches 0; Indels 0; Gaps 0;
Matches 475; Conservative 0; CC 1 MILLARCLLVVSSLLVVCSSGLACGPRGFGRPKKLTPLAKQFVNVAEKTGLGAG 60
Db 1 MILLARCLLVVSSLLVVCSSGLACGPRGFGRPKKLTPLAKQFVNVAEKTGLGAG 60
Cc 61 RYEKGKISRNSRFKELTPNPDIFKDENTGADRMLTORCKDKLNALAIISVNKNOWPVE 120
Db 61 RYEKGKISRNSRFKELTPNPDIFKDENTGADRMLTORCKDKLNALAIISVNKNOWPVE 120
Cc 121 KLRVTEGWDDEGHHSSESLHVEGRADITTSDRSKYGMRLAVALAEAGFDWVYESKAH 180
Db 121 KLRVTEGWDDEGHHSSESLHVEGRADITTSDRSKYGMRLAVALAEAGFDWVYESKAH 180
Cc 181 IHCSVKTAENSYAAKSGCCFPSSATVHLEQGTTKLVDLSPGDRVLAADDQGRLLSDPFT 240
Db 181 IHCSVKTAENSYAAKSGCCFPSSATVHLEQGTTKLVDLSPGDRVLAADDQGRLLSDPFT 240

Best Local Similarity 100.0%; Pred. No. 2.1e-217; Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 181 IHCsvkaensvaaksgggcpgsatvhleqggtklyvkdlspdrlvlaaddqrllysdelt 240
 QY 241 FLDRDGAKKVFVVIETPREPLLTPAHLIFVAPINDSATGEPEASSGSGPPSGALG 300
 DB 241 FLDRDGAKKVFVVIETPREPLLTPAHLIFVAPINDSATGEPEASSGSGPPSGALG 300
 DB 301 PRALFASRTRPGQRYVVAERDGRLLPAAVHSVTLSEAGAYAATLTAQTGTLINRV 360
 QY 301 PRALFASRTRPGQRYVVAERDGRLLPAAVHSVTLSEAGAYAATLTAQTGTLINRV 360
 DB 301 PRALFASRTRPGQRYVVAERDGRLLPAAVHSVTLSEAGAYAATLTAQTGTLINRV 360
 QY 361 ASCYAVIIEBHSWAHRAAFPLLAALAPARTDGGDSCGGDRGGGRVALTAPGA 420
 DB 361 ASCYAVIIEBHSWAHRAAFPLLAALAPARTDGGDSCGGDRGGGRVALTAPGA 420
 QY 421 ADAGAGATAGIHWYSQQLYQITWLDSAEAHPLGNKAVKSXSRGAGGAREGA 475
 DB 421 ADAGAGATAGIHWYSQQLYQITWLDSAEAHPLGNKAVKSXSRGAGGAREGA 475

RESULT 23
 ADD71383 standard; protein; 475 AA.
 XX ADD71383;
 AC ADD71383;
 DT 29-JAN-2004 (first entry)
 DE Human sonic hedgehog (shh).
 KW hedgehog polypeptide; tissue array generation; tissue array maintenance;
 human; sonic hedgehog; shh.
 OS Homo sapiens.
 PH Key Location/Qualifiers
 FT Misc-difference 463
 FT /note= "Unknown"
 US2003139696-A1.
 XX 09-OCT-2003.
 XX 13-DEC-2000; 2000US-00736476.
 PR 30-DEC-1993; 93US-001764227.
 PR 14-DEC-1994; 94US-00356050.
 PR 04-MAY-1995; 95US-00435093.
 PR 05-JUN-1995; 95US-00460900.
 PA (HARD) HARVARD COLLEGE.
 PI Ingham PW, McMahon AP, Tabin CJ, Bumcrot DA, Marti-Gorostiza E;
 XX WPI; 2003-831623/77.
 DR N-PSDB; ADD71376.
 XX New nucleic acid encoding a hedgehog polypeptide having an amino acid sequence identical or homologous to a vertebrate hedgehog protein, useful for generating or maintaining an array of different vertebrate tissue in vitro and in vivo.
 XX Claim 12; SEQ ID NO 13; 118pp; English.
 PS The invention describes an isolated nucleic acid encoding a hedgehog polypeptide having an amino acid sequence identical or homologous to a vertebrate hedgehog protein or its portion and not identical to a fully defined 471-bp sequence. The nucleic acid is useful for generating and/or maintaining an array of different vertebrate tissue both in vitro and in vivo. This is the amino acid sequence of human sonic hedgehog (shh). Sequence 475 AA;
 XX Query Match 99.9%; Score 2467; DB 7; Length 475;

RESULT 24
 AAB83085 standard; protein; 462 AA.
 XX ID AAB83085;
 AC AAB83085;
 XX DT 22-AUG-2001 (first entry)
 DE Human sonic hedgehog (shh) polypeptide.
 KW Insulin; hedgehog protein; sonic hedgehog; Shh; indian hedgehog; Ihh; desert hedgehog; Dhx; diabetes; pancreatic beta-cell; PBC; IDX-1; neogenesis; hyperinsuliremia.
 XX Homo sapiens.
 OS WO200141766-A1.
 XX PN 14-JUN-2001.
 XX PR 08-DEC-2000; 2000WO-US033575.
 PR 10-DEC-1999; 99US-0170282P.
 PA (GEHO) GEN HOSPITAL CORP.
 XX PI Habener JF, Thomas MK;
 XX DR WPI; 2001-381452/40.
 DR N-PSDB; AAF84005.
 XX PT Treating deficiency of insulin, IDX-1 or pancreatic beta cells in a patient by administering a hedgehog protein, nucleic acid encoding the protein or cells expressing the protein.
 XX PS Disclosure; Fig 1B; 63pp; English.

The invention relates to a method of treating deficiency of insulin, that involves administering a hedgehog protein or nucleic acid encoding the hedgehog protein. The hedgehog proteins that can be used in the method are selected from sonic hedgehog (Shhh), indian hedgehog (Ihh) and desert hedgehog (Dhh). The method is useful for treating deficiency of insulin in a patient afflicted with diabetes, by stimulating insulin production in pancreatic beta-cells (PBC). It is also used to treat deficiency of IDX-1 in a patient, by stimulating IDX-1 production in PBC. The hedgehog protein is useful for modulating IDX-1 gene expression or its protein in PBC. This is used to treat deficiency of PBC in a patient, by stimulating neogenesis from beta-cell pancreatic ductal precursor cells. Inhibitors of the hedgehog Proteins are useful for suppressing secretion of insulin in a patient afflicted with hyperinsulinemia. The present sequence represents a human Shh polypeptide.

SQ Sequence 462 AA;

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Query Match Score 97.5%; Pred. No. 6.6e-212; Length 462;
Best Local Similarity 100.0%; Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MLLARCLLVLVSSLLVCSGLACGPGRGKRRPKCUTPLAYQFIFNVAETTLGAG 60
Db 1 MLLARCLLVLVSSLLVCSGLACGPGRGKRRPKCUTPLAYQFIFNVAETTLGAG 60
Qy 61 RYEKGKRSNSRERKELTTPYNNPDIIKFDDENTGADRMLTORCKDLNAISYMNQPCV 120
Qy 61 RYEKGKRSNSRERKELTTPYNNPDIIKFDDENTGADRMLTORCKDLNAISYMNQPCV 120
Db 121 KLRVTEGWDDEGHHSBESLHYEGRADITTSDRDKSYGMNLARAVEAGDFWYYYESKSH 180
Qy 121 KLRVTEGWDDEGHHSBESLHYEGRADITTSDRDKSYGMNLARAVEAGDFWYYYESKSH 180
Db 121 KLRVTEGWDDEGHHSBESLHYEGRADITTSDRDKSYGMNLARAVEAGDFWYYYESKSH 180
Qy 181 IHCSVRAENSTAAKSGCCPPSASATVLEQCGTLYKDLSDGDRVLAADPOGRLLYSDFLT 240
Db 181 IHCSVRAENSTAAKSGCCPPSASATVLEQCGTLYKDLSDGDRVLAADPOGRLLYSDFLT 240
Qy 241 FLDRDDGAKKYFYVIETREPRERLLTAAHILFVAPHNDSATGEPASSSSGPPSGGAUG 300
Db 241 FLDRDDGAKKYFYVIETREPRERLLTAAHILFVAPHNDSATGEPASSSSGPPSGGAUG 300
Qy 301 PRALFAVRPVGQRTVVAERGDRLPAAVHSTVLSEEAGAYAPLTAQGTILINRVL 360
Db 301 PRALFAVRPVGQRTVVAERGDRLPAAVHSTVLSEEAGAYAPLTAQGTILINRVL 360
Qy 361 ASCYAVEEHSAHRAAAPFRIAHALLAALAPARTDGGDSGGDRGGGRVALTAPGA 420
Db 361 ASCYAVEEHSAHRAAAPFRIAHALLAALAPARTDGGDSGGDRGGGRVALTAPGA 420
Qy 421 ADAPGAGATAGTHWSOLIYQIGTWILDSEALHPLGMVKSS 462
Db 421 ADAPGAGATAGTHWSOLIYQIGTWILDSEALHPLGMVKSS 462

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RESULT 25 ADA09286 ID ADA09286 standard; protein: 462 AA.
XX AC ADA09286;
XX DT 20-NOV-2003 (first entry)
XX DE Human Sonic Hedgehog protein (Shh).
XX KW Human; hedgehog protein; desert; indian; sonic; Dhh; Ihh; Shh;
KW cytostatic; gene therapy; carcinogenic; gastric; colonic; cancer;
KW gastrointestinal tract; colonic adenomatous polyp;
KW invasive adenocarcinoma; intestinal adenoma; desmoid tumour.
OS Homo sapiens.
XX PN WO2003070265-A2.
XX

PD 28-AUG-2003.
XX XX PR 20-FEB-2003; 2003WO-NL000127.
XX XX PR 20-FEB-2002; 2002EP-00075690.

XX PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.

XX PI Van Den Brink GR, Peppelenbosch MP, Hardwick JCH, Van Deventer STH;
XX XX WPI; 2003-697568/66.
XX PT Use of a Hedgehog protein for treating Hedgehog protein deficiency in the
PT gastrointestinal tract, or for preventing gastric or colonic cancer,
PT colonic adenomatous polyps, invasive adenocarcinomas, small intestinal
PT adenomas.

SQ Disclosure; Page 47-49; 67pp; English.

PS XX The invention relates to treating a deficiency of a Hedgehog protein in the gastrointestinal tract. The method of the invention comprises providing a source of Hedgehog protein to the GI tract of a subject suffering from the deficiency of this protein. Hedgehog Proteins include CC Desert (Dhh), Indian (Ihh) and Sonic (Shh). The treatment of the deficiency of a Hedgehog Protein in the GI tract is useful for the prophylaxis of carcinogenesis in the GI tract, gastric or colonic cancer, and for the treatment of a GI tract carcinoma, particularly Gastric or colonic cancer. The source Hedgehog protein may also be administered to prevent or reverse colonic adenomatous polyposis, invasive adenocarcinomas, small intestinal adenomas and cancers, and desmoid tumors. Loss of Indian hedgehog (Ihh) expression was evident in the earliest recognisable stage in the sequence of events that is thought to progress to colon cancer. Ihh was found to be not expressed in malignant colonic epithelial cells. The colon cancer cell HT-29 will only express Ihh protein after differentiation with butyrate. The in vitro differentiation of HT-29 cells with recombinant hedgehog (Ihh) protein was determined. Forty-eight hour treatment of HT-29 cells induces Ihh expression to a similar extent as after treatment with 5 mM butyrate. Data show that exogenous Ihh protein was sufficient to restore differentiation of colon carcinoma cells. Hedgehog proteins may also be used in gene therapy techniques. The current sequence represents the human Sonic hedgehog protein (Shh).

SQ Sequence 462 AA;

Query Match Score 97.5%; Pred. No. 6.6e-212; Length 462;
Best Local Similarity 100.0%; Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MLLARCLLVLVSSLLVCSGLACGPGRGKRRPKCUTPLAYQFIFNVAETTLGAG 60
Db 1 MLLARCLLVLVSSLLVCSGLACGPGRGKRRPKCUTPLAYQFIFNVAETTLGAG 60
Qy 61 RYEKGKRSNSRERKELTTPYNNPDIIKFDDENTGADRMLTORCKDLNAISYMNQPCV 120
Qy 61 RYEKGKRSNSRERKELTTPYNNPDIIKFDDENTGADRMLTORCKDLNAISYMNQPCV 120
Db 121 KLRVTEGWDDEGHHSBESLHYEGRADITTSDRDKSYGMNLARAVEAGDFWYYYESKSH 180
Qy 121 KLRVTEGWDDEGHHSBESLHYEGRADITTSDRDKSYGMNLARAVEAGDFWYYYESKSH 180
Db 121 KLRVTEGWDDEGHHSBESLHYEGRADITTSDRDKSYGMNLARAVEAGDFWYYYESKSH 180
Qy 181 IHCSVRAENSTAAKSGCCPPSASATVLEQCGTLYKDLSDGDRVLAADPOGRLLYSDFLT 240
Db 181 IHCSVRAENSTAAKSGCCPPSASATVLEQCGTLYKDLSDGDRVLAADPOGRLLYSDFLT 240
Qy 241 FLDRDDGAKKYFYVIETREPRERLLTAAHILFVAPHNDSATGEPASSSSGPPSGGAUG 300
Db 241 FLDRDDGAKKYFYVIETREPRERLLTAAHILFVAPHNDSATGEPASSSSGPPSGGAUG 300
Qy 301 PRALFAVRPVGQRTVVAERGDRLPAAVHSTVLSEEAGAYAPLTAQGTILINRVL 360
Db 301 PRALFAVRPVGQRTVVAERGDRLPAAVHSTVLSEEAGAYAPLTAQGTILINRVL 360
Qy 361 ASCYAVEEHSAHRAAAPFRIAHALLAALAPARTDGGDSGGDRGGGRVALTAPGA 420
Db 361 ASCYAVEEHSAHRAAAPFRIAHALLAALAPARTDGGDSGGDRGGGRVALTAPGA 420
Qy 421 ADAPGAGATAGTHWSOLIYQIGTWILDSEALHPLGMVKSS 462
Db 421 ADAPGAGATAGTHWSOLIYQIGTWILDSEALHPLGMVKSS 462

Qy 61 RYEKGKRSNSRERKELTTPYNNPDIIKFDDENTGADRMLTORCKDLNAISYMNQPCV 120
Db 61 RYEKGKRSNSRERKELTTPYNNPDIIKFDDENTGADRMLTORCKDLNAISYMNQPCV 120
Qy 121 KLRVTEGWDDEGHHSSESLHYEGRADITTSDEDRSKYMLARAVEAGDFWYYYESKSH 180
Db 121 KLRVTEGWDDEGHHSSESLHYEGRADITTSDEDRSKYMLARAVEAGDFWYYYESKSH 180
Qy 181 IHCSVRAENSTAAKSGCCPPSASATVLEQCGTLYKDLSDGDRVLAADPOGRLLYSDFLT 240
Db 181 IHCSVRAENSTAAKSGCCPPSASATVLEQCGTLYKDLSDGDRVLAADPOGRLLYSDFLT 240
Qy 241 FLDRDDGAKKYFYVIETREPRERLLTAAHILFVAPHNDSATGEPASSSSGPPSGGAUG 300
Db 241 FLDRDDGAKKYFYVIETREPRERLLTAAHILFVAPHNDSATGEPASSSSGPPSGGAUG 300
Qy 301 PRALFAVRPVGQRTVVAERGDRLPAAVHSTVLSEEAGAYAPLTAQGTILINRVL 360
Db 301 PRALFAVRPVGQRTVVAERGDRLPAAVHSTVLSEEAGAYAPLTAQGTILINRVL 360

Qy 361 ASCYAVEEHSAHRAAAPFRIAHALLAALAPARTDGGDSGGDRGGGRVALTAPGA 420

CC and differentiation, e.g. in cases of wound healing or any of a very wide
 CC range of conditions involving reduced hedgehog signalling such as bone
 CC formation, hyperproliferative or hypoproliferative skin disease, growth
 CC of hair, neurodegeneration (Alzheimer's disease etc.) or autonomic
 CC disorders of the peripheral nervous system, e.g. cardiac arrhythmia; to
 CC study physiological pathways; and to screen for drugs that modulate HH
 CC activity and expression. HH proteins are also useful in vitro for
 CC sustaining reproduction of neural precursor cells. Detecting presence of a tumour;
 CC similar analyses can be done at the protein level using antibodies, which
 CC may also be used to treat human cancers

XX

SQ Sequence 462 AA;

Query Match 97.3%; Score 2403; DB 2; Length 462;

Best Local Similarity 99.8%; Pred. No. 1.5e-21; Length 462;
Matches 461; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLARCLLIVLSSLLIVSGLACGPGRGFGKRRHPKKLTPLAYKFPIVNAEKTIGASG 60
 Db 1 MLLARCLLIVLSSLLIVSGLACGPGRGFGKRRHPKKLTPLAYKFPIVNAEKTIGASG 60
 Qy 61 RYEKGKISRNSERFKELTPTNPNPDIFKDENTGADRIMQRCDKKLNALAISVNQPGV 120
 Db 61 RYEKGKISRNSERFKELTPTNPNPDIFKDENTGADRIMQRCDKKLNALAISVNQPGV 120
 Qy 121 KLRVTEGMDWGDGHSEBESLYHEGRAVDITTSDRDKSYKMLAIAVEAGFDATYYESKAH 180
 Db 121 KLRVTEGMDWGDGHSEBESLYHEGRAVDITTSDRDKSYKMLAIAVEAGFDWVYESKAH 180
 Qy 181 IHCSYKAENSAAKSGGCCFGSATVHLEQCGTKLVKDLSIPGDRVLAADDQGRLLYSDFLT 240
 Db 181 IHCSYKAENSAAKSGGCCFGSATVHLEQCGTKLVKDLSIPGDRVLAADDQGRLLYSDFLT 240
 Qy 241 FLDRDGAKVVFYVETREPRLTAAHLLFTAPINNSATGEPEASGSGPSSGALG 300
 Db 241 FLDRDGAKVVFYVETREPRLTAAHLLFTAPINNSATGEPEASGSGPSSGALG 300
 Qy 301 PRALFASRVPQGYVVAARDGDRRLPAAVHSVTLSSEAAGAYAPLTAQQTILINRVL 360
 Db 301 PRALFASRVPQGYVVAARDGDRRLPAAVHSVTLSSEAAGAYAPLTAQQTILINRVL 360
 Qy 361 ASCYAVIEEHSAWAHAFAPPRLAHLLALAPARTDGGDSGGDRGGGRVALTAGA 420
 Db 361 ASCYAVIEEHSAWAHAFAPPRLAHLLALAPARTDGGDSGGDRGGGRVALTAGA 420
 Qy 421 ADAPGAGATAGIHWYSQLIQIGTMLDSEALHPLGMATSS 462
 Db 421 ADAPGAGATAGIHWYSQLIQIGTMLDSEALHPLGMATSS 462

RESULT 28

ID AAW48735 standard; protein; 462 AA.

AC AAW48735;

DT 14-SEP-1998 (first entry)

XX Human mutated sonic hedgehog (SHH) protein (His133-Tyr).
 XX Sonic hedgehog; SHH protein; tumorigenesis; oncogenesis;
 KW basal cell carcinoma; breast cancer; medulloblastoma; tumour;
 KW cell proliferation; cell differentiation; wound healing; diagnosis;
 KW therapy; human.
 XX Homo sapiens.

OS Homo sapiens.

PN WO9821227-A1.

XX PD 22-MAY-1998.

XX PF 12-NOV-1997; 97WO-US020227.

XX PR 13-NOV-1996; 96US-00748591.
 XX PA (REGG) UNIV CALIFORNIA.

XX PI Epstein E, Hu Z, Bonifas J;
 XX DR WPI: 1998-297857/26.
 DR N-PSDB; AAV18403.

XX PT New nucleic acid encoding oncogenic human hedgehog protein - useful for,
 PT e.g. treatment and diagnosis of cancer and diseases involving cell
 PT proliferation or differentiation.

XX SQ

XX PS Claim 6; Page 28-29; 47PP; English.

XX This human sonic hedgehog (SHH) Protein carries a spontaneously occurring
 CC mutation (H133Y substitution) that is associated with oncogenic
 CC transformation of human cells. The amino acid substitution results from a
 CC mutation of the SHH Gene (see AAV18403). This mutation was identified in
 CC 3 independently arising tumours (a basal cell carcinoma,
 CC medulloblastoma, and breast cancer). A second basal cell carcinoma was
 CC shown to carry a different mutation (see AAV48736). Purified oncogenic HH
 CC proteins, and methods for producing the proteins using mammalian
 CC (preferably human) host cells are claimed. The HH proteins can be used:
 CC in functional mapping; therapeutically for modulating cell proliferation
 CC and differentiation, e.g. in cases of wound healing or any of a very wide
 CC range of conditions involving reduced hedgehog signalling such as bone
 CC formation, hyperproliferative or hypoproliferative skin disease, growth
 CC of hair, neurodegeneration (Alzheimer's disease etc.) or autonomic
 CC disorders of the peripheral nervous system, e.g. cardiac arrhythmia; to
 CC study physiological pathways; and to screen for drugs that modulate HH
 CC activity and expression. HH proteins are also useful *in vitro* for
 CC sustaining reproduction of neural progenitor cells. Detecting presence of
 CC oncogenic HH mutations is used to characterise the phenotype of a tumour;
 CC similar analyses can be done at the protein level using antibodies, which
 CC may also be used to treat human cancers

XX SQ Sequence 462 AA;

Query Match 97.2%; Score 2401; DB 2; Length 462;
 Best Local Similarity 99.8%; Pred. No. 2.4e-21;
 Matches 461; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLARCLLIVLSSLLIVSGLACGPGRGFGKRRHPKKLTPLAYKFPIVNAEKTIGASG 60

Db 1 MLLARCLLIVLSSLLIVSGLACGPGRGFGKRRHPKKLTPLAYKFPIVNAEKTIGASG 60

Qy 61 RYEKGKISRNSERFKELTPTNPNPDIFKDENTGADRIMQRCDKKLNALAISVNQPGV 120

Db 61 RYEKGKISRNSERFKELTPTNPNPDIFKDENTGADRIMQRCDKKLNALAISVNQPGV 120

Qy 121 KLRVTEGMDWGDGHSEBESLYHEGRAVDITTSDRDKSYKMLAIAVEAGFDATYYESKAH 180

Db 121 KLRVTEGMDWGDGHSEBESLYHEGRAVDITTSDRDKSYKMLAIAVEAGFDWVYESKAH 180

Qy 181 IHCSYKAENSAAKSGGCCFGSATVHLEQCGTKLVKDLSIPGDRVLAADDQGRLLYSDFLT 240

Db 181 IHCSYKAENSAAKSGGCCFGSATVHLEQCGTKLVKDLSIPGDRVLAADDQGRLLYSDFLT 240

Qy 241 FLDRDGAKVVFYVETREPRLTAAHLLFTAPINNSATGEPEASGSGPSSGALG 300

Db 241 FLDRDGAKVVFYVETREPRLTAAHLLFTAPINNSATGEPEASGSGPSSGALG 300

Qy 301 PRALFASRVPQGYVVAARDGDRRLPAAVHSVTLSSEAAGAYAPLTAQQTILINRVL 360

Db 301 PRALFASRVPQGYVVAARDGDRRLPAAVHSVTLSSEAAGAYAPLTAQQTILINRVL 360

Qy 361 ASCYAVIEEHSAWAHAFAPPRLAHLLALAPARTDGGDSGGDRGGGRVALTAGA 420

Db 361 ASCYAVIEEHSAWAHAFAPPRLAHLLALAPARTDGGDSGGDRGGGRVALTAGA 420

Qy 421 ADAPGAGATAGIHWYSQLIQIGTMLDSEALHPLGMATSS 462

Db 421 ADAPGAGATAGIHWYSQLIQIGTMLDSEALHPLGMATSS 462

Qy 181 IHCSYKAENSAAKSGGCCFGSATVHLEQCGTKLVKDLSIPGDRVLAADDQGRLLYSDFLT 240

Db 181 IHCSYKAENSAAKSGGCCFGSATVHLEQCGTKLVKDLSIPGDRVLAADDQGRLLYSDFLT 240

Qy 241 FLDRDGAKVVFYVETREPRLTAAHLLFTAPINNSATGEPEASGSGPSSGALG 300

Db 241 FLDRDGAKVVFYVETREPRLTAAHLLFTAPINNSATGEPEASGSGPSSGALG 300

Qy 361 ASCYAVIEEHSAWAHAFAPPRLAHLLALAPARTDGGDSGGDRGGGRVALTAGA 420

Db 361 ASCYAVIEEHSAWAHAFAPPRLAHLLALAPARTDGGDSGGDRGGGRVALTAGA 420

Qy 421 ADAPGAGATAGIHWYSQLIQIGTMLDSEALHPLGMATSS 462

PF

CC in pancreatic beta-cells PBC). It is also used to treat deficiency of IDX-1 in a patient, by stimulating IDX-1 production in PBC. The hedgehog protein is useful for modulating IDX-1 gene expression or its protein in PBC. This is used to treat deficiency of PBC in a patient, by stimulating neogenesis from beta-cell pancreatic ductal precursor cells. Inhibitors of the hedgehog proteins are useful for suppressing secretion of insulin in a patient afflicted with hyperinsulinemia. The present sequence represents a mouse Shh polypeptide.

XX Sequence 437 AA;

Query Match 83 %; Score 2068; DB 4; Length 437;

Best Local Similarity 87.4%; Pred. No. 8.3e-181; Mismatches 8; Conservative Matches 404; Indels 26; Gaps 3;

Qy 1 MILAARCILLYVSSILIVCSLAGCPGRCGKPRHKPKKUTPLAKQFIPNVAEKTIGASG 60

Db 2 LILLARCEFLVASSILIVCPGLACGPGRGKPRHKPKKUTPLAKQFIPNVAEKTIGASG 61

Qy 61 RYEKGTRNSRERKFELTPNPNPDLIFKDENTGADRIMTORCKDKNALAIYMNOPGV 120

Db 62 RYEKGTRNSRERKFELTPNPNPDLIFKDENTGADRIMTORCKDKNALAIYMNOPGV 121

Qy 121 KLRVTEGWDDEGHHSSESHYEGRAVDITTSDRSKYMLRNLAVENGFDWVYESKAH 180

Db 122 KLRVTEGWDDEGHHSSESHYEGRAVDITTSDRSKYMLRNLAVENGFDWVYESKAH 181

Qy 181 IHCSYKAENSYAAKSQGCCFGPSATVHLEQGGTKLVKDLSFGDRYLAADDQGRLLYSDFLT 240

Db 182 IHCSYKAENSYAAKSQGCCFGPSATVHLEQGGTKLVKDLSFGDRYLAADDQGRLLYSDFLT 241

Qy 241 FLDRDGAKKVYYVIE TREPERLILTAHLLFYAPHNDSATGEPEASSGSGPSSGGALG 300

Db 242 FLDRDGAKKVYYVIE TREPERLILTAHLLFYAPHND-----SGPPPG 286

Qy 301 PRALFASRVRPGQRVYVVAERGDRLPRAVHSVTLSSEAAGAYAPLTTAGTGTLINEVLT 360

Db 287 PSALFASRVRPGQRVYVVAERGDRLPRAVHSVTLREAGAYAPLTTAGTGTLINEVLT 346

Qy 361 ASCYAVIEEHSAHRAFAPPLAHLLALAAPARD-----GDRGGGRVVALTAGQA 420

Db 347 ASCYAVIEEHSAHRAFAPPLAHLLALAAPARD-----GGGGSIP-AAQSA 395

Qy 421 ADPGAGTAGIHWSQLYQIGTWILDSEALHPGMAYKSS 462

Db 396 TEARGAEPTAGIHWSQLYQIGTWILDSETMHPGMAYKSS 437

RESULT 31

ID AAE09292 standard; protein; 437 AA.
XX AC AAE09292;
XX DT 19-Nov-2001 (first entry)
DE Mouse sonic hedgehog (Shh) protein.

XX Fibroblast growth factor-4: FGF-4: neuronal formation; dopamine; DA;

KW serotonin; 5-hydroxytryptamine; SH; neuroprogenitor cell; depression; sonic hedgehog; Shh; food intake disorder; stress response; vulnerability; sexual activity; cardiovascular function; temperature regulation; pain; obsessive-compulsive behaviour; violent aggressive behaviour; anorexia; reward-associated behaviour; Parkinson's disease; sensory neglect; drug addiction; lesion; trauma; illness; tremor; rigidity; neuroleptic; postural abnormality; akinesia; aphagia; schizophrenia; adipsia; mouse; bulimia.

XX OS Mus musculus.

XX PN US6277820-B1.

PD 21-AUG-2001.

XX XX 09-APR-1998; 98US-00057860.
XX XX 09-APR-1998; 98US-00057860.
XX PR PT in postural reflux regulation, involves contacting neuroprogenitor cells with fibroblast growth factor-8 and sonic hedgehog polypeptide.

XX XX Claim 1; Fig 11; 40PP; English.

XX PS The present invention relates to neuronal formation and methods of treating diseases characterised by abnormalities in the activity of dopaminergic (DA) and serotonergic (5HT) neurons. The invention also relates to a method of forming serotonergic neurons in vitro by contacting neuroprogenitor cells to an effective amount of native sequence, variants and functional fragments of fibroblast growth factor-8 (FGF-8), FGF-4 and sonic hedgehog (Shh). The method is used to treat disorders relating to food intake, hormone secretion, stress response, pain and immune function; sexual activity, cardiovascular function and temperature regulation, in particular depression, proclivity to suicide, obsessive-compulsive behaviour, violent aggressive behaviour and anorexia/bulimia. The method and the composition are useful for forming dopaminergic neurons by stimulating differentiation of neuroprogenitor cells into dopaminergic neurons which is useful for treating disorders characterised by abnormalities in the regulation of postural reflexes, movement and reward-associated behaviours including Parkinson's disease, schizophrenia, drug addiction, lesions due to trauma or other illness resulting in Parkinson-like conditions such as resting tremor, rigidity, akinesia and postural abnormality, including akinesthesia, adipsia, aphagia and sensory neglect. The present sequence is mouse sonic hedgehog protein.

XX SQ Sequence 437 AA;

XX Query Match 83 %; Score 2068; DB 4; Length 437;
Best Local Similarity 87.4%; Pred. No. 8.3e-181;
Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

XX Qy 1 MILLARCLILLYVSSILIVCSLAGCPGRCGKPRHKPKKUTPLAKQFIPNVAEKTIGASG 60
CC CC The present invention relates to neuronal formation and methods of
CC CC treating diseases characterised by abnormalities in the activity of
CC CC dopaminergic (DA) and serotonergic (5HT) neurons. The invention also
CC CC relates to a method of forming serotonergic neurons in vitro by
CC CC contacting neuroprogenitor cells to an effective amount of native
CC CC sequence, variants and functional fragments of fibroblast growth factor-8
CC CC (FGF-8), FGF-4 and sonic hedgehog (Shh). The method is used to treat
CC CC disorders relating to food intake, hormone secretion, stress response,
CC CC pain and immune function; sexual activity, cardiovascular function and
CC CC temperature regulation, in particular depression, proclivity to suicide,
CC CC obsessive-compulsive behaviour, violent aggressive behaviour and
CC CC anorexia/bulimia. The method and the composition are useful for forming
CC CC dopaminergic neurons by stimulating differentiation of neuroprogenitor
CC CC cells into dopaminergic neurons which is useful for treating disorders
CC CC characterised by abnormalities in the regulation of postural reflexes,
CC CC movement and reward-associated behaviours including Parkinson's disease,
CC CC schizophrenia, drug addiction, lesions due to trauma or other illness
CC CC resulting in Parkinson-like conditions such as resting tremor, rigidity,
CC CC akinesia and postural abnormality, including akinesthesia, adipsia, aphagia
CC CC and sensory neglect. The present sequence is mouse sonic hedgehog
CC protein.

XX SQ Sequence 437 AA;

XX Query Match 83 %; Score 2068; DB 4; Length 437;
Best Local Similarity 87.4%; Pred. No. 8.3e-181;
Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

XX Qy 1 MILLARCLILLYVSSILIVCSLAGCPGRCGKPRHKPKKUTPLAKQFIPNVAEKTIGASG 60
DB 2 LILLARCEFLVASSILIVCPGLACGPGRGKPRHKPKKUTPLAKQFIPNVAEKTIGASG 61
Qy 1 RVEKGTRNSRERKFELTPNPNPDLIFKDENTGADRIMTORCKDKNALAIYMNOPGV 120
DB 2 RVEKGTRNSRERKFELTPNPNPDLIFKDENTGADRIMTORCKDKNALAIYMNOPGV 120
Qy 61 RVEKGTRNSRERKFELTPNPNPDLIFKDENTGADRIMTORCKDKNALAIYMNOPGV 120
DB 62 RVEKGTRNSRERKFELTPNPNPDLIFKDENTGADRIMTORCKDKNALAIYMNOPGV 120
Qy 121 KLRVTEGWDDEGHHSSESHYEGRAVDITTSDRSKYMLRNLAVENGFDWVYESKAH 180
DB 122 KLRVTEGWDDEGHHSSESHYEGRAVDITTSDRSKYMLRNLAVENGFDWVYESKAH 181
Qy 181 IHCSYKAENSYAAKSQGCCFGPSATVHLEQGGTKLVKDLSFGDRYLAADDQGRLLYSDFLT 240
DB 182 IHCSYKAENSYAAKSQGCCFGPSATVHLEQGGTKLVKDLSFGDRYLAADDQGRLLYSDFLT 241
Qy 241 FLDRDGAKKVYYVIE TREPERLILTAHLLFYAPHNDSATGEPEASSGSGPSSGGALG 300
DB 242 FLDRDGAKKVYYVIE TREPERLILTAHLLFYAPHND-----SGPTPG 286
Qy 301 PRALFASRVRPGQRVYVVAERGDRLPRAVHSVTLSSEAAGAYAPLTTAGTGTLINEVLT 360
DB 327 PSALFASRVRPGQRVYVVAERGDRLPRAVHSVTLREAGAYAPLTTAGTGTLINEVLT 346
Qy 361 ASCYAVIEEHSAHRAFAPPLAHLLALAAPARD-----GDRGGGRVVALTAGQA 420
DB 347 ASCYAVIEEHSAHRAFAPPLAHLLALAAPARD-----GGGGSIP-AAQSA 395

Qy	421 ADAPGAGATAIHHWSQLLYQIGRLWLDSEALHPLGMVKSS 462	CC Desert hedgehog, the target pathway of the hedgehog signalling pathway is Wnt or Bmp signalling pathway
Db	396 TEARGAEPPIAGIHWSQLYHIGTWWLSETHPLGMVKSS 437	CC
		XX
		SQ Sequence 437 AA:
RESULT 32		Query Match 63.8%; Score 2068; DB 4; Length 437;
AAV97559	:	Best Local Similarity 87.4%; Prod. No. 8_3e-181;
ID AAV97559	standard; protein; 437 AA.	Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;
XX		Qy 1 MLLIARCLLIVLVLSSLLVCSGLACGPGRGFGRKRHPKLTPLAKQFIPNVAEKTIQGSG 60
AC		Db 2 LLLIARCPFLVLLSLLVCPGLACGPGRGFGRKRHPKLTPLAKQFIPNVAEKTIQGSG 61
XX	05-APR-2001 (first entry)	Qy 61 RYEKGKISRNRSERFELTPYNPNDIFKDENTGADRMTQRCKDKLNALAISTMNQPGV 120
DE	Mouse sonic hedgehog protein sequence	Db 62 RYEKGKTRISERFELTPYNPNDIFKDENTGADRMTQRCKDKLNALAISTMNQPGV 121
XX		Qy 121 KLRVTEGWDDEDGHSEESLHYEGRADIFTSDRSKYGMLARIAVEAGFDWVYYYESKAH 180
KW	Hedgehog signalling pathway; inhibitor; autoimmune disorder; epithelial cell hyperplasia; fibrosis; inflammation; adenocarcinoma; immune disorder; cancer; thyroiditis; insulitis; multiple sclerosis; iridocyclitis; uveitis; orchitis; hepatitis; Addison's disease; asthma; myasthenia gravis; rheumatoid arthritis; lupus erythematosus; emblysema; adult respiratory distress syndrome; chronic bronchitis; atelectasis; sialosis; hypersensitivity pneumonitis; idiopathic pulmonary fibrosis; pneumonia; pleural fibrosis; atherosclerosis; myocardial infarction; gastrointestinal tract disorder; hepatic disease; Alzheimer's disease; Wnt signalling pathway; BMP signalling pathway; sonic hedgehog; SHH.	Db 122 KLRVTEGWDDEDGHSEESLHYEGRADIFTSDRSKYGMLARIAVEAGFDWVYYYESKAH 181
KW		Qy 181 IHCSYKAENSAVAKSGGCPPGSATVHLFEGGTKLVLDSPGDRVLAADDQGRLLYSDFIT 240
KW		Db 182 IHCSYKAENSAVAKSGGCPPGSATVHLFEGGTKLVLDSPGDRVLAADDQGRLLYSDFIT 241
KW		Qy 241 FLDRDDGAKKVPTETREPRERLLTAHLLFVAPHINDSATGEPEASSGSGPPSGALG 300
KW		Db 242 FLDRDDGAKKVPTETREPRERLLTAHLLFVAPHINDSATGEPEASSGSGPPSGALG 306
OS	Mus musculus	Db 286 SGPTEG-----SGPTEG 286
PN	WO2000074706-A1.	Qy 301 PRALFAASRVRPQVRYVVAERDGDRLLLDAVHSVTLSPEAAGAYPLTAQGTLLINRVL 360
XX		Db 287 PSALFAASRVRPQVRYVVAERGGRRLLPAAVHSVTLSPEAAGAYPLTAHGTLLINRVL 346
PD	14-DEC-2000.	Qy 361 ASCYAVIEEHSAWAHAFAPPLAHLALAAPARTDRGGDSGGDRGGCGRAYLTAPA 420
XX		Db 347 ASCYAVIEEHSAWAHAFAPPLAHLALAAPARTDRGGDSGGDRGGCGRAYLTAPA 420
PF	05-JUN-2000; 20000NO-GB002191.	Qy 421 ADAPGAGATAGIHWYQLIYOIGTWLDSLSEALHPLGMVKSS 462
XX		Db 396 TEARGAEPPIAGIHWSQLYHIGTWWLSETHPLGMVKSS 437
PR	08-JUN-1999; 99GB-00013350.	
PR	16-SEP-1999; 99GB-00021953.	
XX	(LORA-) LORANTIS LTD.	
PA		
PI	Lamb JR, Hoyne GF, Dallman MJ;	RESULT 33
XX		AAO21264
DR	WPI; 2001-061652/07.	ID AAO21264 standard; protein; 437 AA.
DR	N-PSDB; AAA37897.	XX
XX		AC AAO21264;
PT	Use of an inhibitor of a Hedgehog signaling pathway in preparation of a medicament for treating epithelial cell hyperplasia, inflammation, cancer or an immune disorder.	DT 05-AUG-2002 (first entry)
PT		XX
PT		DE 437-mer wild-type sonic hedgehog protein.
PS	Disclosure: Page 70; 78pp; English.	XX
XX		XX Sonic hedgehog protein; amino terminal protein; modulate differentiation; signalling developmental process; neural plate; ligand; patched receptor; wild-type.
CC	This sequence is mouse sonic hedgehog (SHH), and is part of the Hedgehog signalling pathway. The invention relates to the use of an inhibitor of the Hedgehog signalling pathway, or an inhibitor of a target pathway of the hedgehog signalling pathway in the preparation of a medicament for treating epithelial cell hyperplasia, fibrosis of tissue, inflammation, cancer (especially adenocarcinoma) or an immune disorder. The immune disorder can be an autoimmune disorder such as thyroiditis, insulinitis, multiple sclerosis, iridocyclitis, uveitis, arthritis, hepatitis, emphysema and chronic bronchitis, atelectasis, occupational lung disease including silicosis, hypersensitivity diseases of lung such as hypersensitivity pneumonitis, idiopathic interstitial lung diseases such as idiopathic pulmonary fibrosis, pneumonia including interstitial pneumonia, desquamative interstitial pneumonia and acute interstitial pneumonia, and pleural fibrosis. They can also be used in the treatment of inflammation associated with atherosclerosis, e.g. myocardial infarction, diseases of the gastrointestinal tract, hepatic diseases and diseases of the central nervous system e.g. Alzheimer's disease. The hedgehog signalling pathway is that of Sonic hedgehog, Indian hedgehog or	XX
CC		OS Unidentified.
CC		XX Key Location/Qualifiers
CC		PH Cleavage-site 198..200 /label= GCF autoprocessing site
CC		FT FT /note= "This is an autoproteolytic site. Cleavage occurs between the Gly-Cys residues"
CC		XX PN WO200224151-A2.
CC		XX PD 28-MAR-2002.
CC		XX PP 24-SEP-2001; 2001WO-US042438.
CC		XX PR 22-SEP-2000; 2000US-0235153P.
CC		XX PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX	Beachy PA;
XX	PI
XX	XX
DR	WPI; 2002-425894/45.
XX	
PT	New isolated Sonic hedgehog amino terminal protein which is involved in a
PT	signaling developmental process, useful for identifying compounds that
PT	modulate differentiation of neural plate cells.
XX	
PS	Claim 1: Fig 4; 50PP; English.
XX	
CC	The invention relates to an isolated protein having the amino acid
CC	sequence of a Sonic hedgehog amino terminal protein involved in a
CC	signaling developmental process, where alanine is substituted for amino
CC	acid residues at a position such as 51, 52, 56, 75, 80, 76, 81, 105, 116,
CC	132, 135, 138, 168, 177, 189 or 195 or their combination, where the
CC	sequence listing of the terminal protein is not given in specification.
CC	The invention generally relates to methods for identifying compounds that
CC	modulate differentiation of neural plates using hedgehog proteins as
CC	ligands for the patched receptor. This sequence represents the 437-mer
CC	wild-type sonic hedgehog protein of the invention
XX	
SQ	Sequence 437 AA;
Query	Best Match Score 2068; DB 5; Length 437;
Query	Best Local Similarity 87.4%; Pred. No. 8.3e-181;
Matches	Mismatches 24;
Matches	Indels 26;
Matches	Gaps 3
Db	1 MLLARCLLIVLSSILIVCSGLAACGGPGRGFGRHRPKKLTPLAKYKQFIPNVAEKTTLGAGS 60
Db	2 LILLARFLVLISSLIVCPGLACGGPGRGFGRHRPKKLTPLAKYKQFIPNVAEKTTLGAGS 61
Qy	61 RYEKGKISRNSERFKELTPTPNYDIIKDEENTGADRIMTQRCKDKLNALAISYNMWNQCV 120
Db	62 RYEKGKTRNSERFKELTPTPNYDIIKDEENTGADRIMTQRCKDKLNALAISYNMWNQCV 121
Qy	121 KLRVTEWDEDHHSBESLHVEGRADITTSDRDISKGMLARLAVEAFDWVYESKAH 180
Db	122 KLRVTEWDEDHHSBESLHVEGRADITTSDRDISKGMLARLAVEAFDWVYESKAH 181
Qy	181 THCSVKAENSYRAKSGGCFPGSATVHLEQGSTKLYRDLISGDRVIAADQGRLLSDFLT 240
Db	182 THCSVRAENSYRAKSGGCFPGSATVHLEQGSTKLYRDLISGDRVIAADQGRLLSDFLT 241
Qy	241 FLDRDDGAKKYVIEETREPRERLITTAHILFVAPHNDSATGGEPEAASSGEPFGSGGALG 300
Db	242 FLDRDEGAKKYVIEETLEPRERLITTAHILFVAPHND-----SGPPGP 286
Qy	301 PRALFASRVRPVPGQRTVVAEDGDRRLIPAVHVSITLSEFAAGAYAPLTAQGTILINRLV 360
Db	328 PSALFASRVRPVPGQRTVVAERGDRRLIPAVHVSITLREEEAGATAPLTAHGTILINRLV 346
Qy	361 ASCYAVTEEHSHAHRAAPERLAHALAALAPARTDRGGDSGGGRVAlTAGPA 420
Db	347 ASCYAVTEEHSHAHRAAPERLAHALAALAPART-----GGGGSIP-AAQQA 395
Qy	421 ADPGAGATAGIHWYSQQLYQIQTGWTILDSEALHPLGMATVKS 462
Db	396 TEARGABPTGATHWYSQQLYHGTWLDSETMPHLGMATVKS 437
XX	RESULT 34
XX	ABG71358
XX	ID ABG71358 standard; protein; 437 AA.
XX	AC
XX	ABG71358;
DT	23-JAN-2003 (first entry)
XX	
DB	Mouse sonic hedgehog (SHH) polypeptide.
XX	
KW	Mouse; Hedgehog signalling pathway; T-cell mediated disease;
KW	T-cell apoptosis; Notch signalling pathway; cancer; breast; prostate;

Qy	301. PRALFAASRPGORYVYVAAERGDRRLIPAAVHSVTLSERAGAYAALTAQGTLLINRVL 360	1. MILIARCLILVLYSSLLVCSGLACGPGRGFGRKRPCKLTPLAYKOFIPNYAEKTIGASG 60
Db	287. PSALFAASRPGRYYVAAERGDRRLIPAAVHSVTLSEREEFAYAALTAQGTLLINRVL 346	2. LLLIARCLFLIVLASSLLVCPGLACGPGRGFGRKRPCKLTPLAYKQIPNYAEKTIGASG 61
Qy	361. ASCYAVIEBHSWAHRAAFERLALLAALAPARTDGGDSGGDRGGGERVALTAPGA 420	61. RYEKISKIENSERFELTPNPDIFKDENTGADRINTQRCKDKUNALATSYMNQPGV 120
Db	347. ASCYAVIEBHSWAHRAAFERLALLAALAPARTDGGDSGGDRGGGERVALTAPGA 420	62. RYEKTRTRSERFELTPNPDIFKDENTGADRINTQRCKDKUNALATSYMNQPGV 121
Qy	421. ADAFGAGATAAGIHWYSQLLYQIGITWLUDSEALHPLGMKAVKSS 462	121. KLRVTEBGWDEGHSESESHYEGRAVDTTSQRDRSRYGMMLARLAVERAGFDNTTYEESKAH 180
Db	396. TEARGAEPPAGIHWYSQLLYQIGITWLUDSEALHPLGMKAVKSS 437	122. RLRTTEGWDEGHSESHYEGRAVDTTSQRDRSRYGMMLARLAVERAGFDVYVYERKAH 181
RESULT 35		
ID	AAR77339 standard; protein; 437 AA.	
XX		
AC	AAR77339;	
XX	08-MAR-1996 (first entry)	
XX	DE Mouse sonic hedgehog protein.	
XX	Mouse; sonic hedgehog protein; probe; primer; diagnostic; nervous system disorder; gene therapy; antibody.	
XX	OS Mus musculus.	
Key	Location/Qualifiers	RESULT 36
Peptide	1. /note= "signal peptide"	AAW94471 standard; protein; 437 AA.
FT	/note= "conserved sequence (AAR77349)"	
Peptide	25. .30	
FT	/note= "conserved sequence (AAR77349)"	
Modified-Site	279	
FT	/note= "N-linked glycosylation site"	
XX	W09518856-A1.	
XX	13-JUL-1995.	
XX	PF 30-DEC-1994; 94NO-US014992.	
XX	30-DEC-1993; 93US-00176427.	
PR	14-DEC-1994; 94US-00356060.	
XX	(HARD) HARVARD COLLEGE.	
PA	(IMCR) IMPERIAL CANCER RES TECHNOLOGY.	
PA	Ingham PW, McMahon AP, Tabin CJ;	
PI	WPI: 1995-255060/33.	
XX	DR N-PSDB; AAQ91337.	
XX	Hedgehog-like protein(s) and nucleic acid(s) encoding them - useful to treat degenerative nervous system disorder(s) and in gene therapy.	
PS	Claim 17: Page 139-41; 210pp; English.	
XX	The sequence represents a mouse sonic hedgehog protein, homologous to a Drosophila hedgehog protein (AAR77337), and is encoded by a cDNA isolated from an 8-5-day post coitum mouse cDNA library. Probes and primers derived from the sonic hedgehog gene may be used as diagnostic agents for neuromuscular, autonomic or central nervous system disorders, and the gene may also be used in gene therapy. Antibodies generated from the protein may be used as therapeutic or research reagents	
XX	Sequence 437 AA;	
SQ	Query Match 83.6%; Score 2065; DB 2; Length 437;	
	Best Local Similarity 87.2%; Pred. No. 1.6e-180;	
	Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;	
CC	A method has been developed for limiting the damage to neuronal cells by ischaemic or epoxic conditions by administering a ptc (patched)	
CC	PT conditions - is used for the treatment and prevention of e.g. cerebral infarction, stroke and transient ischaemic attacks.	
XX	Disclosure: Page 68-70; 104pp; English.	

therapeutic agent to reduce cerebral infarct volume (CIV). Damage to neuronal cells can also be limited by administering a gene activation construct which recombines with the genomic hedgehog gene to provide a heterologous transcription regulator linked to the coding region of this gene. Administration of the ptc therapeutic agent is used to protect this cerebral tissues against ischaemic injury; to treat cerebral infarct or ischaemia, stroke (thrombolic or embolic) and transient ischaemic attacks. It may also be used as a prophylactic in many other cases of injury to the brain or spinal cord, oedema caused by trauma, haemorrhage and encephalomyelitis, or in conjunction with (coronary bypass) surgery. Treatment (which may be prophylactic) is used where ischaemic/reoxic conditions may cause cerebral hypoxia, or progressive loss of neurons due to oxygen depletion, including in patients with hypertension. The treatment reduces CIV by at least 70%. The present sequence represents a hedgehog sequence given in the present invention.

XX SQ Sequence 437 AA;

Query Match Score 83.6%; DB 2; Length 437;

Best Local Similarity 87.2%; Pred. No. 1.6e-180;

Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

PSI-BLAST PSSM PS Score 83.6%; DB 2; Length 437; Use of hedgehog polypeptides on patched therapeutics.

Claim 26; Page 124-125; 146pp; English.

KW ptc therapeutic; patched.
 XX OS Mus musculus.
 XX PN W0920298-A1.
 XX PD 29-APR-1999.
 XX PP 20-OCT-1998; 98WO-US022227.
 XX PR 20-OCT-1997; 97US-0095552.
 XX PR 11-SEP-1998; 98US-0015199.
 XX PA (ONTO-) ONTOGENY INC.
 XX PI Wang EA;
 XX DR WPI; 1999-288170/24.
 XX N-PSDB; AAX25620.
 PR Use of hedgehog polypeptides on patched therapeutics.
 XX PS Claim 26; Page 124-125; 146pp; English.
 CC The present sequence represents mouse Sonic hedgehog protein Shh. The invention relates to a method for modulating the growth state an epithelial cell by ectopically contacting the epithelial cell, in vitro or in vivo, with hedgehog therapeutic (i.e. a hedgehog polypeptide or gene therapy construct) or ptc therapeutic (i.e. a small organic molecule that mimics the effect of hedgehog proteins on patched signalling, or activates or potentiates patched signalling) in an amount effective to alter the rate of proliferation of the epithelial cell. The hedgehog therapeutic preferably comprises at least a bioactive extracellular portion of a hedgehog protein (see AAY03854-62) encoded by a vertebrate hedgehog gene (see AAX25617-25), especially a human hedgehog gene. Promotion of proliferation of epithelial cells can be used to control a wound healing process in e.g. burn treatment, skin regeneration, skin grafting, pressure sore treatment, dermal ulcer treatment, scar reduction or treatment of ulcerative colitis (claimed). It can also be used to induce hair growth for the treatment of alopecia (claimed). Inhibition of the growth of epithelial tissue can be used to treat or prevent hyperplastic or neoplastic conditions, e.g. psoriasis, keratosis, acne, comedogenic lesions, folliculitis and Pseudofolliculitis, keratoacanthoma, callosities, Darier's disease, keloids, hypertrophic scars, or autoimmune disorders, e.g. aphthous ulcers, pemphigus vulgaris, pemphigus foliaceus, pemphigus vegetans, pemphigus erythematosus, epidermolysis, lupus lesions, desquamative lesions or carcinomas. The methods can also be used to counteract the effects of ageing on skin
 XX SQ Sequence 437 AA;
 Query Match Score 83.6%; DB 2; Length 437;
 Best Local Similarity 87.2%; Pred. No. 1.6e-180;
 Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;
 PSI-BLAST PSSM PS Score 83.6%; DB 2; Length 437;
 Best Local Similarity 87.2%; Pred. No. 1.6e-180;
 Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;
 QY 1 MILLARCLLIVVSSLIVCSGLACGPGRGKGKRHPKKLTPLAYQFIPNVAEKTIGASG 60
 DB 2 LILLARCLLIVVSSLIVCSGLACGPGRGKGKRHPKKLTPLAYQFIPNVAEKTIGASG 61
 QY 1 2 RYEGKLRNSERFRKEITPNNDIIFKDEENTGADRIMTQCRKLNALAISVNQWQG 120
 DB 2 RYEGKLRNSERFRKEITPNNDIIFKDEENTGADRIMTQCRKLNALAISVNQWQG 121
 QY 121 KLRVTBQWDEQGHBSBSLHVEGRAVIDTTSDRDKSKGHLARLAVEAGDWTYESKAH 180
 DB 122 RLRTVSGWDEQHHSSSESLHVEGRADTTSDRBSKGHLARLAVEAGDWTYESKAH 181
 QY 181 IHCSVRAENSYAAKSGGCFPGSATVHLEQSTGTLYDLSPGDRVLAADQGRLLYSDFLT 240
 DB 182 IHCSVRAENSYAAKSGGCFPGSATVHLEQSTGTLYDLSPGDRVLAADQGRLLYSDFLT 241
 QY 241 FLDRDGAKKVYYETREPRERLITTAHILFVAPHNDSATGEPEASSSGPPSGGAIG 300
 DB 242 FLDRDEAKKVYYETREPRERLITTAHILFVAPHNDSATGEPEASSSGPPSGGAIG 286
 QY 301 PRALEFSRVRPQRVYVVAERDGDRRLPAVHSSTLSEPAAGAYAPLTAQGTILINRVL 360
 DB 287 PSALFASRVRPQRVYVVAERGDRRLPAVHSSTLSEPAAGAYAPLTAQGTILINRVL 345
 QY 361 ASCYAVTEEHSAWAHRAPFPLAHALLAALAPARTDRGDSGGDRGGGRVALTAPAA 420
 DB 347 ASCYAVTEEHSAWAHRAPFPLAHALLAALAPARTD-----GGGGGSTP-AAQCA 395
 QY 421 ADAPGAGATAGTHWYSQLYQIGTWLDSEALHPLGMATKSS 462
 DB 396 TEARGAEPTAGTHWYSQLYQIGTWLDSEALHPLGMATKSS 437
 RESULT 37
 ID AAY0557 standard; protein: 437 AA.
 XX AC AAY0557;
 XX DT 02-AUG-1999 (First entry)
 XX DE Mouse Sonic hedgehog Shh protein.
 XX KW Sonic hedgehog; Shh; mouse; epithelial tissue; epithelium;
 KW cutaneous tissue; skin; hair; wound healing; vulnary; burn;
 KW skin grafting; pressure sore; ulcer; ulcerative colitis; alopecia;
 KW psoriasis; keratosis; acne; comedogenic lesion; folliculitis;
 KW pseudofolliculitis; keratoacanthoma; callosities; Darier's disease;
 KW autoimmune disease; pemphigus; epidermolysis; lupus lesion;
 KW desquamative lesion; carcinoma; therapy; hedgehog therapeutic;

Db	242 FLDREGAKKVKVVIETLEPRERLLTAALLFLVAPIND-----SGPTPG 286	XX	Sequence 437 AA;
Qy	301 PRALFASRVRPGQVYVVERGDRPLPAVHSUTLSEANAGAYAPITAOGTILLINRV 360	SQ	Query Match 83.6%; Score 2065; DB 2; Length 437;
Db	287 PSALFASRTRPGRVYVAERGDRRLPAVHSUTREEEAGAYAPLTAGTILLINRV 346	ID	Best Local Similarity 87.2%; Pred. No.: 1..6e-10; Mismatches 9; Conservative Matches 403; Conservate
Qy	361 ASCVAVIEHNSWAHRAFPFLAHALLA LAPARTDGGDSGGDRGGGRVALTAGA 420	9:	Indels 24; Gaps 3;
Db	347 ASCVAVIEHNSWAHRAFPFLAHALLA LAPARTDGGDSGGDRGGGRVALTAGA 395	Qy	1 MILLARCLLUVLSSLLVCSGLACGPGRGFGRHPKLTPLAYKQTPVNAEKTLAGS 60
Qy	421 ADAAGAGATAGIHHYSOLIYQIGTWLDSALEHPLGMVAKSS 462	Db	2 LILLARCLVTLASSLLCPCGLACGPGRGFGRHPKLTPLAYKQTPVNAEKTLAGS 61
Db	396 TEARGAEPTAGIHHYSOLIYQIGTWLDSETHPLGMVAKSS 437	Qy	61 RYEKGITRNSERFELTPYNPDLIIFDQEENTCADRIMTORCKDKLNALAIISVNQPGV 120
Db	RESULT 38	Db	62 RYEKGITRNSERFELTPYNPDLIIFDQEENTCADRIMTORCKDKLNALAIISVNQPGV 121
AAW977668	AAW977668 standard; protein; 437 AA.	Qy	121 KLRVTEGWDGHSESHYEGRAVDITTSDEDSKYGMMLARLAVEAGFDWVYYESKAH 180
XX		Db	122 RLRLVTEGWDGHSESHYEGRAVDITTSDEDSKYGMMLARLAVEAGFDWVYYESKAH 181
AC	AAW977668;	Qy	181 IHCSYRAENSAVAKSGCFFPGSATVHLFOGGTKLVLSPGDRVLAADDQGRLLYSDFLT 240
XX	21-MAY-1999 (first entry)	Db	182 IHCSYRAENSAVAKSGCFFPGSATVHLFOGGTKLVLSPGDRVLAADDQGRLLYSDFLT 241
XX	Mouse Sonic hedgehog (Shh) protein.	Qy	241 FLDRDDGAKKVYYTETREPRLLTAAHLLVAPINDSATGEPEASGSGCPGSCGALG 300
DE	Sonic hedgehog; Shh protein; mouse; dopaminergic; GABA-nergic;	Db	242 FLDRDDGAKKVYYTETREPRLLTAAHLLVAPIND-----SGPPPG 286
KW	ptc therapeutic; patched; signal transduction; Parkinson's disease;	Qy	301 PRAFLASRTPGQYVVAERGDGRLLPAHVSUTLSEEANGAYAPITAQSTILINRLV 360
KW	Huntington's disease; amyotrophic lateral sclerosis; cerebral ischaemia;	Db	287 PSALFASRTPGQYVVAERGDGRLLPAHVSUTLSEEANGAYAPITAQSTILINRLV 346
KW	hypoxia; neuroprotective; therapy.	Qy	361 ASCVAVIEHNSWAHRAFPFLAHALLA LAPARTDGGDSGGDRGGGRVALTAGA 420
OS	Mus sp.	Db	347 ASCVAVIEHNSWAHRAFPFLAHALLA LAPARTDGGDSGGDRGGGRVALTAGA 395
XX	WO9904775-A2.	Qy	421 ADAPGRAGATAGIHHYSOLIYQIGTWLDSBEAHPLGMVAKSS 462
XX	04-FEB-1999.	Db	396 TEARGAEPTAGIHHYSOLIYQIGTWLDSETMPLGMVAKSS 437
XX	24-JUL-1998; 98WO-US015419.	XX	RESULT 39
XX	24-JUL-1997; 97US-00900220.	AAV05513	AAY05513 standard; protein; 437 AA.
XX	PA (ONTIO-) ONTOGENY INC.	ID	AAV05513
XX	Miao N, Wang M, Mahanthappa NK, Pang K;	AC	AAV05513;
XX	WPI; 1998-142578/12.	XX	XX
DR	N-PDB; AAX0774.	DT	05-JUL-1999 (first entry)
XX	DR	XX	XX
XX	Increasing the survival of neuronal, dopaminergic and GABA-nergic cells - by using a ptc therapeutic such as a protein kinase inhibitor, or an agent derived from hedgehog polypeptides, useful in the treatment of Parkinson's disease.	DB	Mouse Sonic hedgehog protein Shh.
PT	XX	XX	XX
PT	XX	XX	Sonic hedgehog; Shh protein; mouse; hedgehog therapeutic; ptc therapeutic; patched; signal transduction; muscle atrophy; cachexia; muscular myopathy; myoblastic sarcoma; therapy.
PS	XX	KW	XX
XX	PS Disclosure: Page 89-91; 138pp; English.	OS	Mus sp.
CC	This polypeptide is mouse Shh Sonic hedgehog protein. The invention is based on the finding that hedgehog proteins are useful as protective agents in the treatment and prophylaxis of neurodegenerative disorders resulting from the loss of dopaminergic and/or GABA neric neurons, or the general loss of tissue from the substantia nigra. Exemplary disorders include Parkinson's disease, Huntington's disease (both claimed), amyotrophic lateral sclerosis and cerebral ischaemia. The invention relates to hedgehog therapeutics (i.e. hedgehog polypeptides and gene therapy constructs e.g. constructs encoding recombinant hedgehog polypeptides and trans-activation constructs for altering hedgehog gene regulatory sequences) and ptc therapeutic constructs (i.e. agents which mimic the effect of naturally occurring hedgehog proteins on patched signalling) that are effective in both human and animal subjects. Human Ihh and Dhh polypeptides (see AAW97763-64) are preferred. The products can also be used for the maintenance of differentiated neurons in cultures, and to enhance the implantation of such neuronal cells in an animal. They can be used to prevent or treat neurodegenerative conditions arising from the use of certain drugs, and in prevention and/or treatment of hypoxia, e.g. as a neuroprotective agent	PN	W09910004-A2.
CC	XX	XX	XX
CC	XX	PD	04-MAR-1999.
CC	XX	PF	28-AUG-1998; 98WO-US017922.
CC	XX	PR	29-AUG-1997; 97US-0057394P.
CC	XX	PA	(ONTIO-) ONTOGENY INC.
CC	XX	XX	Bladgen CS, Currie PD, Ingham PW, Hughes SM;
CC	XX	PI	XX
CC	XX	DR	WPI; 1999-243557/20.
CC	XX	DR	N-PSDB; AAX25101.
CC	XX	PT	A new method to regulate muscle growth.

PS Disclosure; Page 115-116; 130pp; English.

XX The present sequence is mouse Sonic hedgehog protein Shh. The invention relates to a method for modulating the formation and/or maintenance of muscle tissue by ectopically contacting muscle cells, especially muscle stem/progenitor cells, in vitro or in vivo, with a hedgehog therapeutic (i.e. hedgehog polypeptides and gene therapy constructs) or ptc therapeutic (i.e. a small organic molecule that mimics the effect of hedgehog proteins on patched signalling, or activates or potentiates patched signalling) in an amount effective to alter the growth state of disorders of, or surgical or cosmetic repair of, such muscle tissues, by administering a hedgehog polypeptide or ptc therapeutic. The disorder may be muscle atrophy, in particular skeletal muscle atrophy or cardiac muscle atrophy, cachexia, or muscular myopathy (all claimed). The hedgehog polypeptide or ptc therapeutic can inhibit growth of myoblastic-derived tissue to provide treatment of hyperplastic or neoplastic growth of muscle tissue such as in myoblastic sarcoma (also claimed). The hedgehog therapeutic preferably comprises at least a bioactive extracellular portion of a hedgehog protein (see AAY05510-19) encoded by a vertebrate hedgehog gene (see AXX25098-107), especially a hedgehog gene

XX

SQ Sequence 437 AA;

Query Match 83.6%; Score 2065; DB 2; Length 437;

Best Local Similarity 87.2%; Pred. No. 1.6e-180; Matches 403; Conservative 9; Wismatches 24; Indels 26; Gaps 3;

Qy 1 MILLARCLLVLVSSLLVCSGLACGPGRGFGRHRPKKLTPAKQFINVAEKTLGAGS 60
Db 2 LLLARCFVILLLVSSLLVCPGLACGPGRGFGRHRPKKLTPAKQFINVAEKTLGAGS 61

Qy 61 RYEKGKTSRNSBEPFKELTPNPDIIKPDFENTGADBLMTQRCDKUNALAISSVNQWCPY 120
Db 62 RYEKGKTRNSERFKEITPNTAPDIIKPDFENTGADBLMTQRCDKUNALAISSVNQWCPY 121

Qy 121 KLRVTECWDDECHSEESLHVEGRADITTSDRDSKYGMRLAVEAGFDWYYESKXH 180
Db 122 RLRYTECWDEDEHSEESLHVEGRADITTSDRDSKYGMRLAVEAGFDWYYESKXH 181

Qy 181 IHCSVKRAENSYAAKSGGCFPSATVLEQGTKLVKDLSPDRVLAADDGGRLLYSDFLT 240
Db 182 IHCSVKRAENSYAAKSGGCFPSATVLEQGTKLVKDLSPDRVLAADDGGRLLYSDFLT 241

Qy 241 FLDRDDGAKKVYVIETREPRRLIITAHLFVAFHNDSATGEBASSSGPPGGALG 300
Db 242 FLDRDEGAKKVYVIETLEPRRLIITAHLFVAFHND-----SGPTPG 286

Qy 301 PRALFAASRVRPGQRTVVAERGDDRILLPAVHSVTLSEEAGAYAPLTAQGTLINRYL 360
Db 287 PSALFAASRVRPGQRTVVAERGDDRILLPAVHSVTLREEAGAYAPLTAQGTLINRYL 346

Qy 361 ASCYAVIEEHSHAHRAAPFLAHLAALAPARTDRGGDSGGDRGGGRVALTAPSA 420
Db 347 ASCYAVIEEHSHAHRAAPFLAHLAALAPARTD-----GGGGSIP-AAQSA 395

Qy 421 ADAPGAGTAGTHWYISOLYLQIGTMWLDSEALHPIGMVAKSS 462
Db 396 TEARGAETTAGTHWYISOLYLQIGTMWLDSEALHPIGMVAKSS 437

KW Guillain-Barre syndrome; peripheral neuropathy; diabetes; alcoholism;
KW chronic inflammatory demyelinating polyneuropathy; CIPP; gene therapy;
KW infection; inflammation; hereditary neuropathy;
KW Charcot-Marie-Tooth disease; vasculitis; lung cancer; tumour;
KW multiple myeloma; nutritional imbalance; kidney disease;
KW hypothyroid neuropathy; trauma; Reuss's disease; Abetalipoproteinemia;
KW Tangier disease; Krabbe's disease; Metachromatic leukodystrophy;
KW Fabry's disease; CMV; GBS; Dejerine-Sottas Syndrome; acute neuropathy;
KW Amyotrophic lateral sclerosis; ALS; Miller-Fisher syndrome; amyloidosis;
KW Waldenstrom's Macroglobulinaemia; Chronic Lymphocytic Leukaemia;
KW neuroprotective; cytoprotective; patched-mediated signal transduction.
XX

OS Mus sp.

XX

PN WO200007422-A2.

XX

DR 2000-387341/33.

XX

PT Novel method of preventing deterioration of peripheral nerves, useful for treating or preventing neuropathy, e.g. where associated with diabetes or viral infection, by administering hedgehog or patched agent.

XX

PT

PR 06-NOV-1998; 98US-00187387.

XX

PA (BIOJ) BIOGEN INC.

PA (ONTO-) ONTOGENY INC.

XX

Galdes A, Mahanthappa N;

XX

PI DR WPT; 2000-387341/33.

XX

DR AAA30277.

XX

PT

PT

PT

XX

Claim 7; Page 131-132; 150pp; English.

XX

CC The present sequence is the partial mouse sonic hedgehog protein Shh. This sequence inhibits expression of the patched gene which has been implicated in neuromuscular disorders (neuropathies). This sequence may therefore be used for treating neuromuscular disorders i.e. preventing degeneration in function of motor or sensory nerves and protecting peripheral nerve cells under conditions that normally cause neuropathy. A variety of neuromuscular disorders may be treated: Guillain-Barre syndrome, GBS; peripheral neuropathy; diabetic neuropathy; alcohol-induced neuropathy; chronic inflammatory demyelinating polyneuropathy, CIDP; infection-induced neuropathy e.g. Charcot Marie-Tooth disease (CMT); Familial Amyloidotic neuropathy, Refsum's disease, Abetalipoproteinemia, Tangier disease, Krabbe's disease, Metachromatic leukodystrophy, Fabry's disease, Dejerine-Sottas syndrome, Hereditary sensory neuropathy Type II (HSN II) and Amyotrophic lateral sclerosis (ALS); acute neuropathy e.g. Miller-Fisher syndrome; neuropathy caused by vasculitis; neuropathy associated with tumours e.g. lung cancer, multiple myeloma, B-cell lymphoma, Waldenstrom's Macroglobulinaemia, Chronic Lymphocytic Leukaemia; neuropathy associated with: amyloidosis, nutritional imbalance, kidney disease, trauma; and hypothyroid neuropathy. The coding sequence may be used in gene therapy of the above disorders

XX

SQ Sequence 437 AA;

Query Match 83.6%; Score 2065; DB 3; Length 437;

Best Local Similarity 87.2%; Pred. No. 1.6e-180; Matches 24; Indels 26; Gaps 3;

Matches 403; Conservative 9; Wismatches 24;

Qy 1 MILLARCLLVLVSSLLVCSGLACGPGRGFGRHRPKKLTPAKQFIPNVAEKTLGAGS 60
Db 2 LLLARCFVILLLVSSLLVCPGLACGPGRGFGRHRPKKLTPAKQFIPNVAEKTLGAGS 61

Qy 61 RYEKGKTSRNSERFKEITPNTAPDIIKPDFENTGADBLMTQRCDKUNALAISSVNQPGV 120
Db 62 RYEKGKTRNSERFKEITPNTAPDIIKPDFENTGADBLMTQRCDKUNALAISSVNQPGV 121

CC deliver polynucleotides encoding these lipid modulators
 XX Sequence 437 AA;

Query Match 83.6%; Score 2065; DB 3; Length 437;
 Best Local Similarity 87.2%; Pred. No. 1.6e-180;

Matches 403; Conservative 9; Mismatches 24; Indels 3; Gaps 3;

Qy 1 MILLARCLLIVSSLLVSGLICPGGFGKRRHPKKTPLAYKQPIPTAABKTIGASG 60

Db 2 LILLIARCFLVLLIVSGLICPGGFGKRRHPKKTPLAYKQPIPTAABKTUGASG 61

Qy 61 RYEKGKTRSERFKELTPTNPNPDIIFDENTGADRIMTQRCKDNALATSMVNQPGV 120

Db 62 RYEKGKTRSERFKELTPTNPNPDIIFDENTGADRIMTQRCKDNALATSMVNQPGV 121

Qy 121 KLRVTEGWDGDGHSEESHYEGAVDTTSDRDSKYMLRAYERGDMVYESKAH 180

Db 122 RLRVTEGWDGDGHSEESHYEGAVDTTSDRDSKYMLRAYERGDMVYESKAH 181

Qy 181 IHCSTKAENSAAKSGGCCPGSATVHLEGGTGLKVLKDLSPGDRVLAADDQGRLLSPFL 240

Db 182 IHCSTKAENSAAKSGGCCPGSATVHLEGGTGLKVLKDLSPGDRVLAADDQGRLLSPFL 241

Qy 241 FLDRDGAKKVYFYETTREPERRILTAHHLLVAPHDNSATGEPEASSGSPPSGALG 300

Db 242 FLDRDGAKKVYFYETTREPERRILTAHHLLVAPHDNSATGEPEASSGSPPSGALG 301

Qy 301 PRALPASRVPRPGQYVAERDGPRLIAAHVSVTLESEAAGAYAALITAQCTTILNRL 360

Db 287 PSALPASRVPRPGQYVAERGGRRLIPAVISVTLESEAAGAYAALITAHGTILNRL 346

Qy 361 ASCVAVIEBHSWAARAFAPPRLAHALLALAPARTDRGDSGGDRGGGRVALTAPGA 420

Db 347 ASCVAVIEBHSWAARAFAPPRLAHALLALAPARTDRGDSGGDRGGGRVALTAPGA 395

Qy 421 ADAPGAGATAGIHWYNSOLLYQIGTWLLDSEALHPLGMVAKSS 462

Db 396 TEARGAEPTAGIHWYNSOLLYQIGTWLLDSETMPLGMVAKSS 437

RESULT 44
 AAB84672 ID AAB84672 standard; protein; 437 AA.

XX AC AAB84672; DT 17-SEP-2001 (first entry)

XX DB Amino acid sequence of a mouse hedgehog (Shh) polypeptide.

XX KW Shh gene; hedgehog gene; T lymphocyte; patched gene; infection; diabetes; nutritional deficiency; graft rejection; hyperacute response; cornea transplant; autoimmune disorder; multiple sclerosis; psoriasis; atopic dermatitis; inflammatory disease; proliferative disease; hyperproliferative disease; eczematous dermatitis; urticaria; vasculitis; scleroderma.

XX OS Mus sp.

XX PN WO200140138-A2.

XX PD 07-JUN-2001.

XX PP 30-NOV-1999; 99US-0168112P.

XX PA (CURI-) CURIS INC.

XX PI Crompton T;

XX DR WPI; 2001-441484/47.

DR N-PSDB; AAH28449.
 XX Modulating immune function comprises administration of a hedgehog or ptc
 PT agent; for treating e.g. diabetes, eczematous dermatitis, urticaria or
 PT vasculitis.

XX Claim 4; Page 81-82; 105pp; English.

CC The present sequence represents a hedgehog (Shh) polypeptide. Hedgehog are
 CC gene products and signal transduction pathways involving hedgehog are
 CC involved in the maturing of T lymphocytes. The specification of a hedgehog
 CC a method for modulating immune response by administration of a hedgehog
 CC or patched (ptc) polypeptide, agonists or antagonists. The method is used to
 CC treat disorders affecting the regulation of lymphocytes, particularly
 CC maturation and/or activation of T lymphocytes. It is used to treat
 CC bacterial or viral infection, diabetes, nutritional deficiencies, graft
 CC reaction or other hyperacute response such as kidney, heart, lung, bone
 CC marrow, spleen skin or cornea transplant or autoimmune disorders such as
 CC multiple sclerosis, psoriasis or atopic dermatitis. The method is used to
 CC treat inflammatory, proliferative and hyper-proliferative diseases, as
 CC well as cutaneous manifestations of immunological disorders such as
 CC eczematous dermatitis, urticaria, vasculitis and scleroderma

XX Sequence 437 AA;

Query Match 83.6%; Score 2065; DB 4; Length 437;
 Best Local Similarity 87.2%; Pred. No. 1.6e-180;

Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MILLARCLLIVSSLLVSGLICPGGFGKRRHPKKTPLAYKQPIPTAABKTIGASG 60

Db 2 LILLIARCFLVLLIVSGLICPGGFGKRRHPKKTPLAYKQPIPTAABKTUGASG 61

Qy 61 RYEKGKTRSERFKELTPTNPNPDIIFDENTGADRIMTQRCKDNALATSMVNQPGV 120

Db 62 RYEKGKTRSERFKELTPTNPNPDIIFDENTGADRIMTQRCKDNALATSMVNQPGV 121

Qy 121 KLRVTEGWDGDGHSEESHYEGAVDTTSDRDSKYMLRAYERGDMVYESKAH 180

Db 122 RLRVTEGWDGDGHSEESHYEGAVDTTSDRDSKYMLRAYERGDMVYESKAH 181

Qy 181 IHCSTKAENSAAKSGGCCPGSATVHLEGGTGLKVLKDLSPGDRVLAADDQGRLLSPFL 240

Db 182 IHCSTKAENSAAKSGGCCPGSATVHLEGGTGLKVLKDLSPGDRVLAADDQGRLLSPFL 241

Qy 241 FLDRDGAKKVYFYETTREPERRILTAHHLLVAPHDNSATGEPEASSGSPPSGALG 300

Db 242 FLDRDGAKKVYFYETTREPERRILTAHHLLVAPHDNSATGEPEASSGSPPSGALG 301

Qy 301 PRALPASRVPRPGQYVAERDGPRLIAAHVSVTLESEAAGAYAALITAQCTTILNRL 360

Db 287 PSALPASRVPRPGQYVAERGGRRLIPAVISVTLESEAAGAYAALITAHGTILNRL 346

Qy 361 ASCVAVIEBHSWAARAFAPPRLAHALLALAPARTDRGDSGGDRGGGRVALTAPGA 420

Db 347 ASCVAVIEBHSWAARAFAPPRLAHALLALAPARTDRGDSGGDRGGGRVALTAPGA 395

Qy 421 ADAPGAGATAGIHWYNSOLLYQIGTWLLDSEALHPLGMVAKSS 462

Db 396 TEARGAEPTAGIHWYNSOLLYQIGTWLLDSETMPLGMVAKSS 437

Qy 181 IHCSTKAENSAAKSGGCCPGSATVHLEGGTGLKVLKDLSPGDRVLAADDQGRLLSPFL 240

Db 182 IHCSTKAENSAAKSGGCCPGSATVHLEGGTGLKVLKDLSPGDRVLAADDQGRLLSPFL 241

Qy 241 FLDRDGAKKVYFYETTREPERRILTAHHLLVAPHDNSATGEPEASSGSPPSGALG 300

Db 242 FLDRDGAKKVYFYETTREPERRILTAHHLLVAPHDNSATGEPEASSGSPPSGALG 301

Qy 301 PRALPASRVPRPGQYVAERDGPRLIAAHVSVTLESEAAGAYAALITAQCTTILNRL 360

Db 287 PSALPASRVPRPGQYVAERGGRRLIPAVISVTLESEAAGAYAALITAHGTILNRL 346

Qy 361 ASCVAVIEBHSWAARAFAPPRLAHALLALAPARTDRGDSGGDRGGGRVALTAPGA 420

Db 347 ASCVAVIEBHSWAARAFAPPRLAHALLALAPARTDRGDSGGDRGGGRVALTAPGA 395

Qy 421 ADAPGAGATAGIHWYNSOLLYQIGTWLLDSEALHPLGMVAKSS 462

Db 396 TEARGAEPTAGIHWYNSOLLYQIGTWLLDSETMPLGMVAKSS 437

RESULT 45
 AAB6063 ID AAB6063 standard; protein; 437 AA.

XX AC AAB6063;

XX DT 30-MAR-2001 (First entry)

XX DE Mouse Sonic hedgehog (Shh) protein, SEQ ID NO:13.

KW Hedgehog protein; polymer conjugate; Polyalkene glycol group;

Db	62	RYEGKLTTRNSRERFKELTNPNDLIFKDEBTNGDRLMTCRDKLNALAIISVNMQPGV	121
Qy	121	KLRVTEGWDGDGHSEESTHYEGRPAVIDTSDRSKYGMRLARLAVEAGFDWYYESKAH	180
Db	122	RLRVTEGWDGDGHSEESTHYEGRPAVIDTSDRSKYGMRLARLAVEAGFDWYYESKAH	181
Qy	181	IHCSTKAENSVAAKGGCPGSATTHLEQGTTKLVKDLSGCDRVIAADDQGRLLSDFLT	240
Db	182	IHCSTKAENSVAAKGGCPGSATTHLEQGTTKLVKDLSGCDRVIAADDQGRLLSDFLT	241
Qy	241	FLDRDGAKKVYVETREPERPLLTAAHLFPAPHNDSATGEPEASSGGPPSSGALG	300
Db	242	FLDRDGAKKVYVETREPERPLLTAAHLFPAPHND-----SCPTPG	286
Qy	301	PRALFAASRVPGQTYVVAARGDGRLLPAVHSVTLSEEAGAYAAPLTAQGTILINRVL	360
Db	287	PSALFAASRVPGQTYVVAARGDGRLLPAVHSVTLREEAGAYAAPLTAHGTILINRVL	346
Qy	361	ASCYAVTEEISWAHRAFAPPRLAALAAAPARTDRGGDSGGGERVALTAPGA	420
Db	347	ASCYAVTEEISWAHRAFAPPRLAALAAAPART-----GGGGSSIP-AAQSA	395
Qy	421	ADAPGAGATACIHWYSQQLYQIGTWILDSEALHPILGMAVKSS	462
Db	396	TEARGAEPTAIGHWYSQQLYQIGTWILDSETMHPIGMAVKSS	437
RESULT 46			
	AAE04685	standard; protein; 437 AA.	
ID	AAE04685		
XX	XX		
AC	AAE04685;		
XX	XX	(first entry)	
DT	04-SEP-2001		
XX	XX	Mouse sonic hedgehog (Shh) protein.	
DE	XX		
KW	Mouse; hedgehog protein; nootropic; neuroprotective; anticonvulsant; cytostatic; therapy; Alzheimer's disease; Parkinson's disease; injury; Huntington's chorea; amylotrophic lateral sclerosis; multiple sclerosis; nervous system aging; neurodegenerative disease; immunological disease; malignant glioma; medulloblastoma; neuroectodermal tumour; cancer; extracellular signalling protein.		
KW	XX		
XX	XX	Mus sp.	
OS	XX		
PN	WO200134654-A1.		
XX	XX		
PD	17-MAY-2001.		
XX	XX		
PF	02-NOV-2000; 2000WO-US030405.		
XX	XX		
PR	05-NOV-1999; 99US-0164025P.		
XX	XX		
PA	(BIOJ) BIOGEN INC.		
XX	XX		
PI	Strauch K;		
XX	XX		
WPI	2001-329075/34.		
DR	N-P5DB; AAD09032.		
XX	XX		
PT	Novel isolated hedgehog fusion polypeptide useful for treating neurological conditions such as Alzheimer's disease, Parkinson's disease, Huntington's chorea, amylotrophic lateral sclerosis, and multiple sclerosis.		
PT	XX		
PT	XX		
PT	XX		
PS	Disclosure; Page 115-116; 178DP; English.		
XX	XX		
CC	The present invention relates to hedgehog fusion proteins. Hedgehog proteins are a family of extracellular signalling proteins that regulate various aspects of embryonic development both in vertebrates and in invertebrates. Hedgehog fusion protein is useful for the prophylaxis or treatment of any condition or disease state for which a hedgehog or		

Patched protein constituent is efficacious and in the diagnosis of disease states in biological system or constituents or conditions of disease states in non-biological systems. Hedgehog fusion protein is useful for treating neurological conditions due to injury, aging of nervous system, including Alzheimer's disease, chronic neurodegenerative diseases of the nervous system, including Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis and chronic immunological diseases of nervous system including multiple sclerosis and malignant gliomas, medulloblastomas, neuroectodermal tumours and to specifically target medical therapies against cancers and tumours which express the receptor for the protein. The present sequence is mouse sonic hedgehog (Shh) protein.

Sequence 437 AA;

Query Match Score 83.6%; Best Local Similarity 87.2%; Pred. No. 1; 6e-190; Length 437;

Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MILLARCHLIVYSSLLVCGLAGCPGRGFRHPPKKLPLAYKOFIPVNAEKTLGASG 60

Db 2 LLLIARCFVILASSLLVCPGLACPGPGRGFRHPPKKLPLAYKOFIPVNAEKTLGASG 61

Qy 61 RYCKISKRSERKELTINYNPDIIIFDENTGADMTRQCKDKLNALISVNQWPGV 120

Db 62 RYCKISKRSERKELTINYNPDIIIFDENTGADMTRQCKDKLNALISVNQWPGV 121

Qy 121 KLRVTEGWDDEGHSEBSLHYEGRADITSDRDSKYGMLARLAVEAGFDWVYESKAH 180

Db 122 RLTVTEGNDDEGHSEESIHYEGRADITSDRDSKYGMLARLAVEAGFDWVYESKAH 181

Qy 181 IHCSVKAEINSVAKSGGCPGSATVHLEGGTQLVDRPSGDRVLAADDQGRLLYSDFLT 240

Db 182 IHCSVKAEINSVAKSGGCPGSATVHLEGGTQLVDRPSGDRVLAADDQGRLLYSDFLT 241

Qy 241 FLDDDGARKVVFYIETTEPREFLLTAAHLLEPAINDSATGEPEASSGSPSGALG 300

Db 242 FLDDDEGAKKVVFYIETTEPREFLLTAAHLLEPAIND-----SGPTPG 286

Qy 301 PRALFASRYTRPGQRVYVVAERCDGDRRLIPAAVHSVTLSEAAGAYAPLTQGTTLINRVL 360

Db 287 PSALFASRYTRPGQRVYVVAERCDGDRRLIPAAVHSVTLSEAAGAYALTAHTTINRVL 346

Qy 361 ASCYAVIEHSHWAFAFPRLAHALLAALAPARTDRCGGDSGGDRGGGRVALTAPGA 420

Db 347 ASCYAVIEHSHWAFAFPRLAHALLAALAPARTD-----EGCGSIP-AQSA 395

Qy 421 ADAGAGAAGIHWYSQLNQIGTMWLLSEALPMGNKSS 462

Db 395 TEARGAEPPAGIHWYSQLHGTWLSETHPLGMGNKSS 437

RESULT 47
ID AAE05375 standard; protein: 437 AA.
XX AC AAE05375;
XX DT 12-SEP-2001 (first entry)

XX DE Mouse Sonic hedgehog protein.

XX Mouse; Sonic hedgehog; Shh; morphogenic signal; neuron; chromosome 5; embryonic patterning; cell culture; cell differentiation; ischaemia; cell proliferative disorder; intracerebral grafting; Huntington's chorea; neurological disorder; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; ALS; multiple sclerosis.

XX OS sp.

XX FH Location/Qualifiers 1 : 24
XX Key Peptide /label= Signal_peptide

FT

CC	Protein	25 . 437
CC	/label= Mature_Shh_Protein	
CC	XX	
CC	US6261786-31.	
CC	XX	
CC	PD 17-JUL-2001.	
CC	XX	
CC	PR 02-JUL-1996;	96US-00674509.
CC	XX	
CC	PR 30-DEC-1993;	93US-0017627.
CC	PR 14-DEC-1994;	94US-0035660.
CC	PR 04-MAY-1995;	95US-0043593.
CC	PR 05-JUN-1995;	95US-0046300.
CC	PR 05-JUN-1995;	95US-00462286.
CC	XX	
SQ	(IMGR) IMPERIAL CANCER RES TECHNOLOGY LTD.	
SQ	PA (HARD) HARVARD COLLEGE.	
SQ	PA XX	
SQ	PI Marigo V, Tabin CJ, Ingham PW, McMahon AP;	
SQ	XX	
SQ	WPI: 2001-440859/47.	
SQ	DR N-FSDB; AAD1049.	
SQ	XX	
SQ	Screening compounds that potentiate or inhibit binding of hedgehog polypeptide to naturally occurring patched receptor, comprises contacting polypeptide with receptor and test compound, and detecting change in binding.	
SQ	PT	
SQ	XX	
SQ	Claim 2; Fig 5A; 127pp; English.	
SQ	XX	
SQ	The present invention relates to assay for screening compounds that potentiate or inhibit binding of hedgehog polypeptide to naturally occurring patched receptor. The hedgehog proteins comprise morphogenic signals produced by embryonic patterning centres, and are involved in the formation and maintenance of ordered spatial arrangements of differentiated tissues in vertebrates, both adult and embryonic. The proteins can be used to generate and/or maintain an array of different vertebrate tissues both in vitro and in vivo. The invention also relates to a method for modulating growth, differentiation or survival of a mammalian cell (e.g. neuron, testicular cell) responsive to hedgehog induction. Hedgehog agonists and antagonists can be used in cell culture techniques to enhance survival and maintenance of neurons and various vertebrate organogenic pathways. The hedgehog gene is useful in determining whether a patient is at the risk of disorder characterised by unwanted cell proliferation or aberrant control of differentiation. The hedgehog proteins or mimetics can be used to induce foetal neurons especially neuronal stem cells in intracerbral grafting. The protein or its mimetic can be used in the treatment of neurological conditions e.g. injury to nervous system, ischaemia resulting from stroke, Alzheimer's disease, Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis (ALS) and multiple sclerosis. The present sequence is mouse Sonic hedgehog (Shh) protein. The Shh gene is mapped to the proximal region of mouse chromosome 5	
SQ	XX	
SQ	Sequence 437 AA;	
SQ	Query Match Score 83.6%; Best Local Similarity 87.2%; Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;	
SQ	Qy 1 MILLARCFLIVSLLVCGLAGCPGRGFRHPPKKLPLAYKOFIPVNAEKTLGASG 60	
SQ	Db 2 LILLARCFLVLLSLLVCGLAGCPGRGFRHPPKKLPLAYKOFIPVNAEKTLGASG 61	
SQ	Qy 61 RYEGKISRNSRFKEITPNPDIIKDEENTGADRMTORCKDKLNALISVNQWPGV 120	
SQ	Db 62 RYEGKISRNSRFKEITPNPDIIKDEENTGADRMTORCKDKLNALISVNQWPGV 121	
SQ	Qy 121 KLRVTEGWDDEGHSEBSLHYEGRADITSDRDSKYGMLARLAVEAGFDWVYESKAH 180	
SQ	Db 122 RLRTVTEGWDDEGHSEBSLHYEGRADITSDRDSKYGMLARLAVEAGFDWVYESKAH 181	
SQ	Qy 181 IHCSVKAEINSVAKSGGCPGSATVHLEGGTQLVDRPSGDRVLAADDQGRLLYSDFLT 240	
SQ	Db 182 IHCSVKAEINSVAKSGGCPGSATVHLEGGTQLVDRPSGDRVLAADDQGRLLYSDFLT 241	
SQ	Qy 241 FLDDDGARKVVFYIETTEPREFLLTAAHLLEPAINDSATGEPEASSGSPSGALG 300	
SQ	Db 242 FLDDDEGAKKVVFYIETTEPREFLLTAAHLLEPAIND-----SGPTPG 286	
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SQ	Db 347 ASCYAVIEHSHWAFAFPRLAHALLAALAPARTD-----EGCGSIP-AQSA 395	
SQ	Qy 421 ADAGAGAAGIHWYSQLNQIGTMWLLSEALPMGNKSS 462	
SQ	Db 395 TEARGAEPPAGIHWYSQLHGTWLSETHPLGMGNKSS 437	

RESULT 48
 ID AAB85736 standard; protein; 437 AA.
 XX AC AAB85736;
 XX DT 29-OCT-2001 (first entry)
 XX DE Mouse sonic hedgehog (Shh) polypeptide.
 XX KW Hedgehog protein; sonic hedgehog; Shh; indian hedgehog; Ihh; Dh_h;
 KW desert hedgehog; cell differentiation; mouse.
 OS Mus sp.
 XX PN US6271363-B1.
 XX PD 07-AUG-2001.
 XX PF 20-OCT-1997; 97US-00954698.
 XX PR 30-DEC-1993; 93US-00176427.
 XX PR 14-DEC-1994; 94US-00356016.
 XX PR 04-MAY-1995; 95US-00430933.
 XX PR 05-JUN-1995; 95US-0046236.
 XX PA (HARD) HARVARD COLLEGE.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
 XX PI Ingham PW, McMahon AP, Tabin CJ;
 XX DR WPI; 2001-456723/49.
 DR N-PSDB; AAI76110.
 XX PT Novel nucleic acid encoding a hedgehog polypeptide, used to produce the
 CC selected from sonic hedgehog (Shh), indian hedgehog (Ihh),
 CC hedgehog (Dhh) polypeptides. The hedgehog genes are involved in the
 CC formation of ordered spatial arrangements of differentiated tissue in
 CC vertebrates. The nucleic acid sequences are useful for producing hedgehog
 CC proteins, used for promoting differentiation of, or survival of
 CC differentiated, neuronal cells, and for promoting proliferation, survival
 CC or differentiation of mesenchymal, endodermal or ectodermal tissue,
 CC particularly chondrocytes, or testicular germ line cells. The present
 CC sequence represents a mouse Shh polypeptide
 XX SQ Sequence 437 AA;

Query Match 83.6%; Score 2065; DB 4; Length 437;
 Best Local Similarity 87.2%; Pred. No. 1. 6e-180;
 Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MLLARCLLIVSSLLVCSGLACSGRGRGKRRHPKLTPLAKEYPAVKTLGASG 60
 Db 2 LLLARFLVLLSSLLVCPLAGGGRGKRRHPKLTPLAKEYPAVKTLGASG 61
 Qy 61 RYEGKTSRNSERFKEETPNPNPDIIFKDEENTGADRMTORCKDKLNALATSVNNQWPGV 120
 Db 62 RYEGKTSRNSERFKEETPNPNPDIIFKDEENTGADRMTORCKDKLNALATSVNNQWPGV 121
 Qy 121 KURVTIEWDEGHHSBESLHYEGRADWITSDRSKYGMARLAVEAGDWWYYESKAH 180
 Db 122 RURVTIEWDEGHHSBESLHYEGRADWITSDRSKYGMARLAVEAGDWWYYESKAH 181
 Qy 181 IHCSVRAENSYAAKSGCCFPSSATVLLQEGSTKLVDLSPDRLVIAADDQRLLYSDFLT 240
 Db 182 IHCSVRAENSYAAKSGCCFPSSATVLLQEGSTKLVDLSPDRLVIAADDQRLLYSDFLT 241
 Qy 241 FLDRDGAKKVYVITREPRERLILTAAHLLFVAFHNDSATGEPPASSGSPSSGALG 300
 Db 242 FLDRDGAKKVYVITREPRERLILTAAHLLFVAFHNDSATGEPPASSGSPSSGALG 300
 Qy 301 PRALFASRVRPGQRYVVAERGDRLRILLPAVHSVTLSEPAAGAYAPLTTAGTTLINRVL 360
 Db 287 PSALFASRVRPGQRYVVAERGDRLRILLPAVHSVTLSEPAAGAYAPLTTAGTTLINRVL 346
 Qy 361 ASCYAVIEEHSHAHRAFAPELAHALAAALAPARTRGDGGDRGGGRVALTAPGA 420
 Db 347 ASCYAVIEEHSHAHRAFAPELAHALAAALAPARTRGDGGDRGGGRVALTAPGA 395
 Qy 421 ADAPGAGATAGTHWYQOLYQIGTWLIDSEALHPIGMAVKSS 462
 Db 396 TEARGAEPTAGTHWYQOLYHGTWILDSETMHPLGMAVKSS 437

RESULT 49
 ID AAG65746 standard; protein; 437 AA.
 XX AC AAG65746;
 XX DT 07-JAN-2002 (first entry)
 DE Mouse sonic hedgehog (Shh) polypeptide.
 XX KW Adipocyte; hedgehog polypeptide; desert hedgehog; indian hedgehog; Dh_h;
 KW Ihh; sonic hedgehog; Shh; therapeutic; cytotatic; tumor.
 XX OS Mus sp.
 PN WO0164238-A2.

(CURIS INC.
 XX PD 07-SEP-2001.
 XX PP 28-FEB-2001; 2001WO-US006450.
 XX PR 29-FEB-2000; 2000US-0186058P.
 XX PA (CURIS INC.
 XX PI Zehentner B, Lesser-Reiff U, Bartscher H;
 XX DR WPI; 2001-607352/69.
 XX N-PSDB; AAI6674.
 XX PT Method for regulating formation and/or maintenance of adipocyte tissue by
 CC contracting pre-adipocyte or adipocyte cells with a hedgehog polypeptide
 PT or Fc therapeutic.
 XX Disclosure; Page 97-99; 132pp; English.

Tue Mar 30 13:00:48 2004

us-09-883-848a-15.rag

Page 37

Db 347 ASCYAVIEHSWAHRAFAPPRLAHALLAALAPARTD-----GGGGSTP-AAQSA 395
Qy 421 ADAPGAGATHGITHWYSQULLYQIGTWLUDSEALHRLGMAYKSS 462
Db 396 TEARGAEPTAGITHWYSQULLYHGTWLLDSTMHPLGNAVKSS 437

Search completed: March 29, 2004, 18:32:03
Job time : 64 secs

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OM protein - protein search, using SW model

Run on: March 29, 2004, 18:30:54 ; Search time 23 Seconds

(without alignments)

Title: US-09-883-848a-15
Perfect score: 2469

Sequence: 1 MILLARCLLIVLVSLLVCS.....GMAVKSSXSRGAGGGAREGA 475

Scoring table: BLOCUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2467	99.9	475	3 US-08-74-519B-13	Sequence 13, App1
4	2467	99.9	475	3 US-08-954-598-13	Sequence 13, App1
5	2467	99.9	475	4 US-08-957-974-13	Sequence 13, App1
6	2467	99.9	475	4 US-09-225-256-22	Sequence 22, App1
7	2467	99.9	475	4 US-09-539-995-13	Sequence 13, App1
8	2467	99.9	475	4 US-09-448-188-13	Sequence 13, App1
9	2467	99.9	475	4 US-08-95-128-13	Sequence 13, App1
10	2467	99.9	475	4 US-09-104-917-15	Sequence 15, App1
11	2467	99.9	475	4 US-08-954-710-13	Sequence 15, App1
12	2467	99.9	475	4 US-09-151-999-15	Sequence 15, App1
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18	2068	83.8	437	3 US-08-729-743A-20	Sequence 20, App1
19	2068	83.8	437	3 US-08-156-050A-11	Sequence 6, App1
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US-08-356-060A-13
; Sequence 13, Application US/08356060A
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

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ALIGNMENTS

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; Sequence 13, Application US/0846000C
; Patent No. 6,165747
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

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Db 301 PRALFASRVRPGQRYYVVAEDGDRLLPAVHSYTLSEAAAGAYAPLTAQGTILINRYL 360
Qy 361 ASCYATEEHSWAHRAFAFRLAHALAALAPARTDGGDSGGDRGGGGRVALTAPGA 420
Db 361 ASCYATEEHSWAHRAFAFRLAHALAALAPARTDGGDSGGDRGGGGRVALTAPGA 420
Qy 421 ADAPGAGATAGIHTYSQIYIGWILDSPEAHPLGMAKSSXSRGAGGAREGA 475
Db 421 ADAPGAGATAGIHTYSQIYIGWILDSPEAHPLGMAKSSXSRGAGGAREGA 475

APPLICANT: Marti-Gorostiza, Elisa
 TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
 Proteins and Uses Related Thereto
 NUMBER OF SEQUENCES: 62
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/460,900C
 FILING DATE: 5-JUNE-1995
 PRIORITY DATA:
 APPLICATION NUMBER: US 08/435,093
 FILING DATE: 4-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/356,060
 FILING DATE: 14-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/176,427
 FILING DATE: 30-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: HMV-006 .05
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 832-1000
 TELEFAX: (617) 832-7000
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 475 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-460-900C-13

Query Match 99.9%; Score 2467; DB 3; Length 475;
 Best Local Similarity 100.0%; Pred. No. 1.9e-238;
 Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLARCLLIVLVSILVCSGLACPGRGKGKHPKKTPLAYQFIPVAEKTIGSG 60
 Db 1 MLLARCLLIVLVSILVCSGLACPGRGKGKHPKKTPLAYQFIPVAEKTIGSG 60
 Qy 61 RYEKGKSRNSERFKELTPNYPDIFKDDEENTGADRMLTQCRDKLNALAIISWNQNPGV 120
 Db 61 RYEKGKSRNSERFKELTPNYPDIFKDDEENTGADRMLTQCRDKLNALAIISWNQNPGV 120
 Qy 121 KLRVTEGWDDEGHSEESLHVEGRADITTSDRDRSKYTMNLARAVEAGFDWVYESKAH 180
 Db 121 KLRVTEGWDDEGHSEESLHVEGRADITTSDRDRSKYTMNLARAVEAGFDWVYESKAH 180
 Qy 241 FLDRDGAKCYFYVETREPERLITTAHFLVAPHNDSATGEPEASGSGPSSGGALG 300
 Db 241 FLDRDGAKCYFYVETREPERLITTAHFLVAPHNDSATGEPEASGSGPSSGGALG 300
 Qy 181 IHCSVKAENSYAAKSGCCFPGSATVHLEQGTKLVDSPGDRYLAADQGRLLYSDFLT 240
 Db 181 IHCSVRAENSYAAKSGCCFPGSATVHLEQGTKLVDSPGDRYLAADQGRLLYSDFLT 240
 Qy 121 KLRVTEGWDDEGHSEESLHVEGRADITTSDRDRSKYTMNLARAVEAGFDWVYESKAH 180
 Db 121 KLRVTEGWDDEGHSEESLHVEGRADITTSDRDRSKYTMNLARAVEAGFDWVYESKAH 180
 Qy 301 PRALFASRVRGQRVVAERDGDRLPAVHSVTLSBAAAGAYPLTAQGTILINRVL 360
 Db 301 PRALFASRVRGQRVVAERDGDRLPAVHSVTLSBAAAGAYPLTAQGTILINRVL 360
 Qy 361 ASCYAVIEHSAWAHRAFAPFRLAHLALAPARTDRGGSGGDRGGGGRVALTAGA 420

Db 361 ASCYAVIEHSAWAHRAFAPFRLAHLALAPARTDRGGSGGDRGGGGRVALTAGA 420
 Qy 421 ADAPGAGATAGIHMYSLQIYQIGTWLSEALHPLGMAYKSSXSRGAGGARGA 475
 Db 421 ADAPGAGATAGIHMYSLQIYQIGTWLSEALHPLGMAYKSSXSRGAGGARGA 475

RESULT 3
 US-08-674-509B-13
 Sequence 13, Application US/08674509B
 ; Paten No. 6,617,866
 ; GENERAL INFORMATION:
 ; APPLICANT: Ingham, Phillip W.
 ; APPLICANT: McMahon, Andrew P.
 ; APPLICANT: Tabin, Clifford J.
 ; APPLICANT: Marigo, Valeria
 ; TITLE OF INVENTION: SCREENING ASSAYS FOR HEDGEHOG AGONISTS
 ; TITLE OF INVENTION: AND ANTAGONISTS
 ; NUMBER OF SEQUENCES: 48
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109-2170
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/674,509B
 FILING DATE: 02-JUL-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/460,900
 FILING DATE: 05-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: HMV-006 .05
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-832-1000
 TELEXFAX: 617-832-7000
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 475 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 US-08-674-509B-13

Query Match 99.9%; Score 2467; DB 3; Length 475;
 Best Local Similarity 100.0%; Pred. No. 1.9e-238;
 Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLLARCLLIVLVSILVCSGLACPGRGKGKHPKKTPLAYQFIPVAEKTIGSG 60
 Db 1 MLLARCLLIVLVSILVCSGLACPGRGKGKHPKKTPLAYQFIPVAEKTIGSG 60
 Qy 61 RYEKGKSRNSERFKELTPNYPDIFKDDEENTGADRMLTQCRDKLNALAIISWNQNPGV 120
 Db 61 RYEKGKSRNSERFKELTPNYPDIFKDDEENTGADRMLTQCRDKLNALAIISWNQNPGV 120
 Qy 121 KLRVTEGWDDEGHSEESLHVEGRADITTSDRDRSKYTMNLARAVEAGFDWVYESKAH 180
 Db 121 KLRVTEGWDDEGHSEESLHVEGRADITTSDRDRSKYTMNLARAVEAGFDWVYESKAH 180
 Qy 241 FLDRDGAKCYFYVETREPERLITTAHFLVAPHNDSATGEPEASGSGPSSGGALG 300
 Db 241 FLDRDGAKCYFYVETREPERLITTAHFLVAPHNDSATGEPEASGSGPSSGGALG 300
 Qy 181 IHCSVKAENSYAAKSGCCFPGSATVHLEQGTKLVDSPGDRYLAADQGRLLYSDFLT 240
 Db 181 IHCSVKAENSYAAKSGCCFPGSATVHLEQGTKLVDSPGDRYLAADQGRLLYSDFLT 240
 Qy 301 PRALFASRVRGQRVVAERDGDRLPAVHSVTLSBAAAGAYPLTAQGTILINRVL 360
 Db 301 PRALFASRVRGQRVVAERDGDRLPAVHSVTLSBAAAGAYPLTAQGTILINRVL 360
 Qy 361 ASCYAVIEHSAWAHRAFAPFRLAHLALAPARTDRGGSGGDRGGGGRVALTAGA 420

Qy 241 FLDRDGAKKVFVVIETREPREULLTAAHLLFVAPRNDSATGEPEASSGGPPSSGALG 300
 Db 241 FLDRDGAKKVFVVIETREPREULLTAAHLLFVAPRNDSATGEPEASSGGPPSSGALG 300
 Qy 301 PRALFASTRPQRGVYVAERDGDRLIPPAVHSVTLSSEAGAYAPLTAQSTILINVL 360
 Db 301 PRALFASTRPQRGVYVAERDGDRLIPPAVHSVTLSSEAGAYAPLTAQSTILINVL 360
 Qy 361 ASCVAVIEEWSWAHRAAFRLAHALLAALAPARTDGGDSGGDRGGGRVALTAPGA 420
 Db 361 ASCVAVIEEWSWAHRAAFRLAHALLAALAPARTDGGDSGGDRGGGRVALTAPGA 420
 Qy 421 ADAPGAGATAGIHWYSQLIYQIGTWLDSSEALHPLGNKVSXSRGAGGAREGA 475
 Db 421 ADAPGAGATAGIHWYSQLIYQIGTWLDSSEALHPLGNKVSXSRGAGGAREGA 475

RESULT 4
 US-08-954-698-13 Application US/08554698
 ; Patent No. 627163
 GENERAL INFORMATION:
 APPLICANT: Ingham, Phillip W.
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.
 TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
 TITLE OF INVENTION: Proteins and Uses Related Thereto
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-2170
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ParentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/954,698
 FILING DATE: 20-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/462,386
 FILING DATE: 05-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/435,093
 FILING DATE: 04-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/356,060
 FILING DATE: 14-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/435,093
 FILING DATE: 30-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 3,6,709
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-532-1000
 TELEFAX: 617-832-7000
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 475
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-954-698-13
 Query Match 99.9%; Score 2467.; DB 3.; Length 475;
 Best Local Similarity 100.0%; Pred. No. 1.9e-238; Indels 0; Gaps 0;

Qy 1 MLLARCLLIVLYSSLVCSGLACGPGRGFGRHPKRLTPPLAYQFIPNVAEKTLGASG 60
 Db 1 MLLARCLLIVLYSSLVCSGLACGPGRGFGRHPKRLTPPLAYQFIPNVAEKTLGASG 60
 Qy 61 RYEKISRNSERFELTPYNPDITIFKDENTSGADRMTQRCKDKNALALISVMNOPGV 120
 Db 61 RYEKISRNSERFELTPYNPDITIFKDENTSGADRMTQRCKDKNALALISVMNOPGV 120
 Qy 121 KLRTEGWDGDEGHESSESHYEGRAVDITTSDRSYCGMLARLAVAGFDWVYESKAH 180
 Db 121 KLRTEGWDGDEGHESSESHYEGRAVDITTSDRSYCGMLARLAVAGFDWVYESKAH 180
 Qy 181 IHCSYKAENSAAKSGCCPGSATVHLFEGGTICLVKOLSPGDRVLAADDGRLLYSDFLT 240
 Db 181 IHCSYKAENSAAKSGCCPGSATVHLFEGGTICLVKOLSPGDRVLAADDGRLLYSDFLT 240
 Qy 241 FLDRDDGAKKVYYTETPRERILLTAHLLFVAAPNDSDATEPEASSGGPPSGGALG 300
 Db 241 FLDRDDGAKKVYYTETPRERILLTAHLLFVAAPNDSDATEPEASSGGPPSGGALG 300
 Qy 301 PRALFASTRPQRGVYVAERDGDRLIPPAVHSVTLSSEAAAGAYAPLTAQSTILINVL 360
 Db 301 PRALFASTRPQRGVYVAERDGDRLIPPAVHSVTLSSEAAAGAYAPLTAQSTILINVL 360
 Qy 361 ASCVAVIEEWSWAHRAAFRLAHALLAALAPARTDGGDSGGDRGGGRVALTAPGA 420
 Db 361 ASCVAVIEEWSWAHRAAFRLAHALLAALAPARTDGGDSGGDRGGGRVALTAPGA 420
 Qy 421 ADAPGAGATAGIHWYSQLIYQIGTWLDSSEALHPLGNKVSXSRGAGGAREGA 475
 Db 421 ADAPGAGATAGIHWYSQLIYQIGTWLDSSEALHPLGNKVSXSRGAGGAREGA 475

RESULT 5
 US-08-957-874-13
 ; Sequence 13, Application US/08957874
 ; Patent No. 638412
 ; GENERAL INFORMATION:
 ; APPLICANT: Ingham, Phillip W.
 ; APPLICANT: McMahon, Andrew P.
 ; APPLICANT: Tabin, Clifford J.
 ; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
 ; TITLE OF INVENTION: Proteins and Uses Related Thereto
 ; NUMBER OF SEQUENCES: 47
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII (text)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/957,874
 ; FILING DATE: 20-OCT-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/462,386
 ; FILING DATE: 14-DEC-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/435,093
 ; FILING DATE: 30-DEC-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Vincent, Matthew P.
 ; REGISTRATION NUMBER: 3,6,709
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-532-1000
 ; TELEFAX: 617-832-7000
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 475
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-08-957-874-13
 Query Match 99.9%; Score 2467.; DB 3.; Length 475;
 Best Local Similarity 100.0%; Pred. No. 1.9e-238; Indels 0; Gaps 0;

NAME: Vincent, Matthew P. 36,709
 REGISTRATION NUMBER: HMV-006.09
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 832-1000
 TELEFAX: (617) 832-7000
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 475 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-957-874-13

Query Match 99.9%; Score 2467; DB 4; Length 475;

Best Local Similarity 100.0%; Pred. No. 1.9e-238; Length 475;

Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MILLARCLLVLVSSLLVCSGLACPGGRGKRPKKLTPLAYKFIPINVAEKTILGASG 60
 Db 1 MILLARCLLVLVSSLLVCSGLACPGGRGKRPKKLTPLAYKFIPINVAEKTILGASG 60
 Qy 61 RYEKGISRSNRSERFKELTNPYNDIIFKDDENTGADRMTQRCKDKLNALAISYMNQNGV 120
 Db 61 RYEKGISRSNRSERFKELTNPYNDIIFKDDENTGADRMTQRCKDKLNALAISYMNQNGV 120
 Qy 121 KLRVTEGWDDEGHHSSESHYEGRAVDITTSDRDRSKYGMNLARAVEAGFDWVYESKAH 180
 Db 121 KLRVTEGWDDEGHHSSESHYEGRAVDITTSDRDRSKYGMNLARAVEAGFDWVYESKAH 180
 Qy 181 IHCSYKAENSYAAKSGGCCFGSATVHLEQGGTKLVKDLSPGDRLVLAADDQGRLLYSDFLT 240
 Db 181 IHCSYKAENSYAAKSGGCCFGSATVHLEQGGTKLVKDLSPGDRLVLAADDQGRLLYSDFLT 240
 Qy 181 IHCSYKAENSYAAKSGGCCFGSATVHLEQGGTKLVKDLSPGDRLVLAADDQGRLLYSDFLT 240
 Db 181 IHCSYVGENSYAAKSGGCCFGSATVHLEQGGTKLVKDLSPGDRLVLAADDQGRLLYSDFLT 240
 Qy 241 FLDRDGAKVVFYVETREPRERLLTAHILFLVAPHNDSATGEPEASSGSPSGGALG 300
 Db 241 FLDRDGAKVVFYVETREPRERLLTAHILFLVAPHNDSATGEPEASSGSPSGGALG 300
 Qy 301 PRALFASRVRQQRTYVVAERDGDRLLPDAVHSVTLSSEAAGYAPLTAQGTILINRVL 360
 Db 301 PRALFASRVRQQRTYVVAERDGDRLLPDAVHSVTLSSEAAGYAPLTAQGTILINRVL 360
 Qy 361 ASCYAVIEHSAWAHAFAPFLAHLLALAPARTDGGDSGGDRGGGRVALTAFGA 420
 Db 361 ASCYAVIEHSAWAHAFAPFLAHLLALAPARTDGGDSGGDRGGGRVALTAFGA 420
 Qy 421 ADAPGAGATAGIHWYSQLIQIGTMLDSEALHPGMATSSISRGAGGCCARGA 475
 Db 421 ADAPGAGATAGIHWYSQLIQIGTMLDSEALHPGMATSSISRGAGGCCARGA 475
 Qy 421 ADAPGAGATAGIHWYSQLIQIGTMLDSEALHPGMATSSISRGAGGCCARGA 475
 Db 421 ADAPGAGATAGIHWYSQLIQIGTMLDSEALHPGMATSSISRGAGGCCARGA 475

RESULT 6

US-09-325-256-12
 Sequence 22, Application US/09325256
 Parent No. 6444793
 GENERAL INFORMATION:
 APPLICANT: PEPINSKY, R. BLAKE
 APPLICANT: BAKER, DARREN P.
 APPLICANT: WEN, DINGTI
 APPLICANT: WILLIAMS, KEVIN P.
 APPLICANT: GARGER, ELLEN A.
 APPLICANT: TAYLOR, FREDERICK R.
 APPLICANT: GALDES, ALPHONSE
 APPLICANT: PORTER, JEFFREY
 TITLE OF INVENTION: HYDROPHOBICALLY-MODIFIED PROTEIN COMPOSITIONS AND METHODS
 FILE REFERENCE: BIV-167-01
 CURRENT APPLICATION NUMBER: US/09-325,256
 CURRENT FILING DATE: 1999-06-03
 PRIOR APPLICATION NUMBER: 60/099,800
 PRIOR FILING DATE: 1998-09-10
 PRIOR APPLICATION NUMBER: 60/078,935
 PRIOR FILING DATE: 1998-03-20

US-09-325-256-22

Query Match 99.9%; Score 2467; DB 4; Length 475;
 Best Local Similarity 100.0%; Pred. No. 1.9e-238; Matches 475; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MILLARCLLVLVSSLLVCSGLACPGGRGKRPKKLTPLAYKFIPINVAEKTILGASG 60
 Db 1 MILLARCLLVLVSSLLVCSGLACPGGRGKRPKKLTPLAYKFIPINVAEKTILGASG 60
 Qy 61 RYEKGISRSNRSERFKELTNPYNDIIFKDDENTGADRMTQRCKDKLNALAISYMNQPGV 120
 Db 61 RYEKGISRSNRSERFKELTNPYNDIIFKDDENTGADRMTQRCKDKLNALAISYMNQPGV 120
 Qy 121 KLRVTEGWDDEGHHSSESHYEGRAVDITTSDRDRSKYGMNLARAVEAGFDWVYESKAH 180
 Db 121 KLRVTEGWDDEGHHSSESHYEGRAVDITTSDRDRSKYGMNLARAVEAGFDWVYESKAH 180
 Qy 181 IHCSYVGENSYAAKSGGCCFGSATVHLEQGGTKLVKDLSPGDRLVLAADDQGRLLYSDFLT 240
 Db 181 IHCSYVGENSYAAKSGGCCFGSATVHLEQGGTKLVKDLSPGDRLVLAADDQGRLLYSDFLT 240
 Qy 241 FLDRDGAKVVFYVETREPRERLLTAHILFLVAPHNDSATGEPEASSGSPSGGALG 300
 Db 241 FLDRDGAKVVFYVETREPRERLLTAHILFLVAPHNDSATGEPEASSGSPSGGALG 300
 Qy 301 PRALFASRVRQQRTYVVAERDGDRLLPDAVHSVTLSSEAAGYAPLTAQGTILINRVL 360
 Db 301 PRALFASRVRQQRTYVVAERDGDRLLPDAVHSVTLSSEAAGYAPLTAQGTILINRVL 360
 Qy 361 ASCYAVIEHSAWAHAFAPFLAHLLALAPARTDGGDSGGDRGGGRVALTAFGA 420
 Db 361 ASCYAVIEHSAWAHAFAPFLAHLLALAPARTDGGDSGGDRGGGRVALTAFGA 420
 Qy 421 ADAPGAGATAGIHWYSQLIQIGTMLDSEALHPGMATSSISRGAGGCCARGA 475
 Db 421 ADAPGAGATAGIHWYSQLIQIGTMLDSEALHPGMATSSISRGAGGCCARGA 475
 Qy 421 ADAPGAGATAGIHWYSQLIQIGTMLDSEALHPGMATSSISRGAGGCCARGA 475
 Db 421 ADAPGAGATAGIHWYSQLIQIGTMLDSEALHPGMATSSISRGAGGCCARGA 475

RESULT 7

US-09-639-695-13
 Sequence 13, Application US/09639695
 Patent No. 6576237
 GENERAL INFORMATION:
 APPLICANT: Ingham, Phillip W.
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.
 APPLICANT: Bumcrot, David A.
 APPLICANT: Marti-Gorostiza, Elisa
 TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing Proteins and Uses Related Thereto
 NUMBER OF SEQUENCES: 62
 CORRESPONDENCE ADDRESS:
 ADDRESS: FOLEY, HOAG & ELLIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/639,695
 FILING DATE: 16-Aug-2000
 PRIORITY NUMBER: US 08/435,093
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/435,093
 FILING DATE: 14-DEC-1994
 REFERENCE/DOCKET NUMBER: RMTV-006 .05
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: RMTV-006 .05
 TELEPHONE: (617) 832-7000
 TELEFAX: (617) 832-7000
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 475 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 US-09-639-69-13

Query Match 99.9%; Score 2467; DB 4; Length 475;
 Best Local Similarity 100.0%; Pred. No. 1.9e-238; Indels 0; Gaps 0;
 Matches 475; Conservative 0; Mismatches 0;

Qy	1	MILLARCLLIVSSLLIVSGIACGPGRGFGKGRHPKCLTPLAYKQIPYNAEKTIGASG	60
Db	1	MILLARCLLIVSSLLIVSGIACGPGRGFGKGRHPKCLTPLAYKQIPYNAEKTIGASG	60
Qy	61	RYEGKISRSRSERFELTPNYPDILPKDEENTGADRINTQRCKDKLNALAISYMNPQGV	120
Db	61	RYEGKISRSRSERFELTPNYPDILPKDEENTGADRINTQRCKDKLNALAISYMNPQGV	120
Qy	121	KLRVTEGWDDEDGHSEESIHYEGRAVDITTSDRSKYGMMLRLLAVEAGFDWVYESKAH	180
Db	121	KLRVTEGWDDEDGHSEESIHYEGRAVDITTSDRSKYGMMLRLLAVEAGFDWVYESKAH	180
Qy	181	IHCSYKAENSAVAKSGCPGSAATHLEGKGLDQGRLLYSPLT	240
Db	181	IHCSYKAENSAVAKSGCPGSAATHLEGKGLDQGRLLYSPLT	240
Qy	241	FLDRDGAKVYYETRBRERLLTAHHLLTVAHDSDATGEPEASGSPPSGALG	300
Db	241	FLDRDGAKVYYETRBRERLLTAHHLLTVAHDSDATGEPEASGSPPSGALG	300
Qy	301	PRALPASRYRPQGYVYVVERDGDRLLIPIAVHSVTLSSEAAGAYAPITAQCTILINRVL	360
Db	301	PRALPASRYRPQGYVYVVERDGDRLLIPIAVHSVTLSSEAAGAYAPITAQCTILINRVL	360
Qy	361	ASCAVIEHSMWAHAFAPRLAHLALAPARTDRGDSCGDGGGGVVALTARGA	420
Db	361	ASCAVIEHSMWAHAFAPRLAHLALAPARTDRGDSCGDGGGGVVALTARGA	420
Qy	421	ADAPANGATGIAHWYSQLYQIGWLLDSEALPHLGMAWKSYSRGAGGAREGA	475
Db	421	ADAPANGATGIAHWYSQLYQIGWLLDSEALPHLGMAWKSYSRGAGGAREGA	475
Qy	481	FIDRDGAKVYYETRBRERLLTAHHLLTVAHDSDATGEPEASGSPPSGALG	300
Db	481	FIDRDGAKVYYETRBRERLLTAHHLLTVAHDSDATGEPEASGSPPSGALG	300
Qy	541	PRALPASRVPGQTYVVAERDGDRLLPAAVHSVTLSSEAAGAYAPITAQGTILINRVL	360
Db	541	PRALPASRVPGQTYVVAERDGDRLLPAAVHSVTLSSEAAGAYAPITAQGTILINRVL	360

RESULT 8
 US-09-448-188-13
 Sequence 13, Application US/09448188
 Patent No. 6607913
 GENERAL INFORMATION:

APPLICANT: Ingham, Phillip W.
 McMahon, Andrew P.
 Tabin, Clifford J.
 TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing Proteins and Uses Related Thereto
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-2170
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/448,188
 FILING DATE: 23-NO- 6607913-1999
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/462,386
 FILING DATE: 05-JUN-1995
 PRIORITY NUMBER: US 08/435,093
 FILING DATE: 04-MAY-1995
 APPLICATION NUMBER: US 08/356,060
 FILING DATE: 14-DEC-1994
 APPLICATION NUMBER: US 08/176,427
 FILING DATE: 30-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: RMTV-006 .12
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-832-1000
 TELEFAX: 617-832-7000
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 475 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 US-09-448-188-13

Query Match 99.9%; Score 2467; DB 4; Length 475;
 Best Local Similarity 100.0%; Pred. 1.9e-238; Indels 0; Gaps 0;
 Matches 475; Conservative 0; Mismatches 0;

Qy	1	MILLARCLLIVSSLLIVSGIACGPGRGFGKGRHPKCLTPLAYKQIPYNAEKTIGASG	60
Db	1	MILLARCLLIVSSLLIVSGIACGPGRGFGKGRHPKCLTPLAYKQIPYNAEKTIGASG	60
Qy	61	RYEGKISRSRSERFELTPNYPDILPKDEENTGADRINTQRCKDKLNALAISYMNPQGV	120
Db	61	RYEGKISRSRSERFELTPNYPDILPKDEENTGADRINTQRCKDKLNALAISYMNPQGV	120
Qy	121	KLRVTEGWDDEDGHSEESIHYEGRAVDITTSDRSKYGMMLRLLAVEAGFDWVYESKAH	180
Db	121	KLRVTEGWDDEDGHSEESIHYEGRAVDITTSDRSKYGMMLRLLAVEAGFDWVYESKAH	180
Qy	181	IHCSYKAENSAVAKSGCPGSAATHLEGKGLDQGRLLYSPLT	240
Db	181	IHCSYKAENSAVAKSGCPGSAATHLEGKGLDQGRLLYSPLT	240
Qy	241	FLDRDGAKVYYETRBRERLLTAHHLLTVAHDSDATGEPEASGSPPSGALG	300
Db	241	FLDRDGAKVYYETRBRERLLTAHHLLTVAHDSDATGEPEASGSPPSGALG	300
Qy	301	PRALPASRYRPQGYVYVVERDGDRLLIPIAVHSVTLSSEAAGAYAPITAQCTILINRVL	360
Db	301	PRALPASRYRPQGYVYVVERDGDRLLIPIAVHSVTLSSEAAGAYAPITAQCTILINRVL	360
Qy	361	ASCAVIEHSMWAHAFAPRLAHLALAPARTDRGDSCGDGGGGVVALTARGA	420
Db	361	ASCAVIEHSMWAHAFAPRLAHLALAPARTDRGDSCGDGGGGVVALTARGA	420
Qy	421	ADAPANGATGIAHWYSQLYQIGWLLDSEALPHLGMAWKSYSRGAGGAREGA	475
Db	421	ADAPANGATGIAHWYSQLYQIGWLLDSEALPHLGMAWKSYSRGAGGAREGA	475
Qy	481	FIDRDGAKVYYETRBRERLLTAHHLLTVAHDSDATGEPEASGSPPSGALG	300
Db	481	FIDRDGAKVYYETRBRERLLTAHHLLTVAHDSDATGEPEASGSPPSGALG	300
Qy	541	PRALPASRVPGQTYVVAERDGDRLLPAAVHSVTLSSEAAGAYAPITAQGTILINRVL	360
Db	541	PRALPASRVPGQTYVVAERDGDRLLPAAVHSVTLSSEAAGAYAPITAQGTILINRVL	360

RESULT 9
US-08-954-128-13
 ; Sequence 13, Application US/08954128
 ; GENERAL INFORMATION:
 ; APPLICANT: Inham, Phillip W.
 ; APPLICANT: McMahon, Andrew P.
 ; APPLICANT: Tabin, Clifford J.
 ; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
 ; NUMBER OF SEQUENCES: 48
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109-2170
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/954,128
 ; FILING DATE: 20-OCT-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/462,386
 ; FILING DATE: 05-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/435,093
 ; FILING DATE: 04-MAY-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/356,060
 ; FILING DATE: 14-DEC-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/176,427
 ; FILING DATE: 30-DEC-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Vincent, Matthew P.
 ; REGISTRATION NUMBER: 36,709
 ; REFERENCE/DOCKET NUMBER: HRV-006-12
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-832-1000
 ; TELEFAX: 617-832-7000
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 475 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

Qy 361 ASCYAVIEEHSAWAHAFAPRLAHALLAALAPARTDRGGSQGGDRGGGRVALTAPG 420
 Db 361 ASCYAVIEEHSAWAHAFAPRLAHALLAALAPARTDRGDSQGGDRGGGRVALTAPG 420

Qy 421 ADAPGAGATAGIHWISQLIQIGTMLDSEALHPLGMATKSSXSRGAGGCARGA 475
 Db 421 ADAPGAGATAGIHWISQLIQIGTMLDSEALHPLGMATKSSXSRGAGGCARGA 475

Db 61 RYEGKISRNNSERFKELTPTNYPDIIFKDEENTGADBLMTQCKDKNALAISVNQNQPGV 120
 Qy 121 KURVTGEWDEGHHSSESLSLHVEGRAVDITTSDRSKYGMALARAVEAGFDWVYYESKAH 180
 Db 121 KURVTGEWDEGHHSSESLSLHVEGRAVDITTSDRSKYGMALARAVEAGFDWVYYESKAH 180

Qy 181 IHCSVKAENSYAAKSQGCFPSATVHLEQGTTKLVTKDLSPGDRVLADDQGRLLYSDFLT 240
 Db 181 IHCSVKAENSYAAKSQGCFPSATVHLEQGTTKLVTKDLSPGDRVLADDQGRLLYSDFLT 240

Qy 241 FLDRDQAKVKEYVIETRPERLLTAHILFVAPNDATGEPEASSSGGPPSGAIG 300
 Db 241 FLDRDQAKVKEYVIETRPERLLTAHILFVAPNDATGEPEASSSGGPPGGALG 300

Qy 301 PRALPASRVRVPQRQVYVVAERGDPRLLPAVHSUTLSEAAAGAYAPLTAQGTILINRVL 360
 Db 301 PRALPASRVRPQRQVYVVAERGDPRLLPAVHSUTLSEAAAGAYAPLTAQGTILINRVL 360

Qy 361 ASCYAVIEEHSAWAHAFAPRLAHALLAALAPARTRGDGCGGGRRGVLTAPGA 420
 Db 361 ASCYAVIEEHSAWAHAFAPRLAHALLAALAPARTRGDGCGGGRRGVLTAPGA 420

Qy 421 ADAPGAGATAGIHWISQLIQIGTMLDSEALHPLGMATKSSXSRGAGGCAREGA 475
 Db 421 ADAPGAGATAGIHWISQLIQIGTMLDSEALHPLGMATKSSXSRGAGGCAREGA 475

RESULT 10
US-09-704-917-15
 ; Sequence 15, Application US/09704917
 ; Patent No. 6616926
 ; GENERAL INFORMATION:
 ; APPLICANT: Biogen, Inc.
 ; APPLICANT: Burky, Linda
 ; APPLICANT: Wang, Li Chun
 ; TITLE OF INVENTION: METHODS OF MODULATING LIPID METABOLISM AND STORAGE
 ; FILE REFERENCE: A069PCT
 ; CURRENT APPLICATION NUMBER: US/09/704,917
 ; CURRENT FILING DATE: 2000-11-02
 ; PRIOR APPLICATION NUMBER: 60/122,640
 ; PRIOR FILING DATE: 1999-03-03
 ; PRIOR APPLICATION NUMBER: 60/124,446
 ; PRIOR FILING DATE: 1999-03-15
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 15
 ; LENGTH: 475
 ; TYPE: PPT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Xaa at position 463 is any or unknown amino acid

Qy 1 MILLARCLLIVLVSLLIVCSGLACGPGRGFGRHKPKLTPLAYKOFIPNVAEKTIGASG 60
 Db 1 MILLARCLLIVLVSLLIVCSGLACGPGRGFGRHKPKLTPLAYKOFIPNVAEKTIGASG 60

Qy 61 RYEGKISRNNSERFKELTPTNYPDIIFKDEENTGADBLMTQCKDKNALAISVNQNQPGV 120
 Db 61 RYEGKISRNNSERFKELTPTNYPDIIFKDEENTGADBLMTQCKDKNALAISVNQNQPGV 120

Qy 121 KURVTGEWDEGHHSSESLSLHVEGRAVDITTSDRSKYGMALARAVEAGFDWVYYESKAH 180
 Db 121 KURVTGEWDEGHHSSESLSLHVEGRAVDITTSDRSKYGMALARAVEAGFDWVYYESKAH 180

Qy 181 IHCSVKAENSYAAKSQGCFPSATVHLEQGTTKLVTKDLSPGDRVLADDQGRLLYSDFLT 240
 Db 181 IHCSVKAENSYAAKSQGCFPSATVHLEQGTTKLVTKDLSPGDRVLADDQGRLLYSDFLT 240

Qy 61 RYEGKISRNNSERFKELTPTNYPDIIFKDEENTGADBLMTQCKDKNALAISVNQNQPGV 120

Qy 241 FLDRDGAKKVFVYIETPRERLTLAAHLLVAPHDNSATGEPEASSGSGPPSGALG 300
 Db 241 FLDRDGAKKVFVYIETPRERLTLAAHLLVAPHDNSATGEPEASSGSGPPSGALG 300

Qy 301 PRALFASRTRPGQVYVYERDGRRLIFAAVSTLSEAGAYAATQAQTILNRL 360
 Db 301 PRALFASRTRPGQVYVYERDGRRLIFAAVSTLSEAGAYAATQAQTILNRL 360

Qy 361 ASCYAVIEBESWAHRAFAFLAHALLAALAPARTDRGCGDSGGDRGGGRVALTAPGA 420
 Db 361 ASCYAVIEBESWAHRAFAFLAHALLAALAPARTDRGCGDSGGDRGGGRVALTAPGA 420

Qy 421 ADAPGAGATAGIHWYSQLIYQIGTWLDEALHPLGMAVKSSXSRGAGGCAREGA 475
 Db 421 ADAPGAGATAGIHWYSQLIYQIGTWLDEALHPLGMAVKSSXSRGAGGCAREGA 475

RESULT 11
 US-08-954-740-13
 Sequence 13, Application US/08954740
 i Patent No. 6630148
 i GENERAL INFORMATION:
 i APPLICANT: Irgham, Phillip W.
 i APPLICANT: McMahon, Andrew P.
 i APPLICANT: Tabin, Clifford J.
 i TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
 i TITLE OF INVENTION: Proteins and Uses Related Thereto
 i NUMBER OF SEQUENCES: 48
 i CORRESPONDENCE ADDRESS:
 i ADDRESSEE: FOLEY, HONG & ELIOT LLP
 i STREET: One Post Office Square
 i CITY: Boston
 i STATE: MA
 i COUNTRY: USA
 i ZIP: 02109-2170

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/954,740
 FILING DATE: 20-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/462,386
 FILING DATE: 05-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/435,093
 FILING DATE: 04-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/356,060
 FILING DATE: 14-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/176,427
 FILING DATE: 30-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-832-1000
 TELEFAX: 617-832-7000
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 475 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-954-740-13
 Query Match 99.9%; Score 2467; DB 4; Length: 475;
 Best Local Similarity 100.0%; Pred. No. 1.9e-238;
 Matches 475; Conservative 0; M:matches 0; Indels 0; Gaps 0;

Qy 1 MILLARCLLIVSSLVCSGLACGPGRCGFKRHKPLTPLAYKFIPVAEKTIGASG 60
 Db 1 MILLARCLLIVSSLVCSGLACGPGRCGFKRHKPLTPLAYKFIPVAEKTIGASG 60

Qy 61 RYEKGKRSRNSERFKEIUPNFDIIFKDEENTGADLMTORCKDKLNALAIISVNQWPGV 120
 Db 61 RYEKGKRSRNSERFKEIUPNFDIIFKDEENTGADLMTORCKDKLNALAIISVNQWPGV 120

Qy 121 KLRVTEGWDDEGHSEESLHYEGRAVDITSDRSKYGMALARVEAGFDWVYESKAH 180
 Db 121 KLRVTEGWDDEGHSEESLHYEGRAVDITSDRSKYGMALARVEAGFDWVYESKAH 180

Qy 181 THCSYKAENSAVAKSGCFCPSATVHLEGGTLYKVLSPGDRVLAADDQGRLLSDPFT 240
 Db 181 THCSYKAENSAVAKSGCFCPSATVHLEGGTLYKVLSPGDRVLAADDQGRLLSDPFT 240

Qy 241 FLDRDGAKKVFVYIETREPRELLTAHLLFVAPHDNSATGEPEASSGSGPPSGALG 300
 Db 241 FLDRDGAKKVFVYIETREPRELLTAHLLFVAPHDNSATGEPEASSGSGPPSGALG 300

Qy 301 PRALFASRVRPGQRYVVAERDGRDLPAAVHSVTLSSEAAGAYPLAQGTLLINRVL 360
 Db 301 PRALFASRVRPGQRYVVAERDGRDLPAAVHSVTLSSEAAGAYPLAQGTLLINRVL 360

Qy 361 ASCYATEEWSWAHRAFAFLAHALLAALAPARTDRGSGGDRGGGGRVALTAGA 420
 Db 361 ASCYATEEWSWAHRAFAFLAHALLAALAPARTDRGSGGDRGGGGRVALTAGA 420

Qy 421 ADAPGAGATAGIHWYSQLIYQIGTWLDEALHPLGMAVKSSXSRGAGGCAREGA 475
 Db 421 ADAPGAGATAGIHWYSQLIYQIGTWLDEALHPLGMAVKSSXSRGAGGCAREGA 475

RESULT 12
 US-09-151-999-15
 ; Sequence 15, Application US/09151999
 ; Patent No. 6630151
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Elizabeth
 ; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE
 ; FILE REFERENCE: ONV-031.02
 ; CURRENT APPLICATION NUMBER: US/09/151,999
 ; CURRENT FILING DATE: 198-08-11
 ; EARLIER APPLICATION NUMBER: US 08/955,552
 ; EARLIER FILING DATE: 1997-10-20
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 15
 ; LENGTH: 475
 ; TYPE: PRT
 ; ORGANISM: Homo sapien Shh
 ; PUBLISHER:
 ; OTHER INFORMATION: Xaa at position 463 is any or unknown amino acid
 US-09-151-999-15
 Query Match 99.9%; Score 2467; DB 4; Length: 475;
 Best Local Similarity 100.0%; Pred. No. 1.9e-238;
 Matches 475; Conservative 0; M:matches 0; Indels 0; Gaps 0;

Qy 1 MILLARCLLIVSSLVCSGLACGPGRCGFKRHKPLTPLAYKFIPVAEKTIGASG 60
 Db 1 MILLARCLLIVSSLVCSGLACGPGRCGFKRHKPLTPLAYKFIPVAEKTIGASG 60

Qy 61 RYEKGKRSRNSERFKEIUPNFDIIFKDEENTGADLMTORCKDKLNALAIISVNQWPGV 120
 Db 61 RYEKGKRSRNSERFKEIUPNFDIIFKDEENTGADLMTORCKDKLNALAIISVNQWPGV 120

Qy 121 KLRVTEGWDDEGHSEESLHYEGRAVDITSDRSKYGMALARVEAGFDWVYESKAH 180
 Db 121 KLRVTEGWDDEGHSEESLHYEGRAVDITSDRSKYGMALARVEAGFDWVYESKAH 180

RESULT 13
 Sequence 13, Application US/09736476
 Patent No. 6664075
 GENERAL INFORMATION:
 APPLICANT: Ingham, Phillip W.
 McMahon, Andrew P.
 Tabin, Clifford J.
 Bumrict, David A.
 Marti-Goroztegi, Elisa
 TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
 Proteins and Uses Related Thereto
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHTY & COCKFIELD
 STREET: 60 State Street
 CITY: Boston
 STATE: MA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 09/736,476
 FILING DATE: 4-MAY-1995
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION NUMBER: US 08/435,093
 FILING DATE: 13-Dec-2000
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REFERENCE/DOCKET NUMBER: HMI-006CP4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 13:
 LENGTH: 475 amino acids
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 LENGTH: 462 amino acids

Query Match 99.9%; Score 2467; DB 4; Length 475;
 Best Local Similarity 100.0%; Pred. No. 1.9e-238;
 Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MILLARCLLVLVSSLLVCSLAGGGRGGRKPKKLPLAKQFIDNVAEKTIGASG 60
 Db 1 MILLARCLLVLVSSLLVCSLAGGGRGGRKPKKLPLAKQFIDNVAEKTIGASG 60
 Qy 61 RYEKGSRNSRERKEITPNYNPDIIKFDEENTGADRIMTQRCDKDNALANISVNQWPGV 120
 Db 61 RYEKGSRNSRERKEITPNYNPDIIKFDEENTGADRIMTQRCDKDNALANISVNQWPGV 120
 Qy 121 KURVTBWDDEGHHSDESLSHYEGRAVDITTSDRDRSKYMLARLAVEAGFDWVYTESKAH 180
 Db 121 KURVTBWDDEGHHSDESLSHYEGRAVDITTSDRDRSKYMLARLAVEAGFDWVYTESKAH 180
 Qy 181 IHCSVKAENSYAAKSGGCFPGSATVHLEOGGTLYKDLSPCDRVIAADDGRLYSDFLT 240
 Db 181 IHCSVKAENSYAAKSGGCFPGSATVHLEOGGTLYKDLSPCDRVIAADDGRLYSDFLT 240
 Qy 241 FLDRDGAKKVYYVETREPRERLITAHHFLVAPHNDSATGEPEASSGSPGSGALG 300
 Db 241 FLDRDGAKKVYYVETREPRERLITAHHFLVAPHNDSATGEPEASSGSPGSGALG 300
 Qy 301 PRALPASRVRCQRYVVAERGDRLPLPAAVHSYTSLSERAGAYAPLTAQGTILINRVL 360
 Db 301 PRALPASRVRCQRYVVAERGDRLPLPAAVHSYTSLSERAGAYAPLTAQGTILINRVL 360
 Qy 361 ASCYAVTBESWAHRAPFRLAHALLAALAPARTRGDSGGRRGGGRVVALTAGA 420
 Db 361 ASCYAVTBESWAHRAPFRLAHALLAALAPARTRGDSGGRRGGGRVVALTAGA 420
 Qy 421 ADAPGAGATAGIHWSQLIQIGTMLDSEALHPLMAVKSSXSGAGGAREGA 475
 Db 421 ADAPGAGATAGIHWSQLIQIGTMLDSEALHPLMAVKSSXSGAGGAREGA 475
 RESULT 14
 US-08-736-476-13
 ; Sequence 4, Application US/08748591
 ; Patent No. 5759811
 ; GENERAL INFORMATION:
 ; APPLICANT: Epstein, Ervin
 ; APPLICANT: Hu, Zhilan
 ; APPLICANT: Bonifas, Jeanette
 ; TITLE OF INVENTION: Mutant Human Hedgehog Gene
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish and Richardson
 ; STREET: 220 Sand Hill Road
 ; CITY: Menlo Park
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US 09/736,476
 ; FILING DATE: 13-Dec-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY APPLICATION NUMBER: US 08/435,093
 ; FILING DATE: 4-MAY-1995
 ; APPLICATION NUMBER: US 08/356,060
 ; FILING DATE: 14-DEC-1994
 ; APPLICATION NUMBER: US 08/176,427
 ; FILING DATE: 30-DEC-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Vincent, Matthew P.
 ; REFERENCE/DOCKET NUMBER: HMI-006CP4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 227-7400
 ; TELEFAX: (617) 227-5941
 ; INFORMATION FOR SEQ ID NO: 13:
 ; LENGTH: 475 amino acids
 ; SEQUENCE CHARACTERISTICS:
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 ; LENGTH: 462 amino acids

TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-748-591-4

Query Match 97.5%; Score 2407; DB 1; Length 462;
 Best Local Similarity 100.0%; Pred. No. 1. 9e-232;
 Matches 462; Conservative 0; Mismatches 0; Gaps 0;
 / SEQUENCE FOR SEQ ID NO: 9;

Qy 1 MILLARCLLIVSLLVSGCGLACGPGRGFGKRRHPKKLPLAKOPIRNPVAKTIGASG 60
 Db 1 MILLARCLLIVSLLVSGCGLACGPGRGFGKRRHPKKLPLAKOPIRNPVAKTIGASG 60
 Qy 61 RYEKISRSNTERFELTPNYPNDLIKDDENTGADRINTQRCKDNALIASYMNPVG 120
 Db 61 RYEKISRSNTERFELTPNYPNDLIKDDENTGADRINTQRCKDNALIASYMNPVG 120
 Qy 121 KLRVTEGMDDEGHSEESIHYEGRADITTSDEDRSKYGMARLAVAGFDWVYESKAH 180
 Db 121 KLRVTEGMDDEGHSEESIHYEGRADITTSDEDRSKYGMARLAVAGFDWVYESKAH 180
 Qy 181 IHCSYKAENSAVAKSGCCPGSATVHLECGGTLYVKDLSPGDRVLADDQGRLLYSDFLT 240
 Db 181 IHCSYKAENSAVAKSGCCPGSATVHLECGGTLYVKDLSPGDRVLADDQGRLLYSDFLT 240
 Qy 241 FLDRDGAKKVYYETTRPRERLITAAHLLFVAPHDNSATGPBEAASSGSPSGCALG 300
 Db 241 FLDRDGAKKVYYETTRPRERLITAAHLLFVAPHDNSATGPBEAASSGSPSGCALG 300
 Qy 301 PRALFASRTRPGORYVYVAERGDPRRLPAAVHSVTLSSEAAGAYAPLTAAQGTILINRL 360
 Db 301 PRALFASRTRPGORYVYVAERGDPRRLPAAVHSVTLSSEAAGAYAPLTAAQGTILINRL 360
 Qy 361 ASCAVIEHSAWAFAFPRLAHALLALAPARTDRGDSGGDRGGGERVALTAPGA 420
 Db 361 ASCAVIEHSAWAFAFPRLAHALLALAPARTDRGDSGGDRGGGERVALTAPGA 420
 Qy 421 ADAPGAGATAGIHWYSQLYQIGWLDSBALHPLGMWKSS 462
 Db 421 ADAPGAGATAGIHWYSQLYQIGWLDSBALHPLGMWKSS 462

RESULT 15
 US-08-748-591-9
 Sequence 9, Application US/08748591
 Patient No. 5759811
 GENERAL INFORMATION:
 APPLICANT: Epstein, Ervin
 APPLICANT: Hu, Zhiyan
 APPLICANT: Bonifas, Jeanette
 TITLE OF INVENTION: Mutant Human Hedgehog Gene
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish and Richardson
 STREET: 2200 Sand Hill Road
 CITY: Menlo Park
 STATE: CA
 COUNTRY: USA
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent-In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/748,591
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Sherwood, Pamela J.
 REGISTRATION NUMBER: 36,677
 REFERENCE/DOCKET NUMBER: 08510/067001

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 322-5070
 TELEFAX: (415) 854-0875
 INFORMATION FOR SEQ ID NO: 9;
 LENGTH: 462 amino acids
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-748-591-9

Query Match 97.5%; Score 2407; DB 1; Length 462;
 Best Local Similarity 100.0%; Pred. No. 1. 9e-232;
 Matches 462; Conservative 0; Mismatches 0; Gaps 0;
 / SEQUENCE FOR SEQ ID NO: 9;

Qy 1 MILLARCLLIVSLLVSGCGLACGPGRGFGKRRHPKKLPLAKOPIRNPVAKTIGASG 60
 Db 1 MILLARCLLIVSLLVSGCGLACGPGRGFGKRRHPKKLPLAKOPIRNPVAKTIGASG 60
 Qy 61 RYEKISRSNTERFELTPNYPNDLIKDDENTGADRINTQRCKDNALIASYMNPVG 120
 Db 61 RYEKISRSNTERFELTPNYPNDLIKDDENTGADRINTQRCKDNALIASYMNPVG 120
 Qy 121 KLRVTEGMDDEGHSEESIHYEGRADITTSDEDRSKYGMARLAVAGFDWVYESKAH 180
 Db 121 KLRVTEGMDDEGHSEESIHYEGRADITTSDEDRSKYGMARLAVAGFDWVYESKAH 180
 Qy 181 IHCSYKAENSAVAKSGCCPGSATVHLECGGTLYVKDLSPGDRVLADDQGRLLYSDFLT 240
 Db 181 IHCSYKAENSAVAKSGCCPGSATVHLECGGTLYVKDLSPGDRVLADDQGRLLYSDFLT 240
 Qy 241 FLDRDGAKKVYYETTRPRERLITAAHLLFVAPHDNSATGPBEAASSGSPSGCALG 300
 Db 241 FLDRDGAKKVYYETTRPRERLITAAHLLFVAPHDNSATGPBEAASSGSPSGCALG 300
 Qy 301 PRALFASRTRPGORYVYVAERGDPRRLPAAVHSVTLSSEAAGAYAPLTAAQGTILINRL 360
 Db 301 PRALFASRTRPGORYVYVAERGDPRRLPAAVHSVTLSSEAAGAYAPLTAAQGTILINRL 360
 Qy 361 ASCAVIEHSAWAFAFPRLAHALLALAPARTDRGDSGGDRGGGERVALTAPGA 420
 Db 361 ASCAVIEHSAWAFAFPRLAHALLALAPARTDRGDSGGDRGGGERVALTAPGA 420
 Qy 421 ADAPGAGATAGIHWYSQLYQIGWLDSBALHPLGMWKSS 462
 Db 421 ADAPGAGATAGIHWYSQLYQIGWLDSBALHPLGMWKSS 462

RESULT 16
 US-08-946-329A-20
 Sequence 20, Application US/08946329A
 / Sequence 20, Application US/08946329A
 / Patent No. 6057091
 / GENERAL INFORMATION:
 / APPLICANT: Beachy, Phillip A.
 / APPLICANT: Portier, Jeffrey A.
 / TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
 / NUMBER OF SEQUENCES: 109
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Fish & Richardson P.C.
 / STREET: 4225 Executive Square, Suite 1400
 / CITY: La Jolla
 / STATE: CA
 / ZIP: 92037
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: Windows 95
 / SOFTWARE: FactSeq For Windows Version 2.0b
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/946,329A
 / FILING DATE: 07-OCT-1997
 / CLASSIFICATION: 435
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Sherwood, Pamela J.
 / REGISTRATION NUMBER: 36,677
 / REFERENCE/DOCKET NUMBER: 08510/067001

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/061,323
 FILING DATE: 07-OCT-1996
 APPLICATION NUMBER: 08/729,743
 FILING DATE: 10-JUL-1996
 APPLICATION NUMBER: 08/567,357
 FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: 08/349,498
 FILING DATE: 02-DEC-1994

ATTORNEY/AGENT INFORMATION:
 NAME: Haile, Lisa A.
 REGISTRATION NUMBER: 38,147
 REFERENCE/DOCKET NUMBER: 07265/1400001
 TELEPHONE: 619/676-5070
 TELEFAX: 619/676-5099

INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US - 08-946-329A-20

Query Match 83.8%; Score 2068; DB 3; Length 437;
 Best Local Similarity 87.4%; Pred. No. 1.6e-198; Indels 26; Gaps 3;
 Matches 404; Conservative 8; Mismatches 24;

Qy 1 MLLARCLLIVLVSSILVCGSLACPGRGGRKHPKLTPLAKQFENVAEKTIGASG 60
 Db 2 ILLIARCLFLVASSILVCPGLACPGRGGRKHPKLTPLAKQFENVAEKTIGASG 61

Qy 61 RYEKGKISRNSERFKELTTPNYPDIIKDENTGADRIMTQRCKDNALAIYSWNQPGV 120
 Db 62 RYEKGKITRNSERFKELTTPNYPDIIKDENTGADRIMTQRCKDNALAIYSWNQPGV 121

Qy 121 KLRVTEGWDEGHSEESLHYEGRAVDITTSDRSKYGMRLAVAEAGFDWVYYYESKAH 180
 Db 122 KLRVTEGWDEGHSEESLHYEGRAVDITTSDRSKYGMRLAVAEAGFDWVYYYESKAH 181

Qy 181 IHCsvkaenstyaaksSGCFPSATVHLEQSGTKLVQDLSFGDRVLAADDQGRLLYSDFT 240
 Db 182 IHCsvkaenstyaaksSGCFPSATVHLEQSGTKLVQDLSFGDRVLAADDQGRLLYSDFT 241

Qy 241 FLDRDGAKKVYVETREPERLILTAHILYAPHDNSATGEPEASSGSGPPSGGALG 300
 Db 242 FLDRDGAKKVYVETLEPERLILTAHILYAPHDNSATGEPEASSGSGPPSGGALG 286

Qy 301 PRALPASRVPGQRTVYVAERGDGRILLPAVHSVTLSEAAAGAYAPLTAQGTTLINRVL 360
 Db 287 PSALPASRVPGQRTVYVAERGDGRILLPAVHSVTLSEAAAGAYAPLTAQGTTLINRVL 346

Qy 361 ASCYAVIEHSWAHRATAFPRIAHALLAALAPARTDGGDSGGDRGGGRVALTAPAA 420
 Db 347 ASCYAVIEHSWAHRATAFPRIAHALLAALAPARTDGGGSIP-AAQEA 395

Qy 421 ADAPGAGTAGIHWYSQLYQIGTWILDSEALHPLGMVAKSS 462
 Db 396 TEARGAEPDTAGIHWYSQLYQIGTWILDSEALHPLGMVAKSS 437

RESULT 17
 US-08-567-357A-20
 Sequence 20, Application US/08567357A
 General Information:
 Applicant: Beachy, Philip A.
 Applicant: Moon, Randall T.
 Applicant: Porter, Jeffrey A.
 Title of Invention: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
 Number of Sequences: 37
 Correspondence Address:
 Addressee: Fish & Richardson P.C.

RESULT 18
 US-08-729-743A-20
 Sequence 20, Application US/08729743A
 Patent No. 6214794
 General Information:

APPLICANT: Beachy, Philip A.
 APPLICANT: Moon, Randall T.
 APPLICANT: Porter, Jeffrey A.
 TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Fish & Richardson P.C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US08/729,745A
 FILING DATE: 07-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/567,357
 FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: 08/349,498
 FILING DATE: 02-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Hale, Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE DOCKET NUMBER: 07265/099001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619/678-5070
 TELEFAX: 619/678-5099
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-729-743A-20

Query	Match	Score	Length	Prd.	No.	Mismatches	Indels
Qy	1 MILLARCLLIVYSSLLVCSGLACGPGRGFKRRHRPKKLTPLAYKOFV	83.8%	DB 3;				
Db	2 LLLIARCLIVLLSLLCPGLAGPGRGFKRRHRPKKLTPLAYKQFV	87.4%		Prd. No. 1	5e-18;		
Qy	61 RYECKISSNSRKELTINNPDLIKEEENTGADRIMTQRCKDKNL	87.4%					
Db	62 RYESKITTNSRKELTINNPDLIKEEENTGADRIMTQRCKDKNL	87.4%					
Qy	121 KLRVTEGNDEDGHISEESESHYEGRAVIDTTSDRDRSKYGMARLAVEL	87.4%					
Db	122 KLRVTEGNDEDGHISEESESHYEGRAVIDTTSDRDRSKYGMARLAVEL	87.4%					
Qy	181 IHCsvKAENsVAAKSGCCPGSATVHLQCGTALKVDSLPGDRVLAA	87.4%					
Db	182 IHCsvKAENsVAAKSGCCPGSATVHLQCGTALKVDSLPGDRVLAA	87.4%					
Qy	241 FLDRDGACKVVFVYETREPRERLILTAHLLFVAPNHDATGPEEA	87.4%					
Db	242 FLDRDGACKVVFVYETREPRERLILTAHLLFVAPNHDATGPEEA	87.4%					
Qy	301 PRALFASRYRPGRQRYVVAERDGDRRLPAVHSVTLSEEAGAYA	87.4%					
Db	302 PSALFASRYRPGRQRYVVAERDGDRRLPAVHSVTLSEEAGAYA	87.4%					
Qy	361 ASCYAVIEEHSSWAHRAFAAPPRLAHLLAALAPARTDRGGDSGGDRG	87.4%					
Db	347 ASCYAVIEEHSSWAHRAFAAPPRLAHLLAALAPARTDRGGDSGGDRG	87.4%					
Qy	421 ADAPPAGATGIAHWSQLYQIGWILDSLEAHPLGMAVKSS 462	87.4%					

RESULT 19
US-09-057-860A-6
Sequence 6, Application US/09057860A
Patent No. 6277820
GENERAL INFORMATION:
APPLICANT: Aaron Rosenthal
APPLICANT: Mary Hynes
APPLICANT: Weilan Ye
TITLE OF INVENTION: Method Of Dopaminergic And Serotonergic Neuron Formation From Neutroprogeni
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94060
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057, 860A
FILING DATE: 09-Apr-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1364
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/552-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-057-860A-6

Query Match 83.8%; Score 2068; DB 3; Length 121
Best Local Similarity 87.4%; Pct. No. 1.6e-198;
Matches 404; Conservative 8; Missmatches 24; InDel 1

Qy 1 MLLIARCLIVLVLSSLLVCGSLACGPGRGFGRHPKLTPLAKCK
Db 2 LILLARCFLVILLSSLLVCPGLACGPGRGFGRHPKLTPLAKCK

Qy 61 RYEGKISNSRERKELTNPNNPDLIFDEENTGADMTRDKDKL
Db 62 RYEGRITRNSRERKELTNPNNPDLIFDEENTGADMTRDKDKL

Qy 121 KLRVTEGMDGHSEESLHYEGRADITTSRDRSKYGMARLA
Db 122 KLRVTEGMDGHSEESLHYEGRADITTSRDRSKYGMARLA

Qy 181 IHCSTKAENVAAKS GGCPGSATVHLEQGGTKLVQDLSPGDRVL
Db 182 IHCSTKAENVAAKS GGCPGSATVHLEQGGTKLVQDLSPGDRVL

Qy 241 FLDREDDGAKKVVFVETEPREPLLTAHLLFVAPINDSATGEPP
Db 242 FLDRBEGAKKVVFVETEPREPLLTAHLLFVAPINDSATGEPP

Qy 301 PRALPASRVPGQCVVVAERGDRRLPAAVHSVTLSSEAGAY
Db 302 PRALPASRVPGQCVVVAERGDRRLPAAVHSVTLSSEAGAY

Qy 287 PSALPASRVPGQCVVVAERGDRRLPAAVHSVTLSSEAGAY

RESULT 20 -
US-08-349-498-20
Sequence 20, Application US/08349498

GENERAL INFORMATION:
Patent No. 6281312
APPLICANT: Beachy, Philip A.
APPLICANT: Moon, Randall T.
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: U.S.A.
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/349,498
FILING DATE: 02-DEC-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/043001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-349-498-20

Query Match 83.8%; Score 2068; DB 3; Length 437;
Best Local Similarity 87.4%; Pred. No. 1..6..198;
Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MILLARCLLVLVSSLLVCSGLACGPRGRKPKLTPLAYKOFIPNVAEKTIGASG 60
Db 2 LILLARCLVLIASSLIVPGLAGCPGPRGPKRHKPKLTPLAYKOFIPNVAEKTIGASG 61
Qy 61 RYEGKISRNSRNSRFKELTPTPNYNPDLIFKDENTGADRMTQRCKDNLALAISVNQPGV 120
Db 62 RYEGKISRNSRNSRFKELTPTPNYNDLIFKDDENTGADRMTQRCKDNLALAISVNQPGV 121
Qy 121 KLRVTEGWDGHSEESLHYGRAVDTTSQRDRSKYGMARLAYAEFDWVYESKAH 180
Db 122 KLRVTEGWDGHSEESLHYGRAVDTTSQRDRSKYGMARLAYAEFDWVYESKAH 181
Qy 181 IHCVKVAKNSVAKSGGGPPGSATVHLQGGTKLVRDQGRLLSDFLT 240
Db 182 IHCVKVAKNSVAKSGGGPPGSATVHLQGGTKLVRDQGRLLSDFLT 241
Qy 241 FLDRDDGAKKVFTVIEPREPLLTAHLLVEPINDSATGEPEAASSGSPPSGALG 300
Db 242 FLDRDEGAKKVFTVIEPREPLLTAHLLVEPINDSATGEPEAASSGSPPSGALG 300
Qy 301 PRALFAASRVRPQRVTVAAERDGDRRLPAAVHSVTLSSEEAGAYPLTAGTILNRL 360
Db 287 PSALFAASRVRPQRVTVAAERGDGRRLPAAVHSVTIREEAGAYPLTAGTILNRL 346
Qy 361 ASCYAVIEEHSAHRAFAFPFLAHALLAALAPARTDRGGDSGGDRGGGRVALPAGA 420
Db 347 ASCYAVIEEHSAHRAFAFPFLAHALLAALAPARTDRGGDSGGDRGGGRVALPAGA 420
Qy 421 ADAPGAGATAGIHWYSQLYQIGTWILDSEALHPGMKSS 462
Db 396 TEARGAEPFTAGIHWYSQLYHIGTWILDSETMPGMKSS 437

RESULT 21 -
PCT-US95-15463-20
Sequence 20, Application PC/US9515463
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: U.S.A.
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15463
FILING DATE: 01-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/080W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-15463-20

Query Match 83.8%; Score 2068; DB 5; Length 437;
Best Local Similarity 87.4%; Pred. No. 1..6..198;
Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MILLIARCLLVLVSSLLVCSGLACGPRGRKPKLTPLAYKOFIPNVAEKTIGASG 60
Db 2 LILLARCLVLIASSLIVPGLAGCPGPRGPKRHKPKLTPLAYKOFIPNVAEKTIGASG 61
Qy 61 RYEGKISRNSRNSRFKELTPTPNYNPDLIFKDENTGADRMTQRCKDNLALAISVNQPGV 120
Db 62 RYEGKISRNSRNSRFKELTPTPNYNDLIFKDDENTGADRMTQRCKDNLALAISVNQPGV 121
Qy 121 KLRVTEGWDGHSEESLHYGRAVDTTSQRDRSKYGMARLAYAEFDWVYESKAH 180
Db 122 KLRVTEGWDGHSEESLHYGRAVDTTSQRDRSKYGMARLAYAEFDWVYESKAH 181
Qy 181 IHCVKVAKNSVAKSGGGPPGSATVHLQGGTKLVRDQGRLLSDFLT 240
Db 182 IHCVKVAKNSVAKSGGGPPGSATVHLQGGTKLVRDQGRLLSDFLT 241
Qy 241 FLDRDDGAKKVFTVIEPREPLLTAHLLVEPINDSATGEPEAASSGSPPSGALG 300
Db 242 FLDRDEGAKKVFTVIEPREPLLTAHLLVEPINDSATGEPEAASSGSPPSGALG 300
Qy 301 PRALFAASRVRPQRVTVAAERDGDRRLPAAVHSVTLSSEEAGAYPLTAGTILNRL 360
Db 287 PSALFAASRVRPQRVTVAAERGDGRRLPAAVHSVTIREEAGAYPLTAGTILNRL 346

RESUL 22
PCT-US95-15923-20
Sequence 20, Application PC/TUS9515923
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine, et al.
TITLE OF INVENTION: NOVEL HEDGEROG-DERIVED POLYPEPTIDES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: U.S.A.
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.3.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15923
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REFERENCE/DOCKET NUMBER: 38,347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-15923-20

Query Match Score 83.8%; DB 5; Length 437;
Best Local Similarity 87.4%; Pred. No. 1.6e-198;
Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MILLARCLLIVVSSILVCSGLACGPGRGCKRHPKUTPLAKQFIPNVAKTIGASG 60
Db 2 LILLARCFVLIASSLIVCPGIACGFGRGFCKRHPKUTPLAKQFIPNVAKTIGASG 61
Qy 61 RYEKGKISRNSERFKELTNPDIIFKDENTGADRMLTRCKDNALAIISWNQWPGV 120
Db 62 RYEKGKITRNSERFKELTNPDIIFKDENTGADRMLTRCKDNALAIISWNQWPGV 121
Qy 121 KLRVTECWDEOHHHSESLHYEGRAITTSDRDSKYGMNLAIRAVEAGDWWYYESKAH 180
Db 122 KLRVTEBWDEOHHHSESLHYEGRAITTSDRDSKYGMNLAIRAVEAGDWWYYESKAH 181
Qy 181 IHCSVKAENSYAAKSGCCFPGSATVHLEQGCKTLKDSLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSYAAKSGCCFPGSATVHLEQGCKTLKDSLSPGDRVLAADDQGRLLYSDFLT 241

RESUL 23
US-08-176-427B-8
Sequence 8, Application US/08176427B
GENERAL INFORMATION:
APPLICANT: Ingram, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADRESSEE: LAHTIE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION NUMBER: US/08/176,427B
APPLICATION NUMBER: US/08/176,427B
FILING DATE: 30-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMI-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-176-427B-8

Query Match Score 2065; DB 1; Length 437;
Best Local Similarity 87.2%; Pred. No. 3.3e-198;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MILLARCLLIVVSSILVCSGLACGPGRGCKRHPKUTPLAKQFIPNVAKTIGASG 60
Db 2 LILLARCFVLIASSLIVCPGIACGFGRGFCKRHPKUTPLAKQFIPNVAKTIGASG 61
Qy 61 RYEKGKISRNSERFKELTNPDIIFKDENTGADRMLTRCKDNALAIISWNQWPGV 120
Db 62 RYEKGKITRNSERFKELTNPDIIFKDENTGADRMLTRCKDNALAIISWNQWPGV 121
Qy 121 KLRVTECWDEOHHHSESLHYEGRAITTSDRDSKYGMNLAIRAVEAGDWWYYESKAH 180
Db 122 KLRVTEBWDEOHHHSESLHYEGRAITTSDRDSKYGMNLAIRAVEAGDWWYYESKAH 181
Qy 181 IHCSVKAENSYAAKSGCCFPGSATVHLEQGCKTLKDSLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAENSYAAKSGCCFPGSATVHLEQGCKTLKDSLSPGDRVLAADDQGRLLYSDFLT 241

RESULT 24
US 08-356-060A-11
; Sequence 1_1, Application US/08356060A
; Patent No. 5844079
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,427
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/0356,060A
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HNI-006CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-356-060A-11

RESULT 25
US-08-460-900C-11
; Sequence 1_1, Application US/08460900C
; Patent No. 6165747
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; APPLICANT: Bumcrot, David A.
; APPLICANT: Marti-Gorostiza, Elisa
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; TITLE OF INVENTION: Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HONG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,900C
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,093
; FILING DATE: 4-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/356,060
; FILING DATE: 14-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,427
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HNI-006CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-356-060A-11

Query Match 83.6% Score 2065; DB 2; Length 437;
Best Local Similarity 87.2% Fred. No. 3.3e-198;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

1 MILLIARCLLVLVSSLLVCSGLACGPGRGFGRHRPKKLTPLAYQFIPNVAEKTGAGSG 60

Qy

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 832-1000
 TELEX: (617) 832-7000
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-460-900C-11

Query Match 83.6%; Score 2065; DB 3; Length 437;
 Best Local Similarity 87.2%; Pred. No. 3. 3e-198;
 Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MLLIARCLLVLVSSLYVSGHLACGPGRGFGGRHPKLTPLAKOPIVNTAEEKTLGASG 60
 Db 2 LLLIARCPFLVASSLLVCPGLACGPGRGFGGRHPKLTPLAKOPIVNTAEEKTLGASG 61

Qy 61 RYEGKISRNNSRERPKELTPNYPDIFKDEBENTGADRIMTQRCKDNALATSMVNQPGV 120
 Db 62 RYEKRITRSEERPKELTPNYPDIFKDEBENTGADRIMTQRCKDNALATSMVNQPGV 121

Query Match 83.6%; Score 2065; DB 3; Length 437;
 Best Local Similarity 87.2%; Pred. No. 3. 3e-198;
 Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MLLIARCLLVLVSSLYVSGHLACGPGRGFGGRHPKLTPLAKOPIVNTAEEKTLGASG 60
 Db 2 LLLIARCFLVASSLLVCPGLACGPGRGFGGRHPKLTPLAKOPIVNTAEEKTLGASG 61

Qy 61 RYEGKISRNNSRERPKELTPNYPDIFKDEBENTGADRIMTQRCKDNALATSMVNQPGV 120
 Db 62 RYEGKTRNSRERPKELTPNYPDIFKDEBENTGADRIMTQRCKDNALATSMVNQPGV 121

Db 121 KLRVTEGWDDGHSEESLHYEGRAVDITTSDRSKYGMMLARLAVAGEFDWVYESKAH 180
 Qy 181 IHCSVKAENSAAKSGCCPGSATVHLFQGGKLVKVLSGPRVLADDQCRLLYSDFLT 240
 Db 182 IHCSVKAENSAAKSGCCPGSATVHLFQGGKLVKVLDGPRVLADDQCRLLYSDFLT 241

Qy 241 FLDDEGACKVYYTETRPRERLLTAHHLLVAPND SAGEPEASSGSPPSGCALG 300
 Db 242 FLDDEGACKVYYTETRPRERLLTAHHLLVAPND-----SGPTPG 286

Qy 301 PRALFASRVRPGQVYVVAERGDGRRLIAEVHSVTLSBAAAYAPITAQQTILINRVL 360
 Db 287 PSAFAASRVRPGQVYVVAERGDGRRLIAEVHSVTLSBEEAAYAPITAQQTILINRVL 346

Qy 361 ASCYAVIEEWSWAHAFAPRLAHALLALAPARTDRCGDSGGDRGGGRVALTAPGA 420
 Db 347 ASCYAVIEEWSWAHAFAPRLAHALLALAPARTD-----GGGGSIP-AAQSA 395

Qy 421 ADAPGAGATAAGIHVYSSQIQTWLIDSEBALHPLGMAVKSS 462
 Db 396 TEARGAEPTAGIHVYSSQIQTWLIDSEBTMPLGMAVKSS 437

RESULT 26
 US-08-674-509B-11
 Sequence 11 Application US/08674509B
 Patent No. 6261786
 GENERAL INFORMATION:
 APPLICANT: Ingham, Phillip W.
 APPLICANT: McManon, Andrew P.
 APPLICANT: Tabin, Clifford J.
 APPLICANT: Mario, Valeria
 TITLE OF INVENTION: SCREENING ASSAYS FOR HEDGEHOG AGONISTS
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & BLIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-1170
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

RESULT 28

US-0-957-874-11 Sequence 11, Application US/08957874

GENERAL INFORMATION:

APPLICANT: Ingham, Phillip W.
Patent No. 6384192

APPLICANT: McMahon, Andrew P.

APPLICANT: Tabin, Clifford J.

TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing Proteins and Uses Related Thereto

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/462,386

FILING DATE: 05-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/435,093

FILING DATE: 04-MAY-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/356,060

FILING DATE: 14-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/176,427

FILING DATE: 30-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: HMV-006-10

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000

TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 437 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US - 08-954-698-11

Query Match 83. 6%; Score 2065; DB 3; Length 437;

Best Local Similarity 87.2%; Pred. No. 3.3e-198; Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MILLARCLLIVYSSSLIVCSIIACGPGRGFGRHKPKKLTPLAYKOFIPNVAEKTGAGSG 60
Db 2 LLLARCFVLIASSLIVCPGIIACGPGRGFGRHKPKKLTPLAYKOFIPNVAEKTGAGSG 61

Qy 61 RYEKIKRSNSRFKELTPTNPDIIFKDEENTGADRIMTQRCKDKLNALAIISVNKNOWPGV 120
Db 62 RYEKIKTRNSRFKELTPTNPDIIFKDEENTGADRIMTQRCKDKLNALAIISVNQWPGV 121

Qy 121 KLRVTCWDEGHHSSESLHVEGRADITTSDRSKYGMALARAVEAGDWVYYESKAH 180
Db 122 RLRTBGWDDEGHHSSESLHVEGRADITTSDRSKYGMALARAVEAGEWVYYESKAH 181

Qy 181 IHCYKAENSYAAKSGCCFPGSATVHLEQGSTKLVKDLSPCDRVLADDQGRLLYSDFLT 240
Db 182 IHCYKAENSYAAKSGCCFPGSATVHLEQGSTKLVKDLRSPDRVLADDQGRLLYSDFLT 241

Qy 241 FLDRDGAKKVYVIETREPRERLILTAHHHLFVAPINDSATGEPEAASSGGPSSGALG 300
Db 242 FLDRDEGAKKVYVIETLEPRERLILTAHHHLFVAPIND-----SCOPTPG 286

Qy 301 PRALEAFSRVRPGCRVYVAAERGDRRLPAVHSVTLSEEEAGAYAPLTAGTILINRVL 360
Db 287 PSLALFAFRVRPGCRVYVAAERGDRRLPAVHSVTLREEEAGAYAPLTAGTILINRVL 346

Qy 361 ASCYAVIEEHSHAHRAPFLRAFLAALAAAPARTDGGDGGCGRGGGGRRVALTAPGA 420
Db 347 ASCYAVIEEHSHAHRAPFLRAFLAALAAAPARTDGGDGGCGRGGGGRRVALTAPGA 395

Qy 421 ADAPGAGTAGIHWYQOLYQGTWLDSALPHLGMVAKSS 462
Db 296 TRPAGCARTGAWHYSOLYHGTWLDSMTHPMVAKSS 437

Qy 121 KLRVTEGWDGDGHHSSESLHYEGRADITSDRSDESKYGMALARAVEAGG 83.6%; Score 2065; DB 4; Length 437
Best Local Similarity 87.2%; Pred. No. 3.3e-198; Matches 403; Conservative 9; Mismatches 24; Indels 1

Db 2 LLLARCFVLIASSLIVCPGIIACGPGRGFGRHKPKKLTPLAYKOFIPN 61 RYEKIKRSNSRFKELTPTNPDIIFKDEENTGADRIMTQRCKDKLNAL 62 RYEKIKTRNSRFKELTPTNPDIIFKDEENTGADRIMTQRCKDKLNAL 121 KLRVTCWDEGHHSSESLHVEGRADITTSDRSKYGMALARAVEAGDWVYYESKAH 180 122 RLRTBGWDDEGHHSSESLHVEGRADITTSDRSKYGMALARAVEAGEWVYYESKAH 181 181 IHCYKAENSYAAKSGCCFPGSATVHLEQGSTKLVKDLSPCDRVLADDQGRLLYSDFLT 240 182 IHCYKAENSYAAKSGCCFPGSATVHLEQGSTKLVKDLRSPDRVLADDQGRLLYSDFLT 241 241 FLDRDGAKKVYVIETREPRERLILTAHHHLFVAPINDSATGEPEAASSGGPSSGALG 300 242 FLDRDEGAKKVYVIETLEPRERLILTAHHHLFVAPIND-----SCOPTPG 286 301 PRALEAFSRVRPGCRVYVAAERGDRRLPAVHSVTLSEEEAGAYAPLTAGTILINRVL 360 287 PSLALFAFRVRPGCRVYVAAERGDRRLPAVHSVTLREEEAGAYAPLTAGTILINRVL 346 361 ASCYAVIEEHSHAHRAPFLRAFLAALAAAPARTDGGDGGCGRGGGGRRVALTAPGA 420 347 ASCYAVIEEHSHAHRAPFLRAFLAALAAAPARTDGGDGGCGRGGGGRRVALTAPGA 395 421 ADAPGAGTAGIHWYQOLYQGTWLDSALPHLGMVAKSS 462 296 TRPAGCARTGAWHYSOLYHGTWLDSMTHPMVAKSS 437 121 KLRVTEGWDGDGHHSSESLHYEGRADITSDRSDESKYGMALARAVEAGG 61 RYEKIKRSNSRFKELTPTNPDIIFKDEENTGADRIMTQRCKDKLNAL 62 RYEKIKTRNSRFKELTPTNPDIIFKDEENTGADRIMTQRCKDKLNAL 121 KLRVTEGWDGDGHHSSESLHYEGRADITSDRSDESKYGMALARAVEAGG 122 RLRTBGWDDEGHHSSESLHYEGRADITSDRSDESKYGMALARAVEAGG 181 IHCYKAENSYAAKSGCCFPGSATVHLEQGSTKLVKDLSPCDRVLADDQGRLLYSDFLT 240 182 IHCYKAENSYAAKSGCCFPGSATVHLEQGSTKLVKDLRSPDRVLADDQGRLLYSDFLT 241 241 FLDRDGAKKVYVIETREPRERLILTAHHHLFVAPINDSATGEPEAASSGGPSSGALG 300 242 FLDRDEGAKKVYVIETLEPRERLILTAHHHLFVAPIND-----SCOPTPG 286 301 PRALEAFSRVRPGCRVYVAAERGDRRLPAVHSVTLSEEEAGAYAPLTAGTILINRVL 360 287 PSLALFAFRVRPGCRVYVAAERGDRRLPAVHSVTLREEEAGAYAPLTAGTILINRVL 346 361 ASCYAVIEEHSHAHRAPFLRAFLAALAAAPARTDGGDGGCGRGGGGRRVALTAPGA 420 347 ASCYAVIEEHSHAHRAPFLRAFLAALAAAPARTDGGDGGCGRGGGGRRVALTAPGA 395 421 ADAPGAGTAGIHWYQOLYQGTWLDSALPHLGMVAKSS 462 296 TRPAGCARTGAWHYSOLYHGTWLDSMTHPMVAKSS 437

RESULT 29
US-09-325-256-20
; Sequence 20, Application US/0925256
; Patent No. 6444793
; GENERAL INFORMATION:
; APPLICANT: PEPINSKI, R. BLAKE
; APPLICANT: BAKER, DARREN P.
; APPLICANT: WEN, DINGYI
; APPLICANT: WILLIAMS, KEVIN P.
; APPLICANT: GANGER, ELLEN A.
; APPLICANT: TAYLOR, FREDERICK R.
; APPLICANT: GALDES, ALPHONSE
; APPLICANT: PORTER, JEFFREY
; TITLE OF INVENTION: HYDROPHOBICALLY-MODIFIED PROTEIN COMPOSITIONS AND METHODS
; FILE REFERENCE: BIV-067-01
; CURRENT FILING DATE: 1992-06-03
; PRIOR APPLICATION NUMBER: 60/099,800
; PRIOR APPLICATION NUMBER: 60/078,935
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/089,685
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/067,423
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: PC7/US98/25676
; PRIOR FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 20
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Murine sp.
; US-09-325-256-20

Query Match 83.6%; Score 2065; DB 4; Length 437;
Best Local Similarity 87.2%; Pred. No. 3..3e-198;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

Db 182 IHCsvkaensvaaksgggfpgsatvhleqggtklykdrlpgdrvlaaddqgrllysdlft 241
Qy 241 florddgakkvvtvtttpprbrlltaahhlfvaphndsatgbpeassgsgrppggalg 300
Db 242 florddegakkvvtvtttpprbrlltaahhlfvapnd-----sgptpg 286
Db 244 florddegakkvvtvtttpprbrlltaahhlfvapnd-----sgptpg 286 .

Db 301 pralfasvrpgorvvyyaergdrrllpaahtstilseaaayapltaoqtgilnrvl 360
Qy 301 pralfasvrpgorvvyyaergdrrllpaahtstilseaaayapltaoqtgilnrvl 360
Db 287 psafasvrpgorvvyyaergdrrllpaahtstilseaaayapltaoqtgilnrvl 346
Db 361 ascyavitephswahrafaerflahalaalapartdrgdsgcgdrgggrvaltapg 420
Qy 361 ascyavitephswahrafaerflahalaalapartdrgdsgcgdrgggrvaltapg 420
Db 347 ascyavitephswahrafaerflahalaalapartd-----ggggssip-aaqsa 395
Db 421 adargatagtagimysolyoigtwlldsealplgmvakss 462
Qy 421 adargatagtagimysolyoigtwlldsealplgmvakss 462
Db 396 teargaeptaghmysoolyhigtwlldsetmoplgnmvakss 437

RESULT 30
US-09-639-695-11
; Sequence 11, Application US/09639695
; Patent No. 6576237
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; APPLICANT: Bumcrot, David A.
; APPLICANT: Marti-Gorostiza, Elisa
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESS: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/639,695
FILING DATE: 16-Aug-2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/435,093
FILING DATE: 4-May-1995
PRIORITY NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMV-006.05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-1000
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-639-695-11

Query Match 83.6%; Score 2065; DB 4; Length 437;
Best Local Similarity 87.2%; Pred. No. 3..3e-198;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

Db 1 mlliarcllivvssllvcglacpgprgrgkrrhpkktpkltplayqfnpvaektlgasg 60
Qy 2 llliarcpfvllassllvcglacpgprgrgkrrhpkktpkltplayqfnpvaektlgasg 61
Db 61 ryegkisrnserfrkeltptnpyndifkdbeentgadrlnmtqrckdklnalaistymnowfg 120
Qy 62 ryegkisrnserfrkeltptnpyndifkdbeentgadrlnmtqrckdklnalaistymnowfg 121
Db 121 klrtegwmdeghsfeeslhvegravdtttsdrdrskycmnlaraveagfdwyyyeskah 180
Qy 121 klrtegwmdeghsfeeslhvegravdtttsdrdrskycmnlaraveagfdwyyyeskah 181
Db 122 rlrtegwdeghhspeelvyegeavdtttsdrdrskycmnlaraveagfdwyyyeskah 181
Qy 181 ihcsvkkaensvaaksgggfpgsatvhleqggtklykdrlpgdrvlaaddqgrllysdlft 240

QY	1	MLLARCLLIVSSILVSSGLACGPGRGKGRHRPKKLTPPLAYQFIPNVAEKTIGASG	60
Db	2	LLLARCFVLASSLVCFGCLACPGRGKGRHRPKKLTPPLAYQFIPNVAEKTIGASG	61
QY	61	RYEGKISRSNTERKEFLTPNPDIFKDEBENTGADRLMQRCKDNLALISMUNQNGU	120
Db	62	RYEGKICTRNBERKEFLTPNPDIFKDEBENTGADRLMQRCKDNLALISMUNQNGU	121
QY	121	KLRVTEGMDSGHSSEESLHYEGRAVDITSDRDRSKYGMALARAVEAGFDWVYESKAH	180
Db	122	KLRVTEGMDSGHSSEESLHYEGRAVDITSDRDRSKYGMALARAVEAGFDWVYESKAH	181
QY	181	IHCSYKAENSAAKSGCGFCGSATVHLEQGTTKLVKDLSPGDRVLAADDQGRLLYSDEL	240
Db	182	IHCSYKAENSAAKSGCGCPGSATVHLEQGTTKLVKDLRGDRVLAADDQGRLLYSDEL	241
QY	241	FLDRDGAKEYVYIETREPRERLILTAHLLFVAPHNDSATGPEAASSGSPGGALG	300
Db	242	FLDRDEGAKCUVYIETLERERILLTAHLLFVAPHND-----SGPTPG	286
QY	301	PRALFASRVREGQRVYVVAERDGDRRLPAVHSVTLSEEAGAYAPITAQGTLLINRVL	360
Db	287	PSALFASRVREGQRVYVVAERGDGRRLPAVHSVTLREEAGAYAPITAQGTLLINRVL	346
QY	361	ASCYAVIEEHSAWAHAFAPFRLLAHALLAALAPARTDRCGDSSGGDRGGGGRRVALTAPGA	420
Db	347	ASCYAVIEEHSAWAHAFAPFRLLAHALLAALAPARTD-----GGGGSIP-AAOSA	395
QY	421	ADAPGAGATAGIHWYSLQXIGTMILDSEAHPIGMAYKSS	462
Db	396	TEARGAEPTGICHWYSLQXIGTMILDSEAHPIGMATKSS	437

RESULT 31
US-03-448-188-11
; Sequence 11, Application US/09448188
; Patent No. 6607913
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; McMahon, Andrew P.
; Tabir, Clifford J.
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HONG & ELIOT LLP
; STREET: One Post Office Square

STATE : MA
COUNTRY : USA
ZIP : 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/448,188
FILING DATE: 23-NOV-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/462,386
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US/08/435,093
FILING DATE: 04-MAY-1995
APPLICATION NUMBER: US/08/356,060
FILING DATE: 14-DEC-1994
APPLICATION NUMBER: US/08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMV-006.12

RESULT 32
US-08-154-128-11
Sequence 11, Application US/08954128
Patent No. 6610656

GENERAL INFORMATION:

APPLICANT: Ingram, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tablin, Clifford J.

TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELLIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/954,128
 FILING DATE: 20-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/462,386
 FILING DATE: 05-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/435,093
 FILING DATE: 04-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/356,060
 FILING DATE: 14-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/176,427
 FILING DATE: 30-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: HMV-006.12
 COMMUNICATION INFORMATION:
 TELEPHONE: 617-832-1000
 TELEFAX: 617-832-7000
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-954-128-11

Query Match 83.6%; Score: 2065; DB: 4; Length: 437;
 Best Local Similarity 87.2%; Pred. No. 3.3e-198; Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MILLARCFLIVLVLSSLLVCGSLAGCPGRGFKRHPKLTPLAKQFIPNVAEKTIGASG 60
 Db 2 LLLLARCFLIVLVLASSLLVCGSLAGCPGRGFKRHPKLTPLAKQFIPNVAEKTIGASG 61

Qy 61 RYEKGISRSNTERFEKLTPNYNPDIFKDENTGADRMTQRCKDKNALAISYMNCWGV 120
 Db 62 RYEKGKTRNTERFEKLTPNYNPDIFKDENTGADRMTQRCKDKNALAISYMNCWGV 121

Qy 121 KLRVTEGWDGDGHISESHYEGRAVDITTSDRSKYGMALARVAEAGFDWVYYESKAH 180
 Db 122 RLRTVTEGWDGDGHISESHYGRADITTSDRSKYGMALARVAEAGFDWVYYESKAH 181

Qy 181 IHCSYTAENSAVAKSGCFCFGSATVHLEGGTQLVKDLSPGDRVLAADDQGRLLYSDFLT 240
 Db 182 FLDRDGAKKVYYTETREPRERLTTAHLFLVAPHDNSATGEPEASSGSGPFSGAGL 300

Qy 241 FLDRDGAKKVYYTETREPRERLTTAHLFLVAPHDNSATGEPEASSGSGPFSGAGL 300
 Db 242 FLDRDGAKKVYYTETREPRERLTTAHLFLVAPHDNSATGEPEASSGSGPFSGAGL 286

Qy 301 PRALFASRVPGQRTVVAERDGRRLIPANHVSITLSEAAAGAYAPLTAQGTILINRVL 360
 Db 302 PSALFASRVPGQRTVVAERDGRRLIPANHVSITLSEAAAGAYAPLTAQGTILINRVL 360

Qy 361 ASCYAVIEBSWAHAFAPPRLAHLALAPARTRGDSGGDRGGGRVALTAGCA 420
 Db 347 ASCYAVIEBSWAHAFAPPRLAHLALAPARTRGDSGGDRGGGRVALTAGCA 395

Qy 421 ADAPGAGATAGIHWYSQLYQIYWGLDSEAHLPGLMAVKSS 462
 Db 396 TEARGAEPTAGIHWYSQLYHGTWLDSETMHPGLMAVKSS 437

Qy 301 PRALFASRVPGQRTVVAERDGRRLIPAAVSVTLLSEAAAGAYAPLTAQGTILINRVL 360
 Db 287 PSALFASRVPGQRTVVAERDGRRLIPAAVSVTLLSEAAAGAYAPLTAQGTILINRVL 346

Qy 361 ASCYAVIEBSWAHAFAPPRLAHLALAPARTRGDSGGDRGGGRVALTAGCA 420
 Db 347 ASCYAVIEBSWAHAFAPPRLAHLALAPARTRGDSGGDRGGGRVALTAGCA 395

Qy 421 ADAPGAGATAGIHWYSQLYQIYWGLDSEAHLPGLMAVKSS 462
 Db 396 TEARGAEPTAGIHWYSQLYHGTWLDSETMHPGLMAVKSS 437

RESULT 34
 US-08-954-128-11

Sequence 11, Application US/08954740
 Patent No. 663018

GENERAL INFORMATION:
 APPLICANT: McMahon, Andrew P.
 INVENTOR: Ingham, Phillip W.
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-2170

GENERAL INFORMATION:
 APPLICANT: Biogen, Inc.
 INVENTOR: Burkly, Linda

CORRESPONDENCE ADDRESS:
 ADDRESSEE: POLLEY, HORG & ELIOT LLP
 STREET: One Post Office Square
 CITY: Boston

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,740
FILING DATE: 20-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,386
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,093
FILING DATE: 04-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE DOCKET NUMBER: HNV-006-08
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

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; Sequence 13, Application US/09151999
; Patent No. 6639051
; GENERAL INFORMATION:
; APPLICANT: Yang, Elizabeth
; TITLE OF INVENTION: POLYPEPTIDES, AN
; FILE REFERENCE: ONY-031.02
; CURRENT APPLICATION DATE: US/09/11
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: 08/955,8
; EARLIER FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 13
; LENGTH: 437
; TYPE: PRT
; ORGANISM: murine Shh
; US-09-151-999: murine Shh

Query Match          83.6% Score
Best Local Similarity 87.2% Pred
Matches   403; Conservative 9; M:
           1 MLLIARCLLVLYSLLVCGSGLACCE
           2 LLLIARCFLVILASSLLIVCPGIAACC
Qy          1 RYEKGKISRNSERKEELPPTNMYEDI
Qy          2 RYEKETTINNSERKEELPPTNMYEDI
Db          1 KLRVTEGWDEGHSEESLHVYEGRA
Db          2 KLRVTEGWDEGHSEESLHVYEGRA
Qy          1 KLRVTEGWDEGHSEESLHVYEGRA

```

Query Match 83.6%; Score 2065; DB 4; Length 437;
 Best Local Similarity 87.2%; Pred. No. 3.3e-198;
 Mismatches 9; Indels 26
 Matches 403; Conservative 24;
 Nucleotides 24;

1	MILLAROLIIVLVSLLIVCSLACCPGRGFGRKRRHPKQLTPLAYQFIPNTYV
2	LILLARCFLVLIASSLIVCQGACCPGRGFGRKRRHPKQLTPLAYQFIPNTYV
61	RYEGKISRNSRERKELTPTNPNPDIIFKDEENTGADRIMTQRCKDKLNALAI
62	RYEGKTRNSRERKELTPTNPNPDIIFKDEENTGADRIMTQRCKDKLNALAI
121	KURVTEGWDEGHHSSESLIVEGRAVIDITSDRDRSKYGMMLARIAVAGEGDV
122	KURVTEGWDEGHHSSESLIVEGRAVIDITSDRDRSKYGMMLARIAVAGEGDV
181	IHCsvkaensvaaksgcfcposatvhleqgtklvkdlspgdsvlaaddqggs
182	IHCsvkaensvaaksgcfcposatvhleqgtklvkdlspgdsvlaaddqggs
241	FLDRDGAKKYYVIESTREPERLLITAHLFVAPHNDSATGBPEASSGS
242	FLDRDGAKKYYVIETLEPERLLITAHLFVAPHNDSATGBPEASSGS
301	PRALFASRVRQCRRVYVAEFDGDRRLPAAVHSYTLSEBAAAYAPLTAAQ
287	PSLFASRVRQCRRVYVAEFGDRRLPAAVHSYTLSEBAAAYAPLTAAH
361	ASCAYATBEHSMWRAFAPFLAHLLAALAPARTDGGDSGGDRGGGGCF
347	ASCAYATBEHSMWRAFAPFLAHLLAALAPARTDGGDSGGDRGGGGCF
421	ADPGAGATAGTHWYSQLLQYGTWILDSPALHPLGMAVKS 462
396	TEARGAEPTAGTHWYSQLLQYGTWILDSMHPLGMAVKS 437

RESULT 36
US-09-736-476-11
Sequence 11, Application US/09736476
; Patent No. 6665075
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
McMahon, Andrew P.
Tabin, Clifford J.
Buncrot, David A.
Marti-Gorostiza, Elisa
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston

STATE: MA ; Sequence 14, Application US/09293505
 ZIP: 02109 ; Patent No. 6348875
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/736,476
 FILING DATE: 13-Dec-2000
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/435,093
 FILING DATE: 4-May-1995
 APPLICATION NUMBER: US 08/356,060
 FILING DATE: 14-Dec-1994
 APPLICATION NUMBER: US 08/176,427
 FILING DATE: 30-Dec-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 US-09-736-476-11

Query Match 83.5%; Score 2062; DB 4; Length 437;
 Best Local Similarity 87.0%; Pred. No. 6 5e-198;
 Matches 400; Conservative 10; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MLLIARCLLVLVSSLLVSGLAGPGRGFGKRRHPKKLTPLAYKQFIPYVAEKTIGASG 60
 Db 2 LLLIARCFVLILASSLIVPGLAGPGRGFGKRRHPKKLTPLAYKQFIPYVAEKTIGASG 61

Qy 61 RYECKISRSERFELTPYNPDPYLKEENGTADRLMTQRCKDKUNALASVMNQMPGV 120
 Db 62 RYECKITRANSERFELTPYNPDPYLKDENTADRLMTQRCKDKUNALASVMNQMPGV 121

Qy 121 KLRVTEGMDEDGHSEESLYHEGRAVDITTSDRSKYGMALARAVEAGEDFVVYESKAH 180
 Db 122 RLRTVEGMDEDGHSEESLYHEGRAVDITTSDRSKYGMALARAVEAGEDFVVYESKAH 181

Qy 181 IHCSYKAENSAAKSGCCPGSATVHLEQGGTKLVYDLSPGDRVLAADDQGRLLYSDFLT 240
 Db 182 IHCSYKAENSAAKSGCCPGSATVHLEQGGTKLVYDLSPGDRVLAADDQGRLLYSFLT 241

Qy 241 FLDRDDGAKKFVYVETREPRLILTAHLLFVAPNDSATGEPEAASSGSPGSGALG 300
 Db 242 FLDRDEGAKKFVYVETREPRLILTAHLLFVAPNDF-----SGPTPG 286

Qy 301 PRALFASRVRPGQRYVVAERDGDRLLPAAVHSVTLBEAAAGAYAPLTAQGTILIRNL 360
 Db 302 PSALFASRVRPGQRYVVAERGDRRLLPAAVHSVTLREERGAYAPLTAHGTILIRNL 346

Qy 361 ASCYAVIEEHSAWAFAPERLAHALAALAPARTDGGDSGGDRGGGRVALTAPGA 420
 Db 362 ASCYAVIEEHSAWAFAPERLAHALAALAPARTDGGDSGGDRGGGRVALTAPGA 420

Qy 421 ADAPGAGATGTHWYSQLYQIGTWLIDSEAHPLGMVKSS 462
 Db 396 TEARGAEPTAGIHWYSQLYHGTWLIDSETHEPLGMVKAS 437

RESULT 38
 US-08-757-230A-2
 ; Sequence 2, Application US/08757230A
 ; Patent No. 6238855
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas M. Jessell, et al.
 ; TITLE OF INVENTION: RAT HDGEOH PROTEIN-1 (VH-1)
 ; FILE REFERENCE: 057545375-1/JPW/SNS/MVM
 ; CURRENT APPLICATION NUMBER: US/08757-220A
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 2
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: RAT
 ;
 US-08-757-230A-2

Query Match 39 ; Score 2060; DB 3; Length 437;
 Best Local Similarity 83.4%; Pred. No. 1e-197;
 Matches 405; Conservative 8; Mismatches 22; Indels 28; Gaps 4;

Db 182 IHCsvkaensvaaksdgcffgsatvhleqggtkuvkdlspgdrvlaaddogrillysdlft 241
 Qy 241 FLDRDGAKKVYFYVETREPERLITTAHLLFVAPHNDSATGPEASSGSPGSPPSGALG 300
 Db 242 FLDRDGAKKVYFYVETREPERLITTAHLLFVAPHN-----SGPTPG 286
 Qy 301 PRALFASRVRPGQRTYVAERDGDRLPPLPAVHSYTLSBEEAGAYAPLTAQGTILINRVL 360
 Db 287 PSPLFASRVRPGQRTYVAERGDRRLPPLPAVHSYTLPRAAAGYAPLTAQGTILINRVL 346
 Qy 361 ASCYAVIEEWSWAHAFAPPFLAHALLAALAPARTDGGSDGGDRGGGRVALTAP-G 419
 Db 347 ASCYAVIEEWSWAHAFAPPFLAHALLAALAPART-----GGGGG-SIAPQPS 394
 Qy 420 ADDAPAGATAGTIAHWSQLYQIGWILLDSEALHJGMVAKSS 462
 Db 395 VAEARGGPPAGIHWYSQLYHIGTWLMLDSETLHPGMVAKSS 437

RESULT 40 ; US-08-700-393-2
 ; Sequence 2, Application US/08700393A
 ; Patent No. 6566092
 ; GENERAL INFORMATION:
 ; APPLICANT: Jessell, Thomas M.
 ; APPLICANT: Dodd, Jane
 ; APPLICANT: Reilink, Hank
 ; APPLICANT: Edlund, Thomas
 ; TITLE OF INVENTION: DNA ENCODING A VERTEBRATE HOMOLOG OF HEDGEHOG, VHHL-1
 ; FILE REFERENCE: 453758seq
 ; CURRENT APPLICATION NUMBER: US/08/700,393A
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.0 - beta
 ; SEQ ID NO 2
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: RAT
 ; US-08-700-393-2

Query Match 39 ; Score 2060; DB 4; Length 437;
 Best Local Similarity 83.4%; Pred. No. 1e-197;
 Matches 405; Conservative 8; Mismatches 22; Indels 28; Gaps 4;

Db 1 MLLARCLLIVLSSLLIVCSGLACGPGRGFGRKRRPHPKKLTPLAYKOFIPNVAEKTLGASG 60
 Qy 2 LLLARCFVLVALASSLLVCPGLACGPGRGFGRKRRPHPKKLTPLAYKOFIPNVAEKTLGASG 61
 Db 287 PSPLFASRVRPGQRTYVAERGDRRLPPLPAVHSYTLPRAAAGYAPLTAQGTILINRVL 346
 Qy 301 PRALFASRVRPGQRTYVAERDGDRLPPLPAVHSYTLSBEEAGAYAPLTAQGTILINRVL 360
 Db 347 ASCYAVIEEWSWAHAFAPPFLAHALLAALAPARTDGGSDGGDRGGGRVALTAP-G 419
 Qy 361 ASCYAVIEEWSWAHAFAPPFLAHALLAALAPART-----GGGGG-SIAPQPS 394
 Db 395 VAEARGGPPAGIHWYSQLYHIGTWLMLDSETLHPGMVAKSS 437

RESULT 41 ; US-08-757-230A-9
 ; Sequence 9, Application US/08757230A
 ; Patent No. 6235885
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas M. Jessell, et al.
 ; TITLE OF INVENTION: RAT HEDGEHOG PROTEIN-1 (VHH-1)
 ; FILE REFERENCE: 0575/45375-1/JUP/SHS/MM
 ; CURRENT APPLICATION NUMBER: US/08/757,230A
 ; CURRENT FILING DATE: 1996-11-27
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: Rat
 ; US-08-757-230A-9

Query Match 39 ; Score 2060; DB 3; Length 437;
 Best Local Similarity 83.4%; Pred. No. 1e-197;
 Matches 405; Conservative 8; Mismatches 22; Indels 28; Gaps 4;

Db 1 MLLARCLLIVLSSLLIVCSGLACGPGRGFGRKRRPHPKKLTPLAYKOFIPNVAEKTLGASG 60
 Qy 2 LLLARCFVLVALASSLLVCPGLACGPGRGFGRKRRPHPKKLTPLAYKOFIPNVAEKTLGASG 61
 Db 287 PSPLFASRVRPGQRTYVAERGDRRLPPLPAVHSYTLPRAAAGYAPLTAQGTILINRVL 346
 Qy 301 PRALFASRVRPGQRTYVAERDGDRLPPLPAVHSYTLSBEEAGAYAPLTAQGTILINRVL 360
 Db 347 ASCYAVIEEWSWAHAFAPPFLAHALLAALAPARTDGGSDGGDRGGGRVALTAP-G 419
 Qy 361 ASCYAVIEEWSWAHAFAPPFLAHALLAALAPART-----GGGGG-SIAPQPS 394
 Db 395 VAEARGGPPAGIHWYSQLYHIGTWLMLDSETLHPGMVAKSS 437

RESULT 42 ; US-08-757-230A-9
 ; Sequence 9, Application US/08757230A
 ; Patent No. 6235885
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas M. Jessell, et al.
 ; TITLE OF INVENTION: RAT HEDGEHOG PROTEIN-1 (VHH-1)
 ; FILE REFERENCE: 0575/45375-1/JUP/SHS/MM
 ; CURRENT APPLICATION NUMBER: US/08/757,230A
 ; CURRENT FILING DATE: 1996-11-27
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: Rat
 ; US-08-757-230A-9

Query Match 39 ; Score 2060; DB 3; Length 437;
 Best Local Similarity 83.4%; Pred. No. 1e-197;
 Matches 405; Conservative 8; Mismatches 22; Indels 28; Gaps 4;

Db 1 MLLARCLLIVLSSLLIVCSGLACGPGRGFGRKRRPHPKKLTPLAYKOFIPNVAEKTLGASG 60
 Qy 2 LLLARCFVLVALASSLLVCPGLACGPGRGFGRKRRPHPKKLTPLAYKOFIPNVAEKTLGASG 61
 Db 287 PSPLFASRVRPGQRTYVAERGDRRLPPLPAVHSYTLPRAAAGYAPLTAQGTILINRVL 346
 Qy 301 PRALFASRVRPGQRTYVAERDGDRLPPLPAVHSYTLSBEEAGAYAPLTAQGTILINRVL 360
 Db 347 ASCYAVIEEWSWAHAFAPPFLAHALLAALAPARTDGGSDGGDRGGGRVALTAP-G 419
 Qy 361 ASCYAVIEEWSWAHAFAPPFLAHALLAALAPART-----GGGGG-SIAPQPS 394
 Db 395 VAEARGGPPAGIHWYSQLYHIGTWLMLDSETLHPGMVAKSS 437

Query 420 AADPGAGATAGIHWYSQQLYQIGTWILDEAHLPIGMVKSS 462
 Database 395 VABARGGPPAG-IHWYSQQLYHGTWILDESETLHPLGMVKSS 437

RESULT 41
 PCT-US95-02315-2
 Sequence 2, Application PC/TUSS502315
 GENERAL INFORMATION:
 APPLICANT: Jessell, Thomas M.
 APPLICANT: Dodd, Jane
 APPLICANT: Roelink, Henk
 APPLICANT: Edlund, Thomas
 TITLE OF INVENTION: DNA ENCODING A VERTEBRATE HOMOLOG OF TITIE OF INVENTION: HEDGEROG, VH-1, EXPRESSED BY THE NOTOCHORD, AND USES
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 STREET: Cooper & Dunham
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/02315
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: John P. White
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 45375-A-PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0515
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-02315-2

Query Match Score 2060; DB 5; Length 437;
 Best Local Similarity 87.5%; Pred. No. 1e-197;
 Matches 405; Conservative 8; Mismatches 22; Indels 28; Gaps 4;

Query 1 MILLARCLLIVVSSILVCSLACGPGRGKRRPKKKTPLAYKQIFINVAEKTIGASG 60
 Database 2 LILLARCFIVLAVASSILVCPFLACGPGRGKRRPKKKTPLAYKQIFINVAEKTIGASG 61

Query 61 RYEKGKISRNNSERFKELTPNTPDIIKDENTGADRMLTORKDKLNALAIISVNQWPGV 120
 Database 62 RYEKGKTRNSERFKELTPNTPDIIKDENTGADRMLTORKDKLNALAIISVNQWPGV 121

Query 121 KLRVTEGWDEPHHSSESHESLYEGRADITTSDRSKYMLRQHPKKLTPLAYKQIFINVAEKTIGASG 180
 Database 122 KLRVTEBOWDEPHHSSESHESLYEGRADITTSDRSKYMLRQHPKKLTPLAYKQIFINVAEKTIGASG 181

Query 181 IHCsvkaensvaaksgccfpqsaatvhleogsttklydlspsgdrvlaadogrillysdfit 240
 Database 182 IHCsvkaensvaaksgccfpqsaatvhleogsttklydlspsgdrvlaadogrillysdfit 241

Query 241 FLDRDGAKVYYVITREPRERLLTAHILYVAPHNDSATGEPEASSSGGPPSGGAI 300
 Database 242 FLDRDGAKVYYVITREPRERLLTAHILYVAPHND-----SGPTFG 286

Query 301 PRALFASRVRPGORYVVAERGDERRLLPAAVHSVTLSSEANGAYAPLTAQGTIL-NRVL 360
 Database 287 PSPLFASRVPQGVVVAERGDDRLLPAVHSVTLEERAYAPLTAQGTIL-NRVL 346

Query 361 ASCYAVTEEHWSWAFAFRLLAHALLALAPARTDRGGSGGRGGVALT-G 419
 Database 347 ASCYAVTEEHWSWAFAFRLLAHALLALAPARTD----GGGGG-SIPAPQG 394

Query 420 AADAPGAGATAGIHWYSQQLYQIGTWILDESETLHPLGMVKSS 462
 Database 395 VAEARGGPPAG-IHWYSQQLYHGTWILDESETLHPLGMVKSS 437

RESULT 42
 US-08-176-427B-2
 Sequence 2, Application US/08176427B
 General Information:
 Patent No. 5795533
 APPLICANT: Insham, Phillip W.
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.
 TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
 TITLE OF INVENTION: Proteins and Uses Related Thereto
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHTIVE & COCKFIELD
 STREET: 60 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII (text)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/176-427B
 FILING DATE: 30-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: HMI-006
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-5940
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 425 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-176-427B-2

Query Match Score 1807; DB 1; Length 425;
 Best Local Similarity 77.8%; Pred. No. 2.2e-172;
 Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;

Query 1 MILLARCLLIVVSSILVCSLACGPGRGKRRPKKKTPLAYKQIFINVAEKTIGASG 60
 Database 4 MILLTRILLVGFIICALVVSSGLTCGGRGKRRPKKKTPLAYKQIFINVAEKTIGASG 63

Query 61 RYEKGKISRNNSERFKELTPNTPDIIKDENTGADRMLTORKDKLNALAIISVNQWPGV 120
 Database 64 RYEKGKTRNSERFKELTPNTPDIIKDENTGADRMLTORKDKLNALAIISVNQWPGV 123

Query 121 KLRVTEGWDEPHHSSESHESLYEGRADITTSDRSKYMLRQHPKKLTPLAYKQIFINVAEKTIGASG 180
 Database 124 KLRVTEBOWDEPHHSSESHESLYEGRADITTSDRSKYMLRQHPKKLTPLAYKQIFINVAEKTIGASG 183

Query 181 IHCsvkaensvaaksgccfpqsaatvhleogsttklydlspsgdrvlaadogrillysdfit 240
 Database 182 IHCsvkaensvaaksgccfpqsaatvhleogsttklydlspsgdrvlaadogrillysdfit 241

Query 241 FLDRDGAKVYYVITREPRERLLTAHILYVAPHNDSATGEPEASSSGGPPSGGAI 300
 Database 242 FLDRDGAKVYYVITREPRERLLTAHILYVAPHND-----SGPTFG 286

RESULT 43
US-08-356-060A-8

Sequence 8, Application US/08356060A
Patent No. 5844079

GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.

TITLE OF INVENTION: Proteins and Uses Related Thereto

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,060A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993

ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709

REFERENCE DOCKET NUMBER: HNI-006CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-356-060A-8

Query Match 73.2%; Score 1807; DB 2; Length 425;
Best Local Similarity 77.8%; Pred. No. 2.2e-172;
Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;

1 MLLARCLLVLVSSLUVSGIAGPGRGFGRHRPKKLTPAYKPIPNVAEKTIGASG 60
4 MLLTRILVVGFCALLVSSGLTCGPRGIGRBHKKLTPAYKPIPNVAEKTIGASG 63

61 RYEGKISSNSRFSKELTNYNPDIFDEENTGADRMLTQRCXNLALISVNQNQPGV 120

Db 184 IHC SYKAENSAAKSGGCCPGSATVHLIGGTKLVKDLSPGDRVLAADGRLLYSDELT 243
Qy 241 FLDRDDGAKKVVYVETREBRERLLTAAHLLFVAP-HNDS -ATGEPEASSGGPPSGCA 298
Db 244 FLDRDSSRLFLFYVETRQRARLLTAAHLLFVAPQINQSEATG-----STG----- 292
Qy 299 LGPRLPAESVYRGORVTVYTAERODCRRLPAVAVSHTLSEEAGAYAPLTAGTILINR 358
Db 293 --QALFASTVYKPGRVVLLG--GGOOLLPASVSVSREASGAYAPLTAGTILINR 347
Qy 359 VLASCYAVIEBSWAHRAFPFRLLAALAPARTDEGGSDGGDRGGGORVALTAP 418
Db 348 VLASCYAVIEBSWAHRAFPFRLLAALAPARTDEGGSDGGDRGGGORVALTAP 418
Qy 349 VLASCYAVIEBSWAHRAFPFRLLAALAPARTDEGGSDGGDRGGGORVALTAP 418
Db 381 --QALFASTVYKPGRVVYLGE--GGOQLLPASVSVSREASGAYAPLTAGTILINR 347
Qy 419 GAADAPGAGATAGIHWYSQLIQITWLDEAHLPLGMVAKSS 462
Db 382 DGAIAPTAATTGIIHWYSLLYRGSWVLDGDAHLPLGMVAPAS 425

RESULT 44
US-08-460-900C-8

Sequence 8, Application US/08460900C
Patent No. 6165747

GENERAL INFORMATION:
APPLICANT: Ingman, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
APPLICANT: Bumrot, David A.
APPLICANT: Marti-Gorostiza, Elisa

TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patents and Uses Related Thereto

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,900C
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,093
FILING DATE: 4-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709

REFERENCE DOCKET NUMBER: HNI-006CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-356-060A-8

Query Match 73.2%; Score 1807; DB 2; Length 425;
Best Local Similarity 77.8%; Pred. No. 2.2e-172;
Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;

Qy 1 MLLARCLLVLVSSLUVSGIAGPGRGFGRHRPKKLTPAYKPIPNVAEKTIGASG 60
Db 4 MLLTRILVVGFCALLVSSGLTCGPRGIGRBHKKLTPAYKPIPNVAEKTIGASG 63

Qy 61 RYEGKISSNSRFSKELTNYNPDIFDEENTGADRMLTQRCXNLALISVNQNQPGV 120

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
 LENGTH: 425 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-460-300C-8

Query Match Score 1807; DB 3; Length 425;
 Best Local Similarity 77.8%; Pred. No. 2.2e-172; Indels 44; Gaps 6;
 Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;

1 MLLARCLLVSSLYVCSGLACGPGRGFGKRRPKKLTPLAYKOFIPNVAEKTILGASG 60
 1 RYEGKISRSNSERSEKELTPNYYNDIIFDEENGADRLMTQCKDKNALAI SVWNQPGV 120
 1 KLRVTEGMDEDGHSEESLHYGRAVDTTSRDRSKYGMHLARLAVEAGFDWVYTESKAH 180
 1 KLRVTEGMDEDGHSEESLHYGRAVDTTSRDRSKYGMHLARLAVEAGFDWVYTESKAH 183
 1 IHCsvkaensvanksgggpsatvhleggtklvrdlspdrvliaadqcrlysdelt 240
 1 IHCsvkaensvanksgggpsatvhleggtklvrdlspdrvliaadqcrlysdelt 243
 1 FLDRDDGAKVFKVYETREPRLITTAHLIFVAP-HNDS-ATGEPEASSGGPSSGA 298
 1 QY 241 LGPRALFASRVPGQRVTVVAERDGDRLLPAAVSYTSEEAGAYAATPLAQGTILINR 358
 1 Db 244 FLRMDSSERKLKVYETRQPRAVLTTAAHILFVAPQHNOSEATG-----STSG---- 292
 1 QY 299 VLASCYAVIEEWSWAHRAFAPPRLAHALLAALAPARTDRGGSDGGDRGGGRVALTAP 418
 1 Db 348 VLASCYAVIEEWSWAHRAFAPPRLAHALLAALAPARTDRGGSDGGDRGGGRVALTAP 418
 1 QY 359 VLASCYAVIEEWSWAHRAFAPPRLAHALLAALAPARTDRGGSDGGDRGGGRVALTAP 418
 1 Db 348 VLASCYAVIEEWSWAHRAFAPPRLAHALLAALAPARTDRGGSDGGDRGGGRVALTAP 418
 1 QY 382 DGA IPTAATTGITHWYSRSLLYRIGSWLTDGDAHLHPLGMVADAS 425
 1 Db 348 VLASCYAVIEEWSWAHRAFAPPRLAHALLAALAPARTDRGGSDGGDRGGGRVALTAP 418

RESULT 45
 US-08-674-509B-8
 Sequence 8, Application US/08674509B
 Patent No. 6261786

GENERAL INFORMATION:
 APPLICANT: Ingham, Phillip W.
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.

APPLICANT: Marigo, Valeria
 TITLE OF INVENTION: SCREENING ASSAYS FOR HEDGEHOG AGONISTS AND ANTAGONISTS
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 STREET: One Post Office Square
 STATE: MA
 CITY: Boston
 ZIP: 02109-2170

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/674,509B
 FILING DATE: 02-JUL-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/460,900
 FILING DATE: 05-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE DOCKET NUMBER: HNV-006.06
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-832-1100
 TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 425 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-674-509B-8

Query Match Score 1807; DB 3; Length 425;
 Best Local Similarity 77.8%; Pred. No. 2.2e-172; Indels 37; Mismatches 37; Gaps 6;

1 MILLARCLLVSSLYVCSGLACGPGRGFGKRRPKKLTPLAYKOFIPNVAEKTILGASG 60
 1 MLLARCLLVSSLYVCSGLACGPGRGFGKRRPKKLTPLAYKOFIPNVAEKTILGASG 63
 1 RYEGKISRSNSERSEKELTPNYYNDIIFDEENGADRLMTQCKDKNALAI SVWNQPGV 120
 1 RYEGKISRSNSERSEKELTPNYYNDIIFDEENGADRLMTQCKDKNALAI SVWNQPGV 123
 1 RYEGKISRSNSERSEKELTPNYYNDIIFDEENGADRLMTQCKDKNALAI SVWNQPGV 124
 1 KLRVTEGMDEDGHSEESLHYGRAVDTTSRDRSKYGMHLARLAVEAGFDWVYTESKAH 180
 1 KLRVTEGMDEDGHSEESLHYGRAVDTTSRDRSKYGMHLARLAVEAGFDWVYTESKAH 183
 1 IHCsvkaensvanksgggpsatvhleggtklvrdlspdrvliaadqcrlysdelt 240
 1 IHCsvkaensvanksgggpsatvhleggtklvrdlspdrvliaadqcrlysdelt 243
 1 FLDRDDGAKVFKVYETREPRLITTAHLIFVAP-HNDS-ATGEPEASSGGPSSGA 298
 1 QY 241 LGPRALFASRVPGQRVTVVAERDGDRLLPAAVSYTSEEAGAYAATPLAQGTILINR 358
 1 Db 244 FLRMDSSERKLKVYETRQPRAVLTTAAHILFVAPQHNOSEATG-----STSG---- 292
 1 QY 299 VLASCYAVIEEWSWAHRAFAPPRLAHALLAALAPARTDRGGSDGGDRGGGRVALTAP 418
 1 Db 348 VLASCYAVIEEWSWAHRAFAPPRLAHALLAALAPARTDRGGSDGGDRGGGRVALTAP 418
 1 QY 359 VLASCYAVIEEWSWAHRAFAPPRLAHALLAALAPARTDRGGSDGGDRGGGRVALTAP 418
 1 Db 348 VLASCYAVIEEWSWAHRAFAPPRLAHALLAALAPARTDRGGSDGGDRGGGRVALTAP 418
 1 QY 382 DGA IPTAATTGITHWYSRSLLYRIGSWLTDGDAHLHPLGMVADAS 425
 1 Db 348 VLASCYAVIEEWSWAHRAFAPPRLAHALLAALAPARTDRGGSDGGDRGGGRVALTAP 418

RESULT 46
 US-08-954-698-8
 Sequence 8, Application US/08954698
 Patent No. 6271363

GENERAL INFORMATION:
 APPLICANT: Inham, Phillip W.
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.

TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
 NUMBER OF SEQUENCES: 48
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-2170

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/674,509B
 FILING DATE: 02-JUL-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 425 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-674-509B-8

Query Match Score 1807; DB 3; Length 425;
 Best Local Similarity 77.8%; Pred. No. 2.2e-172; Indels 37; Mismatches 37; Gaps 6;

1 MILLARCLLVSSLYVCSGLACGPGRGFGKRRPKKLTPLAYKOFIPNVAEKTILGASG 60
 1 MLLARCLLVSSLYVCSGLACGPGRGFGKRRPKKLTPLAYKOFIPNVAEKTILGASG 63
 1 RYEGKISRSNSERSEKELTPNYYNDIIFDEENGADRLMTQCKDKNALAI SVWNQPGV 120
 1 RYEGKISRSNSERSEKELTPNYYNDIIFDEENGADRLMTQCKDKNALAI SVWNQPGV 123
 1 RYEGKISRSNSERSEKELTPNYYNDIIFDEENGADRLMTQCKDKNALAI SVWNQPGV 124
 1 KLRVTEGMDEDGHSEESLHYGRAVDTTSRDRSKYGMHLARLAVEAGFDWVYTESKAH 180
 1 KLRVTEGMDEDGHSEESLHYGRAVDTTSRDRSKYGMHLARLAVEAGFDWVYTESKAH 183
 1 IHCsvkaensvanksgggpsatvhleggtklvrdlspdrvliaadqcrlysdelt 240
 1 IHCsvkaensvanksgggpsatvhleggtklvrdlspdrvliaadqcrlysdelt 243
 1 FLDRDDGAKVFKVYETREPRLITTAHLIFVAP-HNDS-ATGEPEASSGGPSSGA 298
 1 QY 241 LGPRALFASRVPGQRVTVVAERDGDRLLPAAVSYTSEEAGAYAATPLAQGTILINR 358
 1 Db 244 FLRMDSSERKLKVYETRQPRAVLTTAAHILFVAPQHNOSEATG-----STSG---- 292
 1 QY 299 VLASCYAVIEEWSWAHRAFAPPRLAHALLAALAPARTDRGGSDGGDRGGGRVALTAP 418
 1 Db 348 VLASCYAVIEEWSWAHRAFAPPRLAHALLAALAPARTDRGGSDGGDRGGGRVALTAP 418
 1 QY 359 VLASCYAVIEEWSWAHRAFAPPRLAHALLAALAPARTDRGGSDGGDRGGGRVALTAP 418
 1 Db 348 VLASCYAVIEEWSWAHRAFAPPRLAHALLAALAPARTDRGGSDGGDRGGGRVALTAP 418
 1 QY 382 DGA IPTAATTGITHWYSRSLLYRIGSWLTDGDAHLHPLGMVADAS 425
 1 Db 348 VLASCYAVIEEWSWAHRAFAPPRLAHALLAALAPARTDRGGSDGGDRGGGRVALTAP 418

RESULT 47
 US-08-954-698-8
 Sequence 8, Application US/08954698
 Patent No. 6271363

GENERAL INFORMATION:
 APPLICANT: Inham, Phillip W.
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.

TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
 NUMBER OF SEQUENCES: 48
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-2170

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/674,509B
 FILING DATE: 02-JUL-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/954,698
 FILING DATE: 20-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/462,386
 FILING DATE: 05-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/435,093
 FILING DATE: 04-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/356,060
 FILING DATE: 14-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/176,427
 FILING DATE: 30-DEC-1993
 ATTORNEY / AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,703
 REFERENCE/DOCKET NUMBER: HMV-006.10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-832-1000
 TELEFAX: 617-832-7000
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 425 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-954-698-8

Query Match 73.2%; Score 1807; DB 3; Length 425;
 Best Local Similarity 77.8%; Pred. No. 2.2e-172;
 Matches 361; Conservative 37; Indels 44; Gaps 6;

Qy 1	MILLARCLLIVYSSSLVCSGLACGFGRGFGKRRHPPKKLTPLAYQFIPNVAEKTGASG 60	Db 4	MILLTRLLVLVFGFICLIVSSSLTGGRGIGRRAFKPLTPLAYQFIPNVAEKTGASG 63
Qy 61	RYEGKISRSNSRERPKELTPNPDIFKDEENTGADRMTQRCKDKNALAIISVNQWPGV 120	Db 64	RYEGKTRNSRERPKELTPNPDIFKDEENTGADRMTQRCKDKNALAIISVNQWPGV 123
Qy 121	KLRVTESWDEDGHSEESLHVEGRADITTSDRSKYGMARLAVEAGDWWYESKSH 180	Db 124	KLRVTESWDEDGHSEESLHVEGRADITTSDRSKYGMARLAVEAGDWWYESKSH 183
Qy 181	IHCsvRAENSAAKSGCCFPGSATVLEQGTTKLVKDLSQDRVLAADDGRLLYSDFLT 240	Db 184	IHCsvRAENSAAKSGCCFPGSATVLEQGTTKLVKDLSQDRVLAADDGRLLYSDFLT 243
Qy 241	FIDRDDGAKKVYVIETPRERLILTAHLILFVAP-HNDS-ATGEPEASSGSPGGSA 298	Db 244	FIDRMDSRKLFVVIETQPARILLTAHLILFVAPQHNQSEATG---STSG---- 292
Qy 299	LGPRALFASRVPGQRTVVAARGDGRLLPAVHSVTLSEBAAGAYAATQGTILINR 358	Db 293	--QALPASIVNPQRTVVLGE--GGQQLLPASVHSVSLREASGAYAATQGTILINR 347
Qy 359	VLASCYAVIEEWSWAHRAFAFPRLAHALLAATAPARTDRGGDSGGDRGGGRVALTAP 418	Db 348	VLASCYAVIEEWSWAHRAFAFPRLAHALLAATAPARTDRGGDSGGDRGGGRVALTAP 381
Qy 419	GAADAPGAGTAGIHWYMSOLIYQIGTMILDSFALHPIGLGMATSS 462	Db 382	DGAIPTRATTGHWYSLRLLYRGSWLDGALPHGMVAPAS 425

Query Match 73.2%; Score 1807; DB 4; Length 425;
 Best Local Similarity 77.8%; Pred. No. 2.2e-172;
 Matches 361; Conservative 37; Indels 44; Gaps 6;

Qy 1 MILLARCLLIVYSSSLVCSGLACGFGRGFGKRRHPPKKLTPLAYQFIPNVAEKTGASG 60
 Db 4 MILLTRLLVLVFGFICLIVSSSLTGGRGIGRRAFKPLTPLAYQFIPNVAEKTGASG 63

Qy 121 KLRVTESWDEDGHSEESLHVEGRADITTSDRSKYGMARLAVEAGDWWYESKSH 180
 Db 124 KLRVTESWDEDGHSEESLHVEGRADITTSDRSKYGMARLAVEAGDWWYESKSH 183

Qy 181 IHCsvRAENSAAKSGCCFPGSATVLEQGTTKLVKDLSQDRVLAADDGRLLYSDFLT 240
 Db 184 IHCsvRAENSAAKSGCCFPGSATVLEQGTTKLVKDLSQDRVLAADDGRLLYSDFLT 243

Qy 241 FIDRDDGAKKVYVIETPRERLILTAHLILFVAP-HNDS-ATGEPEASSGSPGGSA 298
 Db 244 FIDRMDSRKLFVVIETQPARILLTAHLILFVAPQHNQSEATG---STSG---- 292

Qy 299 LGPRALFASRVPGQRTVVAARGDGRLLPAVHSVTLSEBAAGAYAATQGTILINR 358
 Db 293 --QALPASIVNPQRTVVLGE--GGQQLLPASVHSVSLREASGAYAATQGTILINR 347

Qy 359 VLASCYAVIEEWSWAHRAFAFPRLAHALLAATAPARTDRGGDSGGDRGGGRVALTAP 418
 Db 348 VLASCYAVIEEWSWAHRAFAFPRLAHALLAATAPARTDRGGDSGGDRGGGRVALTAP 381

Qy 419 GAADAPGAGTAGIHWYMSOLIYQIGTMILDSFALHPIGLGMATSS 462
 Db 382 DGAIPTRATTGHWYSLRLLYRGSWLDGALPHGMVAPAS 425

Qy 241 FIDRDDGAKKVYVIETPRERLILTAHLILFVAP-HNDS-ATGEPEASSGSPGGSA 298
 US-08-257-874-8

RESULT 48
US-09-325-256-17
; Sequence 17, Application US/09325256
; Patent No. 6444793
; GENERAL INFORMATION:
; APPLICANT: PEPINSKY, R. BLAKE
; APPLICANT: BAKER, DARREN P.
; APPLICANT: WEN, DINGYI
; APPLICANT: WILLIAMS, KEVIN P.
; APPLICANT: GANGER, ELLEN A.
; APPLICANT: TAYLOR, FREDRICK R.
; APPLICANT: CALDES, ALPHONSE
; APPLICANT: JEFFREY PORTER,
; TITLE OF INVENTION: HYDROPHOBICALLY-MODIFIED PROTEIN COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; CURRENT APPLICATION NUMBER: US/09/325,256
; FILE REFERENCE: PIY-067.01
; CURRENT FILING DATE: 1995-06-03
; PRIOR APPLICATION NUMBER: 60/099,800
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/078,935
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/089,685
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/067,423
; PRIOR FILING DATE: 1997-12-03
; PRIOR APPLICATION NUMBER: PCT/US98/25676
; PRIOR FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 17
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Gallus sp.
; US-09-325-256-17

Query Match 73.2%; Score 1807; DB 4; Length 425;
Best Local Similarity 77.8%; Pred. No. 2.2e-172;
Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;
Qy 1 MILLARCLILLYVSSLLVCSGLACCPGRGKRPKKTPLAYQFIPNVAEKTIGASG 60
Db 4 MILLARCLILLYVSSLLVCSGLACCPGRGKRPKKTPLAYQFIPNVAEKTIGASG 63
Qy 61 RYEKGKRSRERKELTPTYNPDIIFKDEBENTGADRIMTORCKDKNLAISYMNOFGV 120
Db 64 RYEKGKTRANSFRKELTPTYNPDIIFKDEBENTGADRIMTORCKDKNLAISYMNOFGV 123
Qy 121 KLRVTEGWDEGGHHSBESLYEGRADITTSDRSKYCMRLAVERAGFDWYYYESKAH 180
Db 124 KLRVTEGWDEGGHHSBESLYEGRADITTSDRSKYCMRLAVERAGFDWYYYESKAH 183
Qy 181 IHCsvkaenSYAAKSGGCFFGSATVHLEQGSTKLVDLSFGDRYIAADDGGRLLSDFT 240
Db 184 IHCsvkaenSYAAKSGCFFGSATVHLEGCTKLVDLSFGDRYIAADDGGRLLSDFT 243
Qy 241 FLDRDGCKKVYVIITREPERLLITAHHFLVAP-HNDS-ATCEPEASSGSPPSGGA 298
Db 242 MLLTRILLVFGICALLVSSLLTGCGRGIGKRRHKPLPLAYQFIPNVAEKTIGASG 60
Qy 243 4 MLLTRILLVFGICALLVSSLLTGCGRGIGKRRHKPLPLAYQFIPNVAEKTIGASG 63

RESULT 49
US-09-639-695-8
; Sequence 8, Application US/09639695
; Patent No. 6576237
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; APPLICANT: McMahon, Andrew P.
; APPLICANT: Tabin, Clifford J.
; Bumrot, David A.
; Marti-Grosziza, Elisa
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; Proteins and Uses Related Thereto
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOUDY, HOAG & ELLIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/639,695
; FILING DATE: 16-AUG-2000
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,093
; FILING DATE: 4-MAY-1995
; APPLICATION NUMBER: US 08/356,060
; FILING DATE: 14-DEC-1994
; APPLICATION NUMBER: US 08/176,427
; FILING DATE: 30-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 26,709
; REGISTRATION NUMBER: HMV-006.05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 425 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
; US-09-639-695-8

Query Match 73.2%; Score 1807; DB 4; Length 425;
Best Local Similarity 77.8%; Pred. No. 2.2e-172;
Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;

61 RYEGKISRNNSEREFKELTNPNNPDLIFKDEENTGADRINTQCKDKLNALATSYMNQPGV 120
 64 RYEGKTRSERFELTPYNPDIFKDEENTGADRINTQCKDKLNALATSYMNQPGV 123

121 KLRVTEGWDGDGHSEESIHYGRAVIDITSDRSKYGMMLARLAVAGFDVYYESKAH 180
 124 KLRVTEGWDGDGHSEESIHYGRAVIDITSDRSKYGMMLARLAVAGFDVYYESKAH 183

Qy 181 IHCSYKAENSAAKSGCPGSATVHLEGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 240
 Db 184 IHCSYKAENSAAKSGCPGSATVHLEGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT 243

Qy 241 FLDRDGAKRKYFYETRSPRERLLTAHHLVLAP-INDS ATGEPBASSSSGPPSGA 298
 Db 244 FLDRMDSRLFYETRSPRERLLTAHHLVLAP-QHNQSATG---STSG----- 292

Qy 299 LGPRPALFASRVPGQRVYVAERDGDRLLPAAVSHVTLSSEAAAGAYAPLTAQGTILINR 358
 Db 293 ---QALFASNVKPGQRVYVGE- GGQQLPASVHSVSLREAGAYAPLTAQGTILINR 347

Qy 359 VLASCYAVBEHSHWAHRAFPFLAHALLAALAPARTDRGGDRGGGRVALTAP 418
 Db 348 VLASCYAVBEHSHWAHWAAPFLAQLAAL-----C 381

Qy 419 GAADAPGAGATAAGIHWYSQLYQIGTWILDSEALHPLGMVAKSS 462
 Db 382 DGAIPPAATTGTHWYSRLLYRIGSWLUDGDAHLHPGNVAPAS 425

RESULT 50
 US-09-448-188-8
 Sequence 8, Application US/09448188
 Patent No. 667913

GENERAL INFORMATION:
 APPLICANT: Ingham, Phillip W.
 Mc Mahon, Andrew P.
 Tabin, Clifford J.

TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 STREET: One Post Office Square
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109-2170

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/448,188
 FILING DATE: 23-Nov- 6607913-1939

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/462,386
 FILING DATE: 05-JUN-1995
 APPLICATION NUMBER: US 08/435,093
 FILING DATE: 04-MAY-1995
 APPLICATION NUMBER: US 08/356,060
 FILING DATE: 14-DEC-1994
 APPLICATION NUMBER: US 08/176,427
 FILING DATE: 30-DEC-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-832-1000
 TELEX: 617-832-7000

INFORMATION FOR SEQ ID NO: 8:

Result No.	Score	Query Match	Length	DB ID	Description
1	2467	99.9	475	8	US-09-021-660A-37 Sequence 1, App1
2	2467	99.9	475	8	US-09-021-660A-37 Sequence 1, App1
3	2467	99.9	475	8	US-09-021-660A-37 Sequence 1, App1
4	2467	99.9	475	8	US-09-021-660A-37 Sequence 1, App1
5	2467	99.9	475	9	US-09-021-660A-37 Sequence 1, App1
6	2467	99.9	475	10	US-09-021-660A-37 Sequence 1, App1
7	2467	99.9	475	10	US-09-021-660A-37 Sequence 1, App1
8	2467	99.9	475	10	US-09-021-660A-37 Sequence 1, App1
9	2467	99.9	475	10	US-09-021-660A-37 Sequence 1, App1
10	2467	99.9	475	10	US-09-021-660A-37 Sequence 1, App1
11	2467	99.9	475	10	US-09-021-660A-37 Sequence 1, App1
12	2467	99.9	475	10	US-09-021-660A-37 Sequence 1, App1
13	2467	99.9	475	10	US-09-021-660A-37 Sequence 1, App1
14	2467	97.5	462	10	US-09-021-660A-37 Sequence 1, App1
15	2407	97.5	462	15	US-09-021-660A-37 Sequence 1, App1

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	%
1	2467	99.9	475	8	US-09-021-660A-37 Sequence 1, App1
2	2467	99.9	475	8	US-09-021-660A-37 Sequence 1, App1
3	2467	99.9	475	8	US-09-021-660A-37 Sequence 1, App1
4	2467	99.9	475	9	US-09-021-660A-37 Sequence 1, App1
5	2467	99.9	475	9	US-09-021-660A-37 Sequence 1, App1
6	2467	99.9	475	10	US-09-021-660A-37 Sequence 1, App1
7	2467	99.9	475	10	US-09-021-660A-37 Sequence 1, App1
8	2467	99.9	475	10	US-09-021-660A-37 Sequence 1, App1
9	2467	99.9	475	10	US-09-021-660A-37 Sequence 1, App1
10	2467	99.9	475	10	US-09-021-660A-37 Sequence 1, App1
11	2467	99.9	475	10	US-09-021-660A-37 Sequence 1, App1
12	2467	99.9	475	10	US-09-021-660A-37 Sequence 1, App1
13	2467	99.9	475	10	US-09-021-660A-37 Sequence 1, App1
14	2467	97.5	462	10	US-09-021-660A-37 Sequence 1, App1
15	2407	97.5	462	15	US-09-021-660A-37 Sequence 1, App1

89	10	US-09-883-848A-16	Sequence 16, App1
90	411	10 US-09-187-387-16	Sequence 16, App1
91	51.5	10 US-09-827-110-16	Sequence 16, App1
92	411	10 US-09-845-05C-16	Sequence 16, App1
93	411	10 US-09-451-939-16	Sequence 16, App1
94	411	10 US-09-238-243-16	Sequence 16, App1
95	411	12 US-10-244-095A-16	Sequence 16, App1
96	411	10 US-09-733-634-28	Sequence 28, App1
97	411	15 US-10-294-036-16	Sequence 16, App1
98	449	9 US-09-990-046-29	Sequence 29, App1
99	449	10 US-09-733-634-10	Sequence 30, App1
100	449	15 US-10-294-036-10	Sequence 12, App1
101	411	10 US-09-733-634-12	Sequence 12, App1
102	411	8 US-08-954-771-10	Sequence 10, App1
103	411	8 US-08-462-386D-10	Sequence 10, App1
104	411	9 US-09-151-999-12	Sequence 12, App1
105	411	10 US-09-883-848A-12	Sequence 12, App1
106	411	10 US-09-187-387-12	Sequence 12, App1
107	411	10 US-09-827-110-12	Sequence 12, App1
108	411	10 US-09-845-025C-12	Sequence 12, App1
109	411	10 US-09-451-939-12	Sequence 12, App1
110	411	10 US-09-238-243-12	Sequence 12, App1
111	411	10 US-09-733-634-10	Sequence 10, App1
112	411	12 US-10-244-095A-12	Sequence 12, App1
113	396	8 US-08-950-220C-11	Sequence 11, App1
114	396	8 US-08-354-771-9	Sequence 9, App1
115	396	8 US-08-662-386D-9	Sequence 9, App1
116	396	9 US-09-021-660A-35	Sequence 35, App1
117	396	9 US-09-151-999-11	Sequence 11, App1
118	396	9 US-09-990-046-13	Sequence 13, App1
119	396	10 US-09-733-634-22	Sequence 22, App1
120	396	10 US-09-883-848A-11	Sequence 11, App1
121	396	10 US-09-827-110-11	Sequence 11, App1
122	396	10 US-09-294-016-11	Sequence 11, App1
123	396	10 US-09-845-025C-11	Sequence 11, App1
124	396	10 US-09-151-939-11	Sequence 11, App1
125	396	10 US-09-238-243-11	Sequence 11, App1
126	396	10 US-09-336-476-9	Sequence 9, App1
127	396	12 US-10-244-095A-11	Sequence 11, App1
128	396	15 US-08-900-220C-17	Sequence 17, App1
129	396	8 US-09-151-999-17	Sequence 17, App1
130	396	9 US-09-151-939-17	Sequence 17, App1
131	396	10 US-09-883-848A-17	Sequence 17, App1
132	396	10 US-09-187-387-17	Sequence 17, App1
133	396	10 US-09-827-110-17	Sequence 17, App1
134	396	10 US-09-294-016-11	Sequence 17, App1
135	396	10 US-09-845-05C-17	Sequence 17, App1
136	336	9 US-09-151-939-17	Sequence 17, App1
137	396	10 US-09-338-243-17	Sequence 17, App1
138	396	12 US-10-244-095A-17	Sequence 17, App1
139	47.5	396	15 US-10-394-06-17
140	47.4	396	14 US-10-147-43-3
141	47.1	396	9 US-09-244-466-2
142	42.8	336	9 US-09-021-660A-36
143	42.8	221	8 US-08-900-220C-21
144	41.8	221	8 US-08-954-771-40
145	41.8	221	8 US-08-462-386D-40
146	41.8	221	9 US-09-151-999-21
147	41.8	221	10 US-09-187-387-21
148	41.8	221	10 US-08-827-110-21
149	41.8	221	10 US-09-451-939-21
150	41.8	221	10 US-09-187-387-21

RESULT 1
S-08-90-220C-15
Sequence 15 , Application US/08900220C
Publication No. US20020045206A1
GENERAL INFORMATION:

DD	301	EPALIFASKVKEPQRVVAEFLGQKLLFVAVLWV
QY	361	ASCYAVIEEHSAHRAFAPPRLAHALLAALAPARTDRGGDGGDRGGGGRVALTAPGA 4
Db	361	ASCYAVIEEHSAHRAFAPPRLAHALLAALAPARTDRGGDGGDRGGGGRVALTAPGA 4
QY	421	ADPGAGATAGIHWYBOLLYQGTWILDSEAHPLMNAVSSXSAGGAAEGA 475

Db 421 ADAPGAGATAGTHWSQLYQIGTWWLDEALHPLGNMAVKSSXSRGAGGGAREGA 475

RESULT 2
US-08-954-771-13
Sequence 13, Application US/08954771
GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
ZIP: 02109-2170
COUNTRY: USA

Computer readable form:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent-In Release #1.0, Version #1.3.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,771
FILING DATE: 20-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,386
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,093
FILING DATE: 04-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMV-006-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
NAME FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 475 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-954-771-13

Query Match 99.9%; Score 2467; DB 8; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-207; Mismatches 0; Gaps 0;

Matches 475; Conservative 0; Indels 0;

Db 181 IHCSVKAENSAAKSGCGFPGSATVHLEQGTTKLVDRSKYGMRLAVAEQFDGRLLYSDELT 240

Qy 241 FLDRDGAKKVYVIEPREPRLATAAHLLFVAPHNSDTSATEPEAASSGSPGSGALG 300
Db 241 FLDRDGAKKVYVIEPREPRLATAAHLLFVAPHNSDTSATEPEAASSGSPGSGALG 300

Qy 301 PRALFASTRPQGVVTAERGDRRLPAAVHSVTSEEAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASTRPQGVVTAERGDRRLPAAVHSVTSEEAGAYAPLTAQGTILINRVL 360

Qy 361 ASCYAVIEEHSAWRAFAFRHLAHLALAPARTDGDGGCDRGGGGRVALTAGCA 420
Db 361 ASCYAVIEEHSAWRAFAFRHLAHLALAPARTDGDGGCDRGGGGRVALTAGCA 420

Qy 421 ADAPGAGATAGTHWSQLYQIGTWWLDEALHPLGNMAVKSSXSRGAGGGAREGA 475
Db 421 ADAPGAGATAGTHWSQLYQIGTWWLDEALHPLGNMAVKSSXSRGAGGGAREGA 475

RESULT 3
US-08-462-386D-13
Sequence 13, Application US/08462386D
Publication No. US2003018657A1
GENERAL INFORMATION:
APPLICANT: Ingham, Phillip W.
APPLICANT: McMahon, Andrew P.
APPLICANT: Tabin, Clifford J.
TITLE OF INVENTION: Vertebrate Tissue Pattern-Inducing
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & CCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,386D
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,093
FILING DATE: 4-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,060
FILING DATE: 14-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/176,427
FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMV-006-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7000
TELEFAX: (617) 227-5941
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: HMV-006-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7000
TELEFAX: (617) 227-5941
SEQUENCE CHARACTERISTICS:
LENGTH: 475 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-462-386D-13

Query Match 99.9%; Score 2467; DB 8; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-207; Mismatches 0; Gaps 0;

Matches 475; Conservative 0; Indels 0;

Db 181 IHCSVKAENSAAKSGCGFPGSATVHLEQGTTKLVDRSKYGMRLAVAEQFDGRLLYSDELT 240

Qy 1 MILLARCLLVLVSSLIVSGIACGGRGFGRIPKKPLAKOFIPVAEKTGAGS 60
Db 1 MILLARCLLVLVSSLIVSGIACGGRGFGRIPKKPLAKOFIPVAEKTGAGS 60

Qy 61 RYEKGKTSRNSNRFKELTPNYNPDIIIFDENTGADLMTCQCKDKLNALAIISVNQWPGV 120
Db 61 RYEKGKTSRNSNRFKELTPNYNPDIIIFDENTGADLMTCQCKDKLNALAIISVNQWPGV 120

Qy 121 KLRVTEGNDDEGHSEBELLHYGRAVDITTSRDRSKYGMRLAVAEQFDGRLLYSDELT 240
Db 121 KLRVTEGNDDEGHSEBELLHYGRAVDITTSRDRSKYGMRLAVAEQFDGRLLYSDELT 240

Qy 181 IHCSVKAENSAAKSGCGFPGSATVHLEQGTTKLVDRSKYGMRLAVAEQFDGRLLYSDELT 240

Qy 1 MILLARCLLIVVSSILVCSGLACPGRGFRHKRHPKCLTPLAYKQFIPNVAEKTIGASG 60
 Db 1 MILLARCLLIVVSSILVCSGLACPGRGFRHKRHPKCLTPLAYKQFIPNVEKTIAGS 60

Qy 61 RYECKISNSERFKELTPNYPDIIIFKDENTGADRMTQRCKDKLNALAISVMNQPGV 120
 Db 61 RYECKISNSERFKELTPNYPDIIIFKDENTGADRMTQRCKDKLNALAISVMNQPGV 120

Qy 121 KLRVTEGDEGHSESLHYEGPAUDITTSRDSKYGMRLAVEAGEDWVYYESKAH 180
 Db 121 KLRVTEGDEGHSESLHYEGPAUDITTSRDSKYGMRLAVEAGEDWVYYESKAH 180

Qy 181 IHCSVKAENSAAKSGCOPGSATVHLEQSTKLVDLSPODRVLAAADDGRLLYSDFLT 240
 Db 181 IHCSVKAENSAAKSGCOPGSATVHLEQSTKLVDLSPODRVLAAADDGRLLYSDFLT 240

Qy 241 FLDRDDGAKKVVFVIEPREPRLITTAHILFVAPHNDSATGEPEASSSGPPSGALG 300
 Db 241 FLDRDDGAKKVVFVIEPREPRLITTAHILFVAPHNDSATGEPEASSSGPPSGALG 300

Qy 301 PRALFASSVRPGORVTVAAERGDGRLLPAVHSVTLSSEBAAVAYAPLTQGTILNRYL 360
 Db 301 PRALFASSVRPGORVTVAAERGDGRLLPAVHSVTLSSEBAAVAYAPLTQGTILNRYL 360

Db 181 IHCSVRAENSAAKSGCOPGSATVHLEQSTKLVDLSPODRVLAAADDGRLLYSDFLT 240
 Qy 241 FLDRDDGAKKVVFVIEPREPRLITTAHILFVAPHNDSATGEPEASSSGPPSGALG 300
 Db 241 FLDRDDGAKKVVFVIEPREPRLITTAHILFVAPHNDSATGEPEASSSGPPSGALG 300

Qy 301 PRALFASSVRPGORVTVAAERGDGRLLPAVHSVTLSSEBAAVAYAPLTQGTILNRYL 360
 Db 301 PRALFASSVRPGORVTVAAERGDGRLLPAVHSVTLSSEBAAVAYAPLTQGTILNRYL 360

Qy 421 ADAPGAGATAGIHWYSSLQYQITGWLDSLEAHLPLGMAVKSXSEGAGGAREGA 475
 Db 421 ADAPGAGATAGIHWYSSLQYQITGWLDSLEAHLPLGMAVKSXSEGAGGAREGA 475

Qy 421 ADAPGAGATAGIHWYSSLQYQITGWLDSLEAHLPLGMAVKSXSEGAGGAREGA 475
 Db 421 ADAPGAGATAGIHWYSSLQYQITGWLDSLEAHLPLGMAVKSXSEGAGGAREGA 475

Db 361 ASCYAVIEHSAWAHRAAPPRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420
 Db 361 ASCYAVIEHSAWAHRAAPPRLAHALLAALAPARTDRGDSGGDRGGGRVALTAPGA 420

Db 421 ADAPGAGATAGIHWYSSLQYQITGWLDSLEAHLPLGMAVKSXSEGAGGAREGA 475
 Db 421 ADAPGAGATAGIHWYSSLQYQITGWLDSLEAHLPLGMAVKSXSEGAGGAREGA 475

RESULT 5

US-09-151-999-15

Qy ; Sequence 15; Application US/09151-999
 Db ; Patent No. US2002011460A1
 Db ; GENERAL INFORMATION:
 Db ; APPLICANT: Wang, Elizabeth
 Db ; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE
 Db ; FILE REFERENCE: NY-031-02
 Db ; CURRENT APPLICATION NUMBER: US/09/151,999
 Db ; EARLIER APPLICATION NUMBER: 08-1998-0-11
 Db ; NUMBER OF SEQ ID NOS: 28
 Db ; SEQ ID NO 15
 Db ; SOFTWARE: Patentin Ver. 2.0
 Db ; LENGTH: 475
 Db ; TYPE: PRT
 Db ; ORGANISM: Homo sapien Shh
 Db ; FEATURE:
 Db ; OTHER INFORMATION: Xaa at position 463 is any or unknown amino acid
 US-09-151-999-15

Query Match 99.9%; Score 2467; DB 9; Length 475;

Qy ; Sequence 39; Application US/09021660A
 Db ; Patent No. US20010041668A1
 Db ; GENERAL INFORMATION:
 Db ; APPLICANT: Baron, M.
 Db ; APPLICANT: Parrott, S.
 Db ; APPLICANT: Belaustegui, M.
 Db ; TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR
 Db ; FILE REFERENCE: HUP-P-01-060
 Db ; CURRENT FILING DATE: 2001-08-27
 Db ; PRIOR APPLICATION NUMBER: US/09/021,650A
 Db ; PRIOR FILING DATE: 1997-02-10
 Db ; PRIOR APPLICATION NUMBER: 60/049,763
 Db ; PRIOR FILING DATE: 1997-06-16
 Db ; NUMBER OF SEQ ID NOS: 4
 Db ; SOFTWARE: Patentin Ver. 2.1
 Db ; SEQ ID NO 39
 Db ; TYPE: PRT
 Db ; ORGANISM: Homo sapiens
 Db ; FEATURE:
 Db ; NAME /KEY: SITE
 Db ; LOCATION: (463)
 Db ; OTHER INFORMATION: Xaa=unknown amino acid
 US-09-021-660A-39

Query Match 99.9%; Score 2467; DB 9; Length 475;

Qy ; Best Local Similarity 100.0%; Fred. No. 2.1e-207; Indels 0; Gaps 0;
 Db ; Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
 Db ; Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MILLARCLLIVVSSILVCSGLACPGRGFRHKRHPKCLTPLAYKQFIPNVAEKTIGASG 60
 Db 1 MILLARCLLIVVSSILVCSGLACPGRGFRHKRHPKCLTPLAYKQFIPNVAEKTIGASG 60

Qy 61 RYECKISNSERFKELTPNYPDIIIFKDENTGADRMTQRCKDKLNALAISVMNQPGV 120
 Db 61 RYECKISNSERFKELTPNYPDIIIFKDENTGADRMTQRCKDKLNALAISVMNQPGV 120

Qy 121 KLRVTEGDEGHSESLHYEGPAUDITTSRDSKYGMRLAVEAGEDWVYYESKAH 180
 Db 121 KLRVTEGDEGHSESLHYEGPAUDITTSRDSKYGMRLAVEAGEDWVYYESKAH 180

Qy 181 IHCSVKAENSAAKSGCOPGSATVHLEQSTKLVDLSPODRVLAAADDGRLLYSDFLT 240
 Db 181 IHCSVKAENSAAKSGCOPGSATVHLEQSTKLVDLSPODRVLAAADDGRLLYSDFLT 240

Qy 241 FLDRDDGAKKVVFVIEPREPRLITTAHILFVAPHNDSATGEPEASSSGPPSGALG 300
 Db 241 FLDRDDGAKKVVFVIEPREPRLITTAHILFVAPHNDSATGEPEASSSGPPSGALG 300

QY	301	PRAFLASRVRPGQRVYVVAERDGDRLLPAAVHSTVTLSEAGGAYAPLTAQGTILINRVL	360
Db	301	PRAFLASRVRPGQRVYVVAERDGDRLLPAAVHSTVTLSEAGGAYAPLTAQGTILINRVL	360
Qy	361	ASCYAVIEEWSWAHRAFAFPRLAHALLAALAPARTDRGGTGGGGRRVLTAPGA	420
Db	361	ASCYAVIEEWSWAHRAFAFPRLAHALLAALAPARTDRGGTGGGGRRVLTAPGA	420
Qy	421	ADAPGAGATAGIHWYSQLYQIGTWILDSEALHPGMATKSXSRGAGGAREGA	475
Db	421	ADAPGAGATAGIHWYSQLYQIGTWILDSEALHPGMATKSXSRGAGGAREGA	475
RESULT 6			
	US-09-883-848A-15		
	Sequence 15, Application US/09883848A		
	/ Publication No. US003002281JA1		
	GENERAL INFORMATION:		
	APPLICANT: Ling, L.		
	APPLICANT: Sanicola-Naddei, M.		
	TITLE OF INVENTION: ANGIogenesis-MODULATING COMPOSITIONS AND USES		
	FILE REFERENCE: CIBT-001-119		
	CURRENT APPLICATION NUMBER: US/09-883, 848A		
	CURRENT FILING DATE: 2001-06-18		
	PRIOR APPLICATION NUMBER: 60/211,919		
	PRIOR FILING DATE: 2000-06-16		
	NUMBER OF SEQ ID NOS: 48		
	SOFTWARE: Patentin Ver. 2.1		
	SEQ ID NO 15		
	LENGTH: 475		
	TYPE: PRT		
	ORGANISM: Homo sapiens		
	FEATURE:		
	NAME/KEY: SITE		
	LOCATION: (463)		
	OTHER INFORMATION: Xaa=unknown amino acid residue		
	US -09-883-848A-15		
Query	Query Match	99.9%	Score 2467; DB 10; Length 475;
	Best Local Similarity	100.0%	Pred. No. 2.1e-207;
	Matches	475;	Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1	MILLARCLLIVVSSLVCGSLACGPGRGFGRHRPKLTPLAYKOFIPVNAETKLGASG	60
Db	1	MILLARCLLIVVSSLVCGSLACGPGRGFGRHRPKLTPLAYKOFIPVNAETKLGASG	60
Qy	61	RYGKISRNSENSEKELTPNNDIIIFDEENTGADMINTORKDKLNALAI SVMNQWPGV	124
Db	61	RYGKISRNSENSEKELTPNNDIIIFDEENTGADMINTORKDKLNALAI SVMNQWPGV	124
Qy	121	KLFVTEGDEDGHSEESLHYEGRAVDITTSDRSKYGMALARVEAGEDDWVYYESKAK	184
Db	121	KLFVTEGDEDGHSEESLHYGRRAVDITTSDRSKYGMALARVEAGEDDWVYYESKAK	184
Qy	181	IHSVKAEVSAKSGGGPFGSATVHLEQGGTKLIVKDLSPDRVLADDQRLIISDFLT	244
Db	181	IHSVKAEVSAKSGGGPFGSATVHLEQGGTKLIVKDLSPDRVLADDQRLIISDFLT	244
Qy	241	FLLDDGAKKVVFVTEPRELLIAAHLLFVPHINDSATGEPAASSGGPSSGAGL	300
Db	241	FLLDDGAKKVVFVTEPRELLIAAHLLFVPHINDSATGEPAASSGGPSSGAGL	300
Qy	301	PRAFLASRVRPGQRVYVVAERDGDRLLPAAVHSTVTLSEAGGAYAPLTAQGTILINRVL	360
Db	301	PRAFLASRVRPGQRVYVVAERDGDRLLPAAVHSTVTLSEAGGAYAPLTAQGTILINRVL	360
Qy	361	ASCYAVIEEWSWAHRAFAFPRLAHALLAALAPARTDRGGTGGGGRRVLTAPGA	420
Db	361	ASCYAVIEEWSWAHRAFAFPRLAHALLAALAPARTDRGGTGGGGRRVLTAPGA	420
Qy	421	ADAPGAGATAGIHWYSQLYQIGTWILDSEALHPGMATKSXSRGAGGAREGA	475

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RESULT 7
US-09-187-387-15
Sequence 15, Application US/09187387
; Publication No. US201003008324A1
; GENERAL INFORMATION
; APPLICANT: Galdes, Alphonse
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
; TITLE OF INVENTION: PERIPHERAL NEUROPATHIES
; FILE REFERENCE: ONV-052.01
CURRENT APPLICATION NUMBER: US/09/187,387
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 475
TYPE: PRT
ORGANISM: human Shh
FEATURE:
OTHER INFORMATION: Xaa at position 463 is any or unknown amino acid
US-09-187-387-15

Query Match          99.9%; Score 2467; DB 10; Length 475;
Best Local Similarity 100.0%; Pred. No. 2.1e-207;
Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      1 MLLARCLLIVSSILVCSGLACGPGRGFGCRHPKPLTPLAYKOFIPNVAEKTILGA
Db      1 MLLARCLLIVSSILVCSGLACGPGRGFGCRHPKPLTPLAYKOFIPNVAEKTILGA
Qy      61 RYEGKSRNSRERFKELTPNNPDLIKEENTGADRIMTORCKDKNALAI SVVNQWNP
Db      61 RYEGKSRNSRERFKELTPNNPDLIKEENTGADRIMTORCKDKNALAI SVVNQWNP
Qy      121 KLRVTEGWDDEGHSEESHHYGRAVDITTSDRSKYGMARLAVAGDNVYYSK
Db      121 KLRVTEGWDDEGHSEESHHYGRAVDITTSDRSKYGMARLAVAGDNVYYSK
Qy      181 IHCSTKAENSVAASGGCFFPSATVHLEQGTTKLVKDLSPGIRVLADQGRLLYSDF
Db      181 IHCSTKAENSVAASGGCFFPSATVHLEQGTTKLVKDLSPGIRVLADQGRLLYSDF
Qy      241 FLDRDGAKKVYYTETREPRLLTAAHLFVAPHDNSATGEPEASSGSPPSGCA
Db      241 FLDRDGAKKVYYTETREPRLLTAAHLFVAPHDNSATGEPEASSGSPPSGCA
Qy      301 PRALPASRPQGYIYDPERCDPRLPAATHSVTSEEAGAYAATQTGTILNR
Db      301 PRALPASRPQGYIYDPERCDPRLPAATHSVTSEEAGAYAATQTGTILNR
Qy      361 ASCYAVIEEWSWAIRAFAPRLAHLLALAPARTDGGDSGGDRGGGRVALTAP
Db      361 ASCYAVIEEWSWAIRAFAPRLAHLLALAPARTDGGDSGGDRGGGRVALTAP
Qy      421 ADAPGAGATAGIHWYSQQLQYQIGTWLJLSEALHPLGMVAKSSXSRGAGGAREGA 47
Db      421 ADAPGAGATAGIHWYSQQLQYQIGTWLJLSEALHPLGMVAKSSXSRGAGGAREGA 47

RESULT 8
US-09-827-110-15
Sequence 15, Application US/09827110
; Publication No. US20030104970A1
; GENERAL INFORMATION
; APPLICANT: Wang, Elizabeth
; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE
; POLYPEPTIDES, AND FORMULATIONS AND USES RELATED
; FILE REFERENCE: ONV-031.02
CURRENT APPLICATION NUMBER: US/09/827,110
CURRENT FILING DATE: 2000-04-04

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PRIOR APPLICATION NUMBER: 08/955, 552
 PRIOR FILING DATE: 1997-10-20
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 15
 LENGTH: 475
 TYPE: PRT
 ORGANISM: Homo sapien Shh
 OTHER INFORMATION: Xaa at position 463 is any or unknown amino acid
 US-09-827-110-15

Query Match 99.9%; Score 2467; DB 10; Length 475;
 Best Local Similarity 100.0%; Pred. No. 2.1e-207; Indels 0; Gaps 0;
 Matches 475; Conservative 0; Misatches 0;

Qy 1 MILLARCLLIVSSLLIVCSGLACGPGRGFKRHPKPLTPLAYKOFIPNVAEKTIGASG 60
 Db 1 MILLARCLLIVSSLLIVCSGLACGPGRGFKRHPKPLTPLAYKOFIPNVAEKTIGASG 60

Qy 61 RYEKISNSERKFELTNNDIIFKDEENTGADMTRQCKDKUNALAISVMNQPGV 120
 Db 61 RYEKISNSERKFELTNNDIIFKDEENTGADMTRQCKDKUNALAISVMNQPGV 120

Query Match 99.9%; Score 2467; DB 10; Length 475;
 Best Local Similarity 100.0%; Pred. No. 2.1e-207; Indels 0; Gaps 0;
 Matches 475; Conservative 0; Misatches 0;

Qy 1 MILLARCLLIVSSLLIVCSGLACGPGRGFKRHPKPLTPLAYKOFIPNVAEKTIGASG 60
 Db 1 MILLARCLLIVSSLLIVCSGLACGPGRGFKRHPKPLTPLAYKOFIPNVAEKTIGASG 60

Qy 61 RYEKISNSERKFELTPNPNDIIFKDEENTGADMTRQCKDKUNALAISVMNQPGV 120
 Db 61 RYEKISNSERKFELTPNPNDIIFKDEENTGADMTRQCKDKUNALAISVMNQPGV 120

Qy 121 KLRVTEGNDGDGHSESHYGRAVDTTSDEDRSYGMALARLAVAGEDMWYYESKAH 180
 Db 121 KLRVTEGNDGDGHSESHYGRAVDTTSDEDRSYGMALARLAVAGEDMWYYESKAH 180

Qy 241 FLDDDGAKKVFYVETREPRLILTAHLLFVAPINDSATGEPEASSGSPSGGALG 300
 Db 241 FLDDDGAKKVFYVETREPRLILTAHLLFVAPINDSATGEPEASSGSPSGGALG 300

Qy 301 PRALFASRVRPGQVYVAAERDGDRLLPAAVHSVTLSSEAAGAYAALTAQCTILINRL
 Db 301 PRALFASRVRPGQVYVAAERDGDRLLPAAVHSVTLSSEAAGAYAALTAQCTILINRL

Qy 361 ASCYAVIEEHSWAFAAFRLAHALLAALAPARTDGGDSCGGDRGGGRVALTAPGA 420
 Db 361 ASCYAVIEEHSWAFAAFRLAHALLAALAPARTDGGDSCGGDRGGGRVALTAPGA 420

Qy 421 ADAPGAGATAGIHWYSQIYQIGTWLDSEALPHGMVKSSXSRGAGGAREGA 475
 Db 421 ADAPGAGATAGIHWYSQIYQIGTWLDSEALPHGMVKSSXSRGAGGAREGA 475

RESULT 10
 US-09-451-939-15
 Sequence 15, Application US/09451939
 Publication No. US20030119729A1
 GENERAL INFORMATION:
 APPLICANT: Mi, Ningning
 APPLICANT: Wang, Monica
 APPLICANT: Mahanthappa, Nagesh K.
 APPLICANT: Jin, Ping
 APPLICANT: Fang, Kevin
 TITLE OF INVENTION: Method of Treating Dopaminergic and GABA-ergic Disorders
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 STREET: ONE POST OFFICE SQUARE
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII (text)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/451, 939
 CURRENT FILING DATE: 2001-04-27
 PRIOR APPLICATION NUMBER: 60/200, 765
 PRIOR FILING DATE: 2000-04-28
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 15
 LENGTH: 475
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (463)
 OTHER INFORMATION: Xaa=unknown amino acid residue
 US-09-845-025C-15

RESULT 9
 US-09-845-025C-15
 Sequence 15, Application US/0945025C
 Publication No. US20030104995A1
 GENERAL INFORMATION:
 APPLICANT: Reilly, J.
 TITLE OF INVENTION: NEUROPROTECTIVE METHODS AND COMPOSITIONS
 CURRENT APPLICATION NUMBER: US/09/845, 025C
 CURRENT FILING DATE: 2001-04-27
 PRIOR APPLICATION NUMBER: 60/200, 765
 PRIOR FILING DATE: 2000-04-28
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 15
 LENGTH: 475
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (463)
 OTHER INFORMATION: Xaa=unknown amino acid residue
 US-09-845-025C-15
 REFERENCE/DOCKET NUMBER: OVN-044.01

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 832-1000
 TELEFAX: (617) 832-7000
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-09-451-939-15

Query Match 99.9%; Score 2467; DB 10; Length 475;

Best Local Similarity 100.0%; Pred. No. 2.1e-20; Mismatches 0; Indels 0; Gaps 0;

Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MLLARCLLIVLVSSLVCSGLACPGGRGKRRHPKKLTPLAYQFIPNVAEKTIGASG

Db 1 MLLARCLLIVLVSSLVCSGLACPGGRGKRRHPKKLTPLAYQFIPNVAEKTIGASG

Qy 61 RYEGKISRSNSERFKELTPNYNPDIKFDEBENTGADRMLTQRCKDKNALAIISYNQNQPGV

Db 61 RYEGKISRSNSERFKELTPNYNPDIKFDEBENTGADRMLTQRCKDKNALAIISYNQNQPGV

Qy 121 KLRVTEGWDDEGHSESESLSHYEGRADVTITSDRDKYGMHLARAVEAGPDWVYESKAH

Db 121 KLRVTEGWDDEGHSESESLSHYEGRADVTITSDRDKYGMHLARAVEAGPDWVYESKAH

Qy 181 IHCSVRAENSYAAKSQGCFPQSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT

Db 181 IHCSVRAENSYAAKSQGCFPQSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT

Qy 241 FLDRDGAKVVFYVITREPRERLITTAHILFVAPHNDSATGEPEASSSGPPSGGALG

Db 241 FLDRDGAKVVFYVITREPRERLITTAHILFVAPHNDSATGEPEASSSGPPSGGALG

Qy 61 RYEGKISRSNSERFKELTPNYNPDIKFDEBENTGADRMLTQRCKDKNALAIISYNQNQPGV

Db 61 RYEGKISRSNSERFKELTPNYNPDIKFDEBENTGADRMLTQRCKDKNALAIISYNQNQPGV

Qy 121 KLRVTEGWDDEGHSESESLSHYEGRADVTITSDRDKYGMHLARAVEAGPDWVYESKAH

Db 121 KLRVTEGWDDEGHSESESLSHYEGRADVTITSDRDKYGMHLARAVEAGPDWVYESKAH

Qy 181 IHCSVRAENSYAAKSQGCFPQSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT

Db 181 IHCSVRAENSYAAKSQGCFPQSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLT

Qy 241 FLDRDGAKVVFYVITREPRERLITTAHILFVAPHNDSATGEPEASSSGPPSGGALG

Db 241 FLDRDGAKVVFYVITREPRERLITTAHILFVAPHNDSATGEPEASSSGPPSGGALG

Qy 301 PRALFASRVRGQRVTVVAEDGDRELLPAVHSVTLSEEAAGYAPLTAQGTILINVL

Db 301 PRALFASRVRGQRVTVVAEDGDRELLPAVHSVTLSEEAAGYAPLTAQGTILINVL

Qy 361 ASCYAVIEEHWAHRAPAFFPLAHLAALAPARTRGDSGGDRGGGGRVALTAGA

Db 361 ASCYAVIEEHWAHRAPAFFPLAHLAALAPARTRGDSGGDRGGGGRVALTAGA

Qy 421 ADAPGAGATAGIHWYSQLIQTGWLIDSEALHPGMVAKSSXSRRGAGGAREGA

Db 421 ADAPGAGATAGIHWYSQLIQTGWLIDSEALHPGMVAKSSXSRRGAGGAREGA

RESULT 11 US-09-238-243-15

; Sequence 15, Application US/09238243

; Publication No. US/030162698A1

; GENERAL INFORMATION

; APPLICANT: Galdes, Alphonse

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING DOPAMINERGIC

; TITLE OF INVENTION: AND GABA-ANERGIC DISORDERS

; FILE REFERENCE: ONV-069_01

; CURRENT APPLICATION NUMBER: US/09/238,243

; CURRENT FILING DATE: 1999-01-27

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO: 15

; LENGTH: 475

; TYPE: PRT

; ORGANISM: Homo sapiens Shh

; FEATURE:

; OTHER INFORMATION: Xaa at position 463 is any or unknown amino acid

; US-09-238-243-15

; Query Match 99.9%; Score 2467; DB 10; Length 475;

; Best Local Similarity 100.0%; Pred. No. 2.1e-20;

; Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12

US-09-736-476-13

; Sequence 13, Application US/09736476

; Publication No. US/2003/019069A1

; GENERAL INFORMATION:

; APPLICANT: Ingham, Phillip W.

; McMaham, Andrew P.

; Tabin, Clifford J.

; Bumcrot, David A.

; Marti-Gorostiza, Elisa

; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing Proteins and Uses Related Thereto

; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:

; ADDRESS: LAHIVE & COCKFIELD

; STREET: 60 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII (text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/736,476

; FILING DATE: 13-Dec-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08 / 435,093

; FILING DATE: 4-MAY-1995

; APPLICATION NUMBER: US 08 / 356,060

; FILING DATE: 14-DEC-1994

; APPLICATION NUMBER: US 08 / 176,427

; FILING DATE: 30-DEC-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: HNT-006CP4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEX/FAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 475 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 13;
 US-09-736-476-13

Query Match 99.9%; Score 2467; DB 12; Length 475;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 Matches 475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLVLVSSLLVCSGLACGPGRGFGRKRHKPKLTPLAYKQFIPNVAEKTLGASG 60
 DB 1 MLLARCLLVLVSSLLVCSGLACGPGRGFGRKRHKPKLTPLAYKQFIPNVAEKTLGASG 60
 QY 61 RYEKGKISNSERFKELTNPYNPDIIFKDEENTGADRINTQRCKDKLNALAISYMNONPGV 120
 DB 61 RYEKGKISNSERFKELTNPYNPDIIFKDEENTGADRINTQRCKDKLNALAISYMNONPGV 120
 QY 121 KLRVTEGDEDGHSEESLHYEGRADITTSDRSKYGMALARLAVAEFGDWVYYYESKAH 180
 DB 121 KLRVTEGDEDGHSEESLHYEGRADITTSDRSKYGMALARLAVAEFGDWVYYYESKAH 180
 QY 121 KLRVTEGDEDGHSEELHYEGRADITTSDRSKYGMALARLAVAEFGDWVYYYESKAH 180
 DB 121 KLRVTEGDEDGHSEELHYEGRADITTSDRSKYGMALARLAVAEFGDWVYYYESKAH 180
 QY 181 IHCSVKAENSVAAKSGCOPPGSATVHLBOGGTKLVLDLSPGDVLAAQGRLLYSDFLT 240
 DB 181 IHCSVKAENSVAAKSGCOPPGSATVHLBOGGTKLVLDLSPGDVLAAQGRLLYSDFLT 240
 QY 121 KLRVTEGDEDGHSEESLHYEGRADITTSDRSKYGMALARLAVAEFGDWVYYYESKAH 180
 DB 121 KLRVTEGDEDGHSEESLHYEGRADITTSDRSKYGMALARLAVAEFGDWVYYYESKAH 180
 QY 181 IHCSVKAENSVAAKSGCOPPGSATVHLBOGGTKLVLDLSPGDVLAAQGRLLYSDFLT 240
 DB 181 IHCSVKAENSVAAKSGCOPPGSATVHLBOGGTKLVLDLSPGDVLAAQGRLLYSDFLT 240
 QY 181 IHCSVKAENSVAAKSGCOPPGSATVHLBOGGTKLVLDLSPGDVLAAQGRLLYSDFLT 240
 DB 181 IHCSVKAENSVAAKSGCOPPGSATVHLBOGGTKLVLDLSPGDVLAAQGRLLYSDFLT 240
 QY 241 FLDRDGAKXKVFYIETREPRLLTAAHLLFVAPNHDSDATEPEASSGSPPSGGALG 300
 DB 241 FLDRDGAKXKVFYIETREPRLLTAAHLLFVAPNHDSDATEPEASSGSPPSGGALG 300
 QY 241 FLDRDGAKXKVFYIETREPRLLTAAHLLFVAPNHDSDATEPEASSGSPPSGGALG 300
 DB 241 FLDRDGAKXKVFYIETREPRLLTAAHLLFVAPNHDSDATEPEASSGSPPSGGALG 300
 QY 301 PRALFAASRYPGQRYVYVAERGDGRLLPAAVHSVTLSSEAAGAYAALITAQGTTLINRVL 360
 DB 301 PRALFAASRYPGQRYVYVAERGDGRLLPAAVHSVTLSSEAAGAYAALITAQGTTLINRVL 360
 QY 301 PRALFAASRYPGQRYVYVAERGDGRLLPAAVHSVTLSSEAAGAYAALITAQGTTLINRVL 360
 DB 301 PRALFAASRYPGQRYVYVAERGDGRLLPAAVHSVTLSSEAAGAYAALITAQGTTLINRVL 360
 QY 361 ASCYAVIEEWSWAHRAAFPLAHALLAALAPARTDRGGSGDRGGGGRVALTAPGA 420
 DB 361 ASCYAVIEEWSWAHRAAFPLAHALLAALAPARTDRGGSGDRGGGGRVALTAPGA 420
 QY 421 ADAPAGATAGIHWSQQLYQIGWILDSALHPGMAYKSXSXRGAEGAA 475
 DB 421 ADAPAGATAGIHWSQQLYQIGWILDSALHPGMAYKSXSXRGAEGAA 475
 RESULT 13
 US-10-244-095A-15
 ; Sequence 15, Application US/10244095A
 ; Publication No. US20030038876A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Repinsky, Blake R.
 ; APPLICANT: Taylor, Frederick
 ; APPLICANT: Garber, Ellen A.
 ; TITLE OF INVENTION: POLYMER CONJUGATES OF HEDGEHOG PROTEINS AND USES
 ; FILE REFERENCE: CIBT-P01-17
 ; CURRENT APPLICATION NUMBER: US/10/244,095A
 ; CURRENT FILING DATE: 2002-09-12
 ; PRIOR APPLICATION NUMBER: PCT/US00/14741
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 1999-08-13
 ; PRIOR FILING DATE: 1999-06-01
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 15
 ; LENGTH: 475
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-733-634-14

Query Match 99.9%; Score 2407; DB 10; Length 462;
 Best Local Similarity 100.0%; Pred. No. 3.7e-202;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLVLVSSLLVCSGLACGPGRGFGRKRHKPKLTPLAYKQFIPNVAEKTLGASG 60
 DB 1 MLLARCLLVLVSSLLVCSGLACGPGRGFGRKRHKPKLTPLAYKQFIPNVAEKTLGASG 60
 QY 61 RYEKGKISNSERFKELTNPYNPDIIFKDEENTGADRINTQRCKDKLNALAISYMNONPGV 120
 DB 61 RYEKGKISNSERFKELTNPYNPDIIFKDEENTGADRINTQRCKDKLNALAISYMNONPGV 120
 QY 121 KLRVTEGDEDGHSEESLHYEGRADITTSDRSKYGMALARLAVAEFGDWVYYYESKAH 180
 DB 121 KLRVTEGDEDGHSEESLHYEGRADITTSDRSKYGMALARLAVAEFGDWVYYYESKAH 180
 QY 121 KLRVTEGDEDGHSEELHYEGRADITTSDRSKYGMALARLAVAEFGDWVYYYESKAH 180
 DB 121 KLRVTEGDEDGHSEELHYEGRADITTSDRSKYGMALARLAVAEFGDWVYYYESKAH 180
 QY 181 IHCSVKAENSVAAKSGCOPPGSATVHLBOGGTKLVLDLSPGDVLAAQGRLLYSDFLT 240
 DB 181 IHCSVKAENSVAAKSGCOPPGSATVHLBOGGTKLVLDLSPGDVLAAQGRLLYSDFLT 240
 QY 241 FLDRDGAKXKVFYIETREPRLLTAAHLLFVAPNHDSDATEPEASSGSPPSGGALG 300
 DB 241 FLDRDGAKXKVFYIETREPRLLTAAHLLFVAPNHDSDATEPEASSGSPPSGGALG 300
 QY 301 PRALFAASRYPGQRYVYVAERGDGRLLPAAVHSVTLSSEAAGAYAALITAQGTTLINRVL 360
 DB 301 PRALFAASRYPGQRYVYVAERGDGRLLPAAVHSVTLSSEAAGAYAALITAQGTTLINRVL 360
 QY 361 ASCYAVIEEWSWAHRAAFPLAHALLAALAPARTDRGGSGDRGGGGRVALTAPGA 420
 DB 361 ASCYAVIEEWSWAHRAAFPLAHALLAALAPARTDRGGSGDRGGGGRVALTAPGA 420
 QY 421 ADAPAGATAGIHWSQQLYQIGWILDSALHPGMAYKSXSXRGAEGAA 475
 DB 421 ADAPAGATAGIHWSQQLYQIGWILDSALHPGMAYKSXSXRGAEGAA 475
 RESULT 14
 US-09-733-634-14
 ; Sequence 14, Application US/09733634
 ; Publication No. US20030013646A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Massachusetts General Hospital
 ; FILE REFERENCE: 1763/1240
 ; CURRENT APPLICATION NUMBER: US/09/733 , 634
 ; CURRENT FILING DATE: 2000-12-08
 ; PRIOR APPLICATION NUMBER: US 60/170,282
 ; PRIOR FILING DATE: 1999-12-10
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 14
 ; LENGTH: 462
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-733-634-14

Query Match 97.5%; Score 2407; DB 10; Length 462;
 Best Local Similarity 100.0%; Pred. No. 3.7e-202;
 Matches 462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLARCLLVLVSSLLVCSGLACGPGRGFGRKRHKPKLTPLAYKQFIPNVAEKTLGASG 60
 DB 1 MLLARCLLVLVSSLLVCSGLACGPGRGFGRKRHKPKLTPLAYKQFIPNVAEKTLGASG 60
 QY 61 RYEKGKISNSERFKELTNPYNPDIIFKDEENTGADRINTQRCKDKLNALAISYMNONPGV 120
 DB 61 RYEKGKISNSERFKELTNPYNPDIIFKDEENTGADRINTQRCKDKLNALAISYMNONPGV 120

61 RYEKGKSRNSERFKELTPYNPDIFKDENTGADRMLQRCKDNLNALAISYMNQPGV 120
Db 61 RYEKGKSRNSERFKELTPYNPDIFKDENTGADRMLQRCKDNLNALAISYMNQPGV 120
Qy 121 KLRVTEGWDGHSEESLHYEGRADITTSDRSKYMLARLAVEAGFDWVYYESKAH 180
Db 121 KLRVTEGWDGHSEESLHYEGRADITTSDRSKYMLARLAVEAGFDWVYYESKAH 180
Qy 181 IHCSYKAENSAVAATSGGCFCFGSATVHLEGGTLYKVDLSPGDRYLAADQGRILYSDFLT 240
Db 181 IHCSYKAENSAVAATSGGCFCFGSATVHLEGGTLYKVDLSPGDRYLAADQGRILYSDFLT 240
Qy 241 FLDRDGAKKVFYVIETREPERERLLTAAHLLFVAPHNDSATGEPEASSGSPPSGGALG 300
Db 241 FLDRDGAKKVFYVIETREPERERLLTAAHLLFVAPHNDSATGEPEASSGSPPSGGALG 300
Db RESULT 16 US-09-021-660A-37
Qy 301 PRALFASRVRFGORYVVAERDGDRILLPAAVHSVTLSPEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVRFGORYVVAERDGDRILLPAAVHSVTLSPEAAGAYAPLTAQGTILINRVL 360
Qy 361 ASCYATEEERSWAHAFAPRLAHLAALAPARTDRGGDSGGDRGGGGRRVALTAGA 420
Db 361 ASCYATEEERSWAHAFAPRLAHLAALAPARTDRGGDSGGDRGGGGRRVALTAGA 420
Qy 421 ADAPGAGATAGIHWYSQLIQIGTMILDSPEALHPGMAYKSS 462
Db 421 ADAPGAGATAGIHWYSQLIQIGTMILDSPEALHPGMAYKSS 462
Qy 421 ADAPGAGATAGIHWYSQLIQIGTMILDSPEALHPGMAYKSS 462
Db 421 ADAPGAGATAGIHWYSQLIQIGTMILDSPEALHPGMAYKSS 462
Db RESULT 17 US-09-021-660A-37
Qy Sequence 37, Application US/09021660A
Db Patent No. US2010041668A1
Db GENERAL INFORMATION:
Qy APPLICANT: Baron, M.
Db APPLICANT: Barrington, S.
Qy APPLICANT: Belauhoff, M.
Db TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR GROWTH
Db FILE REFERENCE: HU1P-P01-060
Db CURRENT APPLICATION NUMBER: US/09/021,660A
Db CURRENT FILING DATE: 2001-08-27
Db PRIORITY APPLICATION NUMBER: 60/037,513
Db PRIORITY FILING DATE: 1999-02-10
Db PRIORITY APPLICATION NUMBER: 60/049,763
Db PRIORITY FILING DATE: 1999-06-16
Db NUMBER OF SEQ ID NOS: 42
Db SOFTWARE: PatentIn Ver. 2.1
Db SEQ ID NO: 37
Db TYPE: PRT
Db ORGANISM: Mus musculus
Db US-09-021-660A-37
Qy Query Match 83.8%; Score 2068; DB 9; Length 437;
Db Best Local Similarity 87.4%; Pred. No. 1; e-172; Indels 26; Gaps 3;
Db Matches 404; Conservative 404;
Qy 1 MULLARCLLVLVSSLLVCSGLACGPGRGFGRHRPKLTPPLAYKFIPNVAEKTGAGS 60
Db 2 LULLARCLLVLASSLLVCPGLACGPGRGFGRHRPKLTPPLAYKFIPNVAEKTGAGS 61
Qy 61 RYEGKLRNSERFKELTPYNPDIIKDEENTGADRMLQRCKDNLNALAISYMNQPGV 120
Db 62 RYEGKLRNSERFKELTPYNPDIIKDEENTGADRMLQRCKDNLNALAISYMNQPGV 121
Qy 121 KURVTEGWDGHSEESLHYEGRADITTSDRSKYMLARLAVEAGFDWVYYESKAH 180
Db 122 KURVTEGWDGHSEESLHYEGRADITTSDRSKYMLARLAVEAGFDWVYYESKAH 181
Qy 181 IHCSVRAENSAVAKSGCFCFGSATVHLEGGTLYKVDLSPDRLAADDQGRILYSDFLT 240
Db 182 IHCSVRAENSAVAKSGCFCFGSATVHLEGGTLYKVDLSPDRLAADDQGRILYSDFLT 241
Qy 241 FLDRDGAKKVFYVIETREPERERLLTAAHLLFVAPHNDSATGEPEASSGSPPSGGALG 300
Db 242 FLDRDGAKKVFYVIETREPERERLLTAAHLLFVAPHNDSATGEPEASSGSPPSGGALG 300
Qy 301 PRALFASRVRFGORYVVAERDGDRILLPAAVHSVTLSPEAAGAYAPLTAQGTILINRVL 360
Db 301 PRALFASRVRFGORYVVAERDGDRILLPAAVHSVTLSPEAAGAYAPLTAQGTILINRVL 360
Qy 361 ASCYATEEERSWAHAFAPRLAHLAALAPARTDRGGDSGGDRGGGGRRVALTAGA 420
Db 361 ASCYATEEERSWAHAFAPRLAHLAALAPARTDRGGDSGGDRGGGGRRVALTAGA 420
Qy 421 ADAPGAGATAGIHWYSQLIQIGTMILDSPEALHPGMAYKSS 462
Db 421 ADAPGAGATAGIHWYSQLIQIGTMILDSPEALHPGMAYKSS 462
Db 396 TEARGAEPTAGIHWYSQLIQIGTMILDSPEALHPGMAYKSS 437

RESULT 17
 US-09-869-520A-1
 i Sequence 1, Application US/09969520A
 i Patent No. US20020177163A1
 i GENERAL INFORMATION:
 i APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
 i FILE REFERENCE: JHU1670-1
 i CURRENT FILING DATE: 2002-06-04
 i PRIORITY APPLICATION NUMBER: US 60/235,153
 i NUMBER OF SEQ ID NOS: 17
 i SOFTWARE: PatentIn version 3.1
 i SEQ ID NO 1
 i LENGTH: 437
 i TYPE: PRT
 i ORGANISM: Mus musculus
 i US-09-869-520A-1

Query Match 83.8%; Score 2068; DB 9; Length 437;
 Best Local Similarity 87.4%; Pred. No. 1.7e-172;
 Matches 404; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MILLARCILLYSSLLVSYLVCSSGIACGPGRGFGRHRPKLTPLAYKFIPNVAEKTIGASG 60
 Db 2 LILLARCFLVLLASSLIVCPGLACPGFGRHFGRHPKLTPLAYKFIPNVAEKTIGASG 61

Qy 61 RYEGKISRNSEPKELPPNYPNDIIFDEENTGADELMTQRCKDKNALALISVNQWPGV 120
 Db 62 RYEGKITENSEPKELPPNYPNDIIFDEENTGADELMTQRCKDKNALALISVNQWPGV 121

Qy 121 KURVTEGMDGHSEESLHYEGRAVDITTSDRSKYGMARLAVEAGFDWVYYESKAH 180
 Db 122 KLRVTEGMDGHSEESLHYEGRAVLITSQRDRSKYGMARLAVEAGFDWVYYESKAH 181

Qy 181 IHCSVKAEINSVAAKSGGFPGSATVHIEQGTKLVQLSPGDRVLAADDQCRRLYSDFLT 240
 Db 182 IHCSVKAEINSVAAKSGGCFPGSATVHIEQGTKLVQLSPGDRVLAADDQCRRLYSDFLT 241

Qy 241 FLRDRGAKKVFVVIETREPRELLTAAHLLFVAPINDSATGEPEASSGGPPSGGALG 300
 Db 242 FLRDEGAKKVFVVIETREPRELLTAAHLLFVAPIND-----SGPTPG 286

Qy 301 PRALFASVRPGQRVYVVAERDGDRLLPAAHTSVTLSEEAGAYAPLTAQCTTILINRVL 360
 Db 302 PSALFASVRPGQRVYVVAERGDRRLLPAAHTSVTLSEEAGAYAPLTAQCTTILINRVL 346

Qy 361 ASCYAVIEHSWAHRAFAPERLAHALAALAPARTDGGDSGGDRGGGRVALTAPGA 420
 Db 347 ASCYAVIEHSWAHRAFAPERLAHALAALAPARTDGGDSGGDRGGGRVALTAPGA 395

Qy 421 ADAGGAGTAGIHWYSQLIQISTWLSEAHLPGMVKSS 462
 Db 396 TEARGAEPAGIHWYSQLIYHISTWLSDETMPLGNMKVKSS 437

RESULT 19
 US-10-012-310-1
 i Sequence 1, Application US/10013310
 i Publication No. US20020192216A1
 i GENERAL INFORMATION:
 i APPLICANT: Lamb, Jonathon Robert
 i HOYNE, Gerard Francis
 i APPLICANT: Dallman, Margaret Jane
 i TITLE OF INVENTION: Therapeutic Use
 i FILE REFERENCE: 674525-2003
 i CURRENT APPLICATION NUMBER: US/10/013,310
 i CURRENT FILING DATE: 2001-12-07
 i PRIOR APPLICATION NUMBER: PCT/GB00/02191
 i PRIOR FILING DATE: 2000-06-05
 i PRIORITY APPLICATION NUMBER: 1999-06-08
 i PRIOR FILING DATE: 1999-09-16
 i NUMBER OF SEQ ID NOS: 8
 i SEQ ID NO 1
 i LENGTH: 437
 i TYPE: PRT
 i ORGANISM: House Mouse
 i US-10-013-310-1

Query Match 83.8%; Score 2068; DB 13; Length 437;
 Best Local Similarity 87.4%; Pred. No. 1.7e-172;
 Matches 404; Mismatches 24; Indels 26; Gaps 3;

RESULT 18
 US-09-733-634-16
 i Sequence 16, Application US/09733634
 i Publication No. US20030011646A1
 i GENERAL INFORMATION:
 i APPLICANT: Massachusetts General Hospital
 i FILE REFERENCE: 1763311240
 i CURRENT APPLICATION NUMBER: US/09/733,634
 i CURRENT FILING DATE: 2000-12-08
 i PRIOR APPLICATION NUMBER: US 60/170,282
 i PRIOR FILING DATE: 1999-12-10
 i NUMBER OF SEQ ID NOS: 32

TELECOMMUNICATION INFORMATION:

1 MILLARCLLIVSSLLVSGLAGCPGRGKGRHKPKKLTPLAKQFIPNVAEKTILGASG 60
 2 LLLIARCFVTLASSLLVCGLAGCPGRGKGRHKPKKLTPLAKQFIPNVAEKTILGASG 61

INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: protein
 SEQ ID NO: 20:
 US-10-460-594-20

SEQUENCE DESCRIPTION:

Query Match 83.8%; Score 2068; DB 15; Length 437;
 Best Local Similarity 87.4%; Pred. No. 1.7e-172;
 Matches 404; Conservative 8; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MILLARCLLIVSSLLVSGLAGCPGRGKGRHKPKKLTPLAKQFIPNVAEKTILGASG 60
 Db 2 LLLIARCFVTLASSLLVCGLAGCPGRGKGRHKPKKLTPLAKQFIPNVAEKTILGASG 61

Qy 1 RYEGKTSRNSERPFKEIIPNPYDIFKDEENTGADLMTORCKDKLNALANISWVQWPGVY 120
 Db 2 RYEGKTRNSERPFKEIIPNPYDIFKDEENTGADLMTORCKDKLNALANISWVQWPGVY 121

Qy 1 KLRVTGWDDEGHSEESLHVEGRADITTSDRSKYGMARLAVAEAGDWVYTESKAH 180
 Db 2 KLRVTGWDDEGHSEESLHVEGRADITTSDRSKYGMARLAVAEAGDWVYTESKAH 181

Qy 1 FUDRDGAKKVYYTETREPERLILTAHLLFYAPHNDSATGEPEASSSGGPSSGGALG 300
 Db 2 FUDRDGAKKVYYTETREPERLILTAHLLFYAPHNDSATGEPEASSSGGPSSGGALG 301

Qy 1 PRALFSPRSVPQGRYYVVAARDGDERLPPAVHSTVLSEAAAGAYAAPTAAQGTLLINVL 360
 Db 2 PSALFSPRSVPQGRYYVVAERGGERDLPPAVHSTVLSEAAAGAYAAPTAAQGTLLINVL 346

Qy 1 ASCYAVIEHSWAHRAFPAPRLAHALLALAPARTDGGDSGGDRGGGGRVALTAGQA 420
 Db 2 ASCYAVIEHSWAHRAFPAPRLAHALLALAPARTDGGDSGGDRGGGGRVALTAGQA 421

Qy 1 ADAPGAGATAGIHWTSQQLQIGTMLDSEALHPGMATKSS 462
 Db 2 TEARGAEPTAGIHWTSQQLQIGTMLDSEALHPGMATKSS 437

RESULT 21

US-10-460-594-20
 Sequence 20, Application US/10460594
 Publication No. US20040018979A1
 GENERAL INFORMATION:
 APPLICANT: Beatty, Philip A.
 PORTER, Jeffrey A.
 TITLE OF INVENTION: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
 NUMBER OF SEQUENCES: 109
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson, P. C.
 STREET: 4225 Executive Square, Suite 1400
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSEQ for Windws Version 2.0b

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/460,594
 FILING DATE: 11-Jun-2003

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/061,323
 FILING DATE: 07-OCT-1997
 APPLICATION NUMBER: 08/729,743
 FILING DATE: 07-OCT-1996
 APPLICATION NUMBER: 08/567,357
 FILING DATE: 10-JUL-1996
 APPLICATION NUMBER: 08/349,498
 FILING DATE: 04-DEC-1995
 APPLICATION NUMBER: <Unknown>
 FILING DATE: 02-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Hallie, Lisa A.
 REGISTRATION NUMBER: 38,347
 REFERENCE/DOCKET NUMBER: 07265/140001

TITLE OF INVENTION: Method of Treating Dopaminergic and GABA-nergic Disorders

NUMBER OF SEQUENCES: 32
 Sequence 13, Application US/08900220C
 CORRESPONDENCE ADDRESS:
 Publication No. US20020045206A1
 GENERAL INFORMATION:
 APPLICANT: Miao, Ningning
 Wang, Monica
 Mahanthappa, Nagesh K.
 PANG, Kevin
 Jin, Ping

NUMBER OF SEQUENCES: 32
 Sequence 13, Application US/08900220C
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 STREET: ONE POST OFFICE SQUARE
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII (text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/900,220C

PILING DATE: 24-Jul-1997

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: ONY-044-01

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 832-1000

TELEFAX: (617) 832-7000

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 437 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-08-900-220C-13

Query Match 83.6%; Score 2065; DB 8; Length 437;

Best Local Similarity 87.2%; Pred. No. 3,2e-12;

Matches 403; Conservative 9; Mismatches 24; Indels 3; Gaps 3;

Db 1 MLLARCLLVLVSSLVSGLAGCPGRGKRRHPKKLTPLAYQFIPNVAEKTIGASG 60

Db 2 LLLARCFVLIASSLVCPGLACPGRGKGRHRPKKLTPLAYQFIPNVAEKTIGASG 61

Qy 61 RYEKGKTRNSERFKELTPNYPNDIFKDENTGADRMTQRCKDKNALAISYMNONPGV 120

Db 62 RYEKGKTRNSERFKELTPNYPNDIFKDENTGADRMTQRCKDKNALAISYMNONPGV 121

Qy 121 KLRVTEGWDGGHISBESHYEGRAVD-TTSDRDRSKYGMRLARLAVEAGFDVYVYESKAH 180

Db 122 RLRVTEGWDGGHISBESHYEGRAVD-TTSDRDRSKYGMRLARLAVEAGFDVYVYESKAH 181

Qy 181 IHCSYKAENSAAKSGGCCPGSATVHLEGGTCKLVKDLSPGDRVLAADDQGRULLYSDFLT 240

Db 182 IHCSYKAENSAAKSGGCCPGSATVHLEGGTCKLVKDLSPGDRVLAADDQGRULLYSDFLT 241

Qy 241 FLDRDGAKKVYVETTERERERLLTAHHLFVAPINDSATSEPEASSGSPSGGALG 300

Db 242 FLDRDGAKKVYVETTERERERLLTAHHLFVAPINDSATSEPEASSGSPSGGALG 286

Qy 301 PRALFASRVPGQRTYVVAERGDRERLLAHAHVSTLSEAAAYAFAITAQGTILINRL 360

Db 287 PSALFASRVPGQRTYVVAERGDRERLLAHAHVSTLSEAAAYAFAITAQGTILINRL 346

Qy 361 ASCYAVIEHSWAHAFAPFLAHALLAALAPARTDRGGDSGGDRGGGRVALTAFGA 420

Db 347 ASCYAVIEHSWAHAFAPFLAHALLAALAPARTDRGGDSGGDRGGGRVALTAFGA 395

Qy 421 ADAPGAGATAGIHWYSQLYQIGTWLLDSEALHPLGMVKSS 462

Db 396 TEARGAEPTAGIHWYSQLYHGTWLLDSETMHPLGMVKSS 437

RESULT 22

US-08-954-771-11

Sequence 11, Application US/08954771

Publication No. US20030054437A1

GENERAL INFORMATION:

APPLICANT: McMahon, Andrew P.

APPLICANT: Insham, Phillip W.

APPLICANT: Tabin, Clifford J.

TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing

TITLE OF INVENTION: Proteins and Uses Related Thereto

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HONG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

RESULT 23
 US-09-462-386D-11
 Sequence 11, Application US/08462386D
 Publication No. US20030186557A1
 GENERAL INFORMATION:
 APPLICANT: Ingham, Phillip W.
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.
 TITLE OF INVENTION: Vertebrate Tissue Pattern-Inducing
 TITLE OF INVENTION: Proteins and Uses Related Thereto
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, Suite 510
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII (text)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/462, 386D
 FILING DATE: 5-JUNE-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/435, 093
 FILING DATE: 4-JAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/356, 060
 FILING DATE: 14-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/176, 427
 FILING DATE: 30-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: HMI-006CP3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEX/FAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-462-386D-11

Query Match Score 2065; DB 8; Length 437;
 Best Local Similarity 87.2%; Pred. No. 3.2e-172;
 Matches 403; Conservative 9; N mismatches 24; Indels 26; Gaps 3;

Db 242 FLDRDGAKKVYVETPLRLLPAVHSVTLSEAAAGAYPLAQGTLLNRL 360
 Qy 301 PRALFASRVPGQRTVVAERDGDRILLPAVHSVTLSEAAAGAYPLAQGTLLNRL 360
 Db 287 PSALFASRVPGQRTVVAERGDGRILLPAVHSVTLSEAAAGAYPLAQGTLLNRL 346
 Qy 361 ASCYATTEHHWAHRAPFLAHLLAALAPARTRGDSGGDRGGGRVALTAGA 420
 Db 347 ASCYATTEHHWAHRAPFLAHLLAALAPARTRGDSGGDRGGGRVALTAGA 420
 Qy 421 ADAPGAGATAGTHWSOLYQIGTMLDSEALHPGMVKSS 462
 Db 396 TEARGAEPTAGTHWSOLYQIGTMLDSEALHPGMVKSS 437

RESULT 24
 US-09-151-999-13
 Sequence 13, Application US/09151999
 ; Patent No. US2002151460A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Elizabeth
 ; TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE
 ; POLYPEPTIDES, AND FORMULATIONS AND USES RELATED THERETO
 ; TITLE OF INVENTION: POLYPEPTIDES, AND FORMULATIONS AND USES RELATED THERETO
 ; FILE REFERENCE: ONV-031.02
 ; CURRENT APPLICATION NUMBER: US/09/151, 999
 ; CURRENT FILING DATE: 1998-08-11
 ; EARLIER APPLICATION NUMBER: 08/955, 552
 ; EARLIER FILING DATE: 1997-10-20
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 13
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: murine Shh
 ; US-09-151-999-13

Query Match Score 2065; DB 9; Length 437;
 Best Local Similarity 87.2%; Pred. No. 3.2e-172;
 Matches 403; Conservative 9; N mismatches 24; Indels 26; Gaps 3;

Db 1 MILLARCLLVLVSSLVCSGLACGGGRGFGRRIPKKTPLAYQFIPVNAEKTLGASG 60
 Db 2 MILLARCLVLASSLVCPCPGLACGGGRGFGRRIPKKTPLAYQFIPVNAEKTLGASG 61
 Qy 61 RYEKGISRSNSERFKELTPTNPDIIFKDEENTGADRLMTORCDKLNALATSVNNQPGV 120
 Db 62 RYEKGITRNSERFKELTPTNPDIIFKDEENTGADRLMTORCDKLNALATSVNNQPGV 121
 Qy 121 KLRVTEGWDEGHHSSESLSHYEGRAVDITTSDRSKYGMALARLAVEAGDFWVYESKAH 180
 Db 122 RLRVTEGWDEGHHSSESLSHYEGRAVDITTSDRSKYGMALARLAVEAGDFWVYESKAH 181
 Qy 181 IHCSVKAENSYAKSGCFCPPSATSYLEQCGSTKLVKDLSPCDRVLAADDQGRLLYSDFLT 240
 Db 182 IHCSVKAENSYAKSGCFCPPSATSYLEQCGSTKLVKDLSPCDRVLAADDQGRLLYSDFLT 241
 Qy 241 FLDRDGAKKVYVETPLRLLPAVHSVTLSEAAAGAYPLAQGTLLNRL 360
 Db 242 FLDRDGAKKVYVETPLRLLPAVHSVTLSEAAAGAYPLAQGTLLNRL 346
 Qy 301 PRALFASRVPGQRTVVAERDGDRILLPAVHSVTLSEAAAGAYPLAQGTLLNRL 360
 Db 287 PSALFASRVPGQRTVVAERGDGRILLPAVHSVTLSEAAAGAYPLAQGTLLNRL 346
 Qy 361 ASCYATTEHHWAHRAPFLAHLLAALAPARTRGDSGGDRGGGRVALTAGA 420
 Db 347 ASCYATTEHHWAHRAPFLAHLLAALAPARTRGDSGGDRGGGRVALTAGA 420
 Qy 421 ADAPGAGATAGTHWSOLYQIGTMLDSEALHPGMVKSS 462
 Db 396 TEARGAEPTAGTHWSOLYQIGTMLDSEALHPGMVKSS 437

Query Match Score 2065; DB 8; Length 437;
 Best Local Similarity 87.2%; Pred. No. 3.2e-172;
 Matches 403; Conservative 9; N mismatches 24; Indels 26; Gaps 3;

Db 1 MILLARCLLVLVSSLVCSGLACGGGRGFGRRIPKKTPLAYQFIPVNAEKTLGASG 60
 Db 2 MILLARCLVLASSLVCPCPGLACGGGRGFGRRIPKKTPLAYQFIPVNAEKTLGASG 61
 Qy 61 RYEKGISRSNSERFKELTPTNPDIIFKDEENTGADRLMTORCDKLNALATSVNNQPGV 120
 Db 62 RYEKGITRNSERFKELTPTNPDIIFKDEENTGADRLMTORCDKLNALATSVNNQPGV 121
 Qy 121 KLRVTEGWDEGHHSSESLSHYEGRAVDITTSDRSKYGMALARLAVEAGDFWVYESKAH 180
 Db 122 RLRVTEGWDEGHHSSESLSHYEGRAVDITTSDRSKYGMALARLAVEAGDFWVYESKAH 181
 Qy 181 IHCSVKAENSYAKSGCFCPPSATSYLEQCGSTKLVKDLSPCDRVLAADDQGRLLYSDFLT 240
 Db 182 IHCSVKAENSYAKSGCFCPPSATSYLEQCGSTKLVKDLSPCDRVLAADDQGRLLYSDFLT 241
 Qy 241 ADAPGAGATAGTHWSOLYQIGTMLDSEALHPGMVKSS 462
 Db 347 ASCYATTEHHWAHRAPFLAHLLAALAPARTRGDSGGDRGGGRVALTAGA 420
 Qy 361 ASCYATTEHHWAHRAPFLAHLLAALAPARTRGDSGGDRGGGRVALTAGA 420
 Db 347 ASCYATTEHHWAHRAPFLAHLLAALAPARTRGDSGGDRGGGRVALTAGA 420
 Qy 421 ADAPGAGATAGTHWSOLYQIGTMLDSEALHPGMVKSS 462
 Db 396 TEARGAEPTAGTHWSOLYQIGTMLDSEALHPGMVKSS 437

Query Match Score 2065; DB 8; Length 437;
 Best Local Similarity 87.2%; Pred. No. 3.2e-172;
 Matches 403; Conservative 9; N mismatches 24; Indels 26; Gaps 3;

Db 1 MILLARCLLVLVSSLVCSGLACGGGRGFGRRIPKKTPLAYQFIPVNAEKTLGASG 60
 Db 2 MILLARCLVLASSLVCPCPGLACGGGRGFGRRIPKKTPLAYQFIPVNAEKTLGASG 61
 Qy 61 RYEKGISRSNSERFKELTPTNPDIIFKDEENTGADRLMTORCDKLNALATSVNNQPGV 120
 Db 62 RYEKGITRNSERFKELTPTNPDIIFKDEENTGADRLMTORCDKLNALATSVNNQPGV 121
 Qy 121 KLRVTEGWDEGHHSSESLSHYEGRAVDITTSDRSKYGMALARLAVEAGDFWVYESKAH 180
 Db 122 RLRVTEGWDEGHHSSESLSHYEGRAVDITTSDRSKYGMALARLAVEAGDFWVYESKAH 181
 Qy 181 IHCSVKAENSYAKSGCFCPPSATSYLEQCGSTKLVKDLSPCDRVLAADDQGRLLYSDFLT 240
 Db 182 IHCSVKAENSYAKSGCFCPPSATSYLEQCGSTKLVKDLSPCDRVLAADDQGRLLYSDFLT 241
 Qy 241 ADAPGAGATAGTHWSOLYQIGTMLDSEALHPGMVKSS 462
 Db 347 ASCYATTEHHWAHRAPFLAHLLAALAPARTRGDSGGDRGGGRVALTAGA 420
 Qy 361 ASCYATTEHHWAHRAPFLAHLLAALAPARTRGDSGGDRGGGRVALTAGA 420
 Db 347 ASCYATTEHHWAHRAPFLAHLLAALAPARTRGDSGGDRGGGRVALTAGA 420
 Qy 421 ADAPGAGATAGTHWSOLYQIGTMLDSEALHPGMVKSS 462
 Db 396 TEARGAEPTAGTHWSOLYQIGTMLDSEALHPGMVKSS 437

RESULT 25
US-09-883-848A-13
Sequence 13, Application US/0983848A
Publication No. US2003002281A1
GENERAL INFORMATION:
APPLICANT: Ling, L.
TITLE OF INVENTION: ANGIOGENESIS-MODULATING COMPOSITIONS AND USES
FILE REFERENCE: CIBT-P01-119
CURRENT APPLICATION NUMBER: US/09/883, 848A
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/211, 919
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 437
TYPE: PRT
ORGANISM: Mus musculus
US-09-883-848A-13

Query Match 83.6%; Score 2065; DB 10; Length 437;
Best Local Similarity 87.2%; Pred. No. 3.2e-172;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MILLIARCLLIVSSLLVCGSLACGPGRGFGRHRPKKLTPLAYKOFIPNVAEKTIGASC 60
Db 2 LILLARCPFLVASSLLVCPGLACGPGRGFGRHRPKKLTPLAYKOFIPNVAEKTIGASC 61

Qy 61 RYEGKISRSNRSERFELTPNYNPDIIFDEENTGADRIMTQRCKDKNALASVNQWPGV 120
Db 62 RYEGKITNSRERFELTPNYNPDIIFDEENTGADRIMTQRCKDKNALASVNQWPGV 121

Qy 121 KLRVTEGMDGEGHSEESLHYGRAVDTTSDRSKYGMMLARAVAGEFDWVYESKAH 180
Db 122 RLRTVEGMDGEGHSEESLHYGRAVDTTSDRSKYGMMLARAVAGEFDWVYESKAH 181

Qy 181 IHCSVKAEINSVAKS GCCFPGSATVHLEQGGTKVLKDLSPGDRVLAADDQGRLLYSDFLT 240
Db 182 IHCSVKAEINSVAKS GCCFPGSATVHLEQGGTKVLKDLSPGDRVLAADDQGRLLYSDFLT 241

Qy 241 FLORDGAKKVFTVETPREBLLTAAHLLFVAPHNDSATGEPEASSGGPPSGALG 300
Db 242 FLDRDEGAKKVFTVETPREBLLTAAHLLFVAPHNDSATGEPEASSGGPPSGALG 286

Qy 301 PRALFASRVRPGORYVVAERGCDRRLPAATHSUTLSEAAAGAYALTAQGTTLINRVL 360
Db 287 PSALFASRVRPGORYVVAERGCDRRLPAATHSUTLREEAAGAYALTAQGTTLINRVL 346

Qy 361 ASCVAVIEHSWAHRAFAPRLAHALLAALAPARTDGDSSGGDRGGGRVALTAPGA 420
Db 347 ASCVAVIEHSWAHRAFAPRLAHALLAALAPARTDGDSSGGDRGGGRVALTAPGA 395

Qy 421 ADAPGAGATAIGHWYSQQLYQIGTWLDSALEHPLGNMVKSS 462
Db 396 TEARGAEPTAGIGHWYSQQLYHIGTWLDSETHPLGNMVKSS 437

RESULT 27
US-09-827-110-13
Sequence 13, Application US/09827110
Publication No. US20030104970A1
GENERAL INFORMATION:
APPLICANT: Wang, Elizabeth
TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE POLYPEPTIDES, AND FORMULATIONS AND USES RELATED THERETO
FILE REFERENCE: ONV-031-02
CURRENT APPLICATION NUMBER: US/09/827, 110
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 08-1955, 552
PRIOR FILING DATE: 1997-10-20
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 437
TYPE: PRT
ORGANISM: murine shh
US-09-827-110-13

Query Match 83.6%; Score 2065; DB 10; Length 437;
Best Local Similarity 87.2%; Pred. No. 3.2e-172;
Matches 403; Conservative 9; Mismatches 24; Indels 26; Gaps 3;

Qy 1 MILLIARCLLIVSSLLVCGSLACGPGRGFGRHRPKKLTPLAYKOFIPNVAEKTIGASC 60
Db 2 LILLARCPFLVASSLLVCPGLACGPGRGFGRHRPKKLTPLAYKOFIPNVAEKTIGASC 61

Qy 61 RYEGKISRSNRSERFELTPNYNPDIIFDEENTGADRIMTQRCKDKNALASVNQWPGV 120

62 RYEKGKTRNSERFKELTNPYNDIFKDENTGADRMLQRCKDNLALAI SVMNQPGV 121
 Db 62 RYEKGKTRNSERFKELTNPYNDIFKDENTGADRMLQRCKDNLALAI SVMNQPGV 121
 Qy 121 KLRVTEGMDDEGHSEESIHYEGRADITTSDRSKYGMRLARLAVEAGFDWVYESKAH 180
 Db 122 RLRTVEGMDDEGHSEESIHYEGRADITTSDRSKYGMRLARLAVEAGFDWVYESKAH 181
 Db 122 RLRTVEGMDDEGHSEESIHYEGRADITTSDRSKYGMRLARLAVEAGFDWVYESKAH 181
 Qy 181 1 HCSVKAEINSVAAKSGCCPGSATVHLEGGTKLVKDLS PGDRVLAADDQGRLLYSDFLT 240
 Db 182 1 HCSVKAEINSVAAKSGCCPGSATVHLEGGTKLVKDLS PGDRVLAADDQGRLLYSDFLT 241
 Qy 241 FLDRDGAKKVYYVETREPRERLLTAHHLEVAPHDNSATGEPEASSGSPPSGGALG 300
 Db 242 FLDRDGAKKVYYVETLEPRERLLTAHHLEVAPHDNSATGEPEASSGSPPSGGALG 300
 Db 242 FLDRDGAKKVYYVETLEPRERLLTAHHLEVAPHDNSATGEPEASSGSPPSGGALG 300
 RESULT 29
 US-09-451-939-13
 ; Sequence 13, Application US/09451939
 ; Publication No. US20030119729A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Miao, Ningning
 ; APPLICANT: Wang, Monica
 ; APPLICANT: Mahanthappa, Nagesh K.
 ; APPLICANT: Jain, Ping
 ; APPLICANT: Pang, Kevin
 ; TITLE OF INVENTION: Method of Treating Dopamnergic and GABA-nergic Disorders
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: POLEY, HOAG & ELLIOT LLP
 ; STREET: ONE POST OFFICE SQUARE
 ; CITY: BOSTON
 ; STATE: MA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-POS/MS-DOS
 ; SOFTWARE: ASCII (text)
 ; CURRENT APPLICATION NUMBER: US/09/451,919
 ; APPLICATION NUMBER: US/09/451,919
 ; FILING DATE:
 ; PRIORITY DATE:
 ; NUMBER OF SEQ ID NOS: 22
 ; SEQ ID NO: 13
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-845-025C-13

RESULT 28
 US-09-845-025C-13
 ; Sequence 13, Application US/09B45025C
 ; PUBLICATION NO. US20030104995A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reilly, J.
 ; TITLE OF INVENTION: NEUROPROTECTIVE METHODS AND COMPOSITIONS
 ; FILE REFERENCE: C1T-P01-098
 ; CURRENT APPLICATION NUMBER: US/09/845,025C
 ; CURRENT FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: 60/200,765
 ; PRIOR FILING DATE: 2000-04-28
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 13
 ; LENGTH: 437
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-845-025C-13

Query Match 83.6%; Score 2065; DB 10; Length 437;
 Best Local Similarity 87.2%; Pred. No. 3.2e-172;
 Matches 403; Conservative 9; Missmatches 24; Indels 26; Gaps 3;

Qy 1 MILLARCLLTVSSLLIVSGLAGPGRGFGRKRIPFKLTPKOFINVAEKTGLSG 60
 Db 2 LILLARCLFVILASSLLIVCPGLACGGRGFGRKRIPFKLTPKOFINVAEKTGLSG 61
 Qy 61 RYEKGKTRNSERFKELTNPYNDIFKDENTGADRMLQRCKDNLALAI SVMNQPGV 120
 Db 62 RYEKGKTRNSERFKELTNPYNDIFKDENTGADRMLQRCKDNLALAI SVMNQPGV 121
 Qy 121 KLRVTEGMDDEGHSEESIHYEGRADITTSDRSKYGMRLARLAVEAGFDWVYESKAH 180
 Db 122 RLRTVEGMDDEGHSEESIHYEGRADITTSDRSKYGMRLARLAVEAGFDWVYESKAH 181
 Qy 181 1 HCSVKAEINSVAAKSGCCPGSATVHLEGGTKLVKDLS PGDRVLAADDQGRLLYSDFLT 240
 Db 182 1 HCSVKAEINSVAAKSGCCPGSATVHLEGGTKLVKDLS PGDRVLAADDQGRLLYSDFLT 241
 Qy 241 FLDRDGAKKVYYVETREPRERLLTAHHLEVAPHDNSATGEPEASSGSPPSGGALG 300
 Db 242 FLDRDGAKKVYYVETLEPRERLLTAHHLEVAPHDNSATGEPEASSGSPPSGGALG 300
 Qy 301 PRALFASRVRPGQRVYVAERGDRRLPAAVHSVTLSSEAGAYAPLTAQGTILINRVL 360

Db	122	RLLRTEGWDDEGHHSBESLHYEGRAVDITTSDRDRSKYGMILLARAVEAGFDFVYBESKAH	181
Qy	181	IHCSTKAENSAAKSGCCPGSATVHLEGGTCKVKDLSPGDRVLAADDQGRLLYSDFLT	240
Db	182	IHCSTKAENSAAKSGCCPGSATVHLEGGTCKVKDLSPGDRVLAADDQGRLLYSDFLT	241
Db	241	FLDRDGAKKVYVIEPREPLLTAAHLLFYAPANDSACEPEASSGSPGGALG	300
Qy	242	FLDRDGAKKVYVIEPREPLLTAAHLLFYAPND-----SOPPTPG	286
Db	301	PRALPASRYVRPGQRVYVVAERDGDRLLAAVHSVTLSBEAGAYAALTAQGTILINRVL	360
Qy	287	PSALPASRYVRPGQRVYVVAERGGDRLLPAAVSITVLREEEAGAYAALTAQGTILINRVL	346
Db	361	ASCYAYTEEHSAWAHAFAPRLLAHAA LAPTDRGCGDGGDRGGGGRVALTAPGA	420
Qy	347	ASCYAYTEEHSAWAHAFAPRLLAHAA LAPTD-----GGGGSIP AAQSA	395
Db	421	ADAPGAGATAGTHTWSQLYHQIGTWLDSPEAHLGMAVKSS	462
Qy	396	TEARGAEPTAGIHWTSQLYHIGTWLDSETMHLGMAVKSS	437
RESULT 30			
US-09-238-243-13			
Qy	; Sequence 13 , Application US/09218243		
Qy	; Publication No. US2003162638A1		
Qy	; GENERAL INFORMATION:		
Qy	; APPLICANT: Galdes, Alphonse		
Qy	; APPLICANT: Mahanthappa, Nagesh		
Qy	; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING DOPAMINERGIC		
Qy	; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING DOPAMINERGIC		
Qy	; TITLE OF INVENTION: AND GABA-NERGIC DISORDERS		
Qy	; FILE REFERENCE: ONV-063-01		
Qy	; CURRENT APPLICATION NUMBER: US/09/238,243		
Qy	; CURRENT FILING DATE: 1999-01-27		
Qy	; NUMBER OF SEQ ID NOS: 32		
Qy	; SOFTWARE: PatentIn Ver. 2.0		
Qy	; SEQ ID NO 13		
Qy	; LENGTH: 437		
Qy	; TYPE: PRT		
Qy	; ORGANISM: murine Shh		
Qy	US-09-238-243-13		
Qy	Query Match Score 2065; DB 10; Length 437;		
Qy	Best Local Similarity 87.2%; Pred: No. 3..2e-172;		
Qy	Matches 403; Conservative 9; Mismatches 24; Gaps 3		
Qy	1 MULARCILLYVSSLLIVCSGLACCGPGRGEKGKRPKQLTPLAKQFIPNVAKRTLGASG		
Db	2 LLIJARCFLVIASSLIVCPGIAAGGGRGEKGKRPKQLTPLAKQFIPNVAKRTLGASG		
Qy	61 RVEGKIGNSNRSERKELTPTPNYPDIIFKDEENTGADRIMTORCKDKLNALAISSYNMNPQVG		
Db	62 RVEGKIGNSNRSERKELTPTPNYPDIIFKDEENTGADRIMTORCKDKLNALAISSYNMNPQVG		
Qy	121 KRFVTEGNDDEGHSESSLHVEGRADITTSDRDRSKYGMILLARAVEAGFDWTVYESKAH		
Db	122 RLFVTEGNDDEGHSESSLHVEGRADITTSDRDRSKYGMILLARAVEAGFDWTVYESKAH		
Qy	181 IHCSTKAENSAAKSGCCPGSATVHLEGGTCKYLDLSPGDRVLAADDQGRLLYSDFLT		
Db	182 IHCSTKAENSAAKSGCCPGSATVHLEGGTCKYLDLSPGDRVLAADDQGRLLYSDFLT		
Qy	241 FLDRDGAKKVYVIEPREPLLTAAHLLFYAPNDSATGPEASSGSPGGALG		
Db	242 FLDRDGAKKVYVIEPREPLLTAAHLLFYAPND-----SGPPG		
Qy	301 PRALFAASRVPGQRVYVVAERGDRLPAAVHSVSEBRAGAYAALTAQGTILINRVL		
Db	287 PSALPASRVPGQRVYVVAERGDRLPAAVHSVSEBRAGAYAALTAQGTILINRVL		
Qy	361 ASCYAYTEEHSAWAHAFAPRLLAHAA LAPTD-----GGGGCGRVLTAPGA		

RESULT 31

US-09-736-476-11 Query Match 83 %; Score 2065; DB 10; Length 437;

; Sequence 11, Application US/09736476
; Publication No. US20030190696A1

QY ; Best Local Similarity 87 %; Pred. No. 3.26E-172; Gaps 3 ;
; GENERAL INFORMATION:
; APPLICANT: Ingham, Phillip W.
; McMahan, Andrew P.
; Tabin, Clifford J.
; Bumrout, David A.
; Marti-Gorostiza, Elisa

Db ; Matches 403; Conservative 9; Mis matches 24; Indels 26; Gaps 6 ;
; TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
; Proteins and Uses Related Thereto

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:
; ADDRESSEES: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII (text)

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/736,476
; FILING DATE: 13-Dec-2000

PRIOR APPLICATION DATA:
; CLASSIFICATION: <Unknown>
; APPLICATION NUMBER: US 06/435,093
; FILING DATE: 4-MAY-1995
; APPLICATION NUMBER: US 08/356,060
; FILING DATE: 14-DEC-1994
; APPLICATION NUMBER: US 08/176,427
; FILING DATE: 30-DEC-1993

ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HMI - 006CP4

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-736-476-11

Query Match 83 %; Score 2065; DB 10; Length 437;

Best Local Similarity 87 %; Pred. No. 3.26E-172; Gaps 3 ;
; Matches 403; Conservative 9; Mis matches 24; Indels 26; Gaps 6 ;
; 1. MILLARCLLVLVSSLLVCGPGLACCPGRFGKRRPKKLTPLAYKQFIPNVAEKTIGASG 60
; :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
; 2. LLLARCFLVLLASSILVCPGLACCPGRFGKRRPKKLTPLAYKQFIPNVAEKTIGASG 61

QY 61 RYEKGISRSRBRKFELTPNYPNPDLIFKQDENTGADRMLTQRCDKLNALAIISMNQWQGV 120
; Db 62 RYEKGITRNSRKFELTPNYPNDIFKDBENTGADRMLTQRCDKLNALAIISMNQWQGV 121

QY 121 KLRVTEGWDDEGHSEESLHYEGRADITTSDRSKYMLARIAVEAGEDWVYYESKAH 180

Sequence 14, Application US/09990046
 Patent No. US200215245A1
 GENERAL INFORMATION:
 APPLICANT: de Sauvage, Frederic
 APPLICANT: Carpenter, David A.
 FILE REFERENCE: PI45RI
 CURRENT APPLICATION NUMBER: US/09/990, 046
 CURRENT FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/293, 505
 PRIOR FILING DATE: EARLIER FILING DATE: 1995-04-15
 SEQ ID NO: 14
 LENGTH: 437
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-990-046-14

Query Match Score 83.5%; Best Local Similarity 87.0%; Pred. No. 5.8e-12; Matches 402; Conservative 8; Mismatches 251; Indels 26; Gaps 3;
 OTHER INFORMATION: Altered sonic hedgehog protein
 US-09-969-520A-3

Query Match Score 2062; DB 9; Length 437;
 Best Local Similarity 87.2%; Pred. No. 5.8e-12; Matches 403; Conservative 8; Mismatches 251; Indels 26; Gaps 3;
 OTHER INFORMATION: Artificial sequence
 US-09-969-520A-3

Query Match Score 2062; DB 9; Length 437;
 Best Local Similarity 87.2%; Pred. No. 5.8e-12; Matches 403; Conservative 8; Mismatches 251; Indels 26; Gaps 3;
 OTHER INFORMATION: Altered sonic hedgehog protein
 US-09-969-520A-3

Qy 1 MILLARCLLIVLSSLLVCSGLACPGGFGKRRPKKLTPLAYKQIPVNAEKTIGASG 60
 Db 2 LILLARCLFLVILASSLLVCPGLACPGGFGKRRPKKLTPLAYKQIPVNAEKTIGASG 61

Qy 61 RYEKGKISRNSRERFELTPYNPDIIKFDDEENTGADRMLTQRCDKKLNALAISVMNQPGV 120
 Db 62 RYEKGKTRNSRERFELTPYNPDIIKFDDEENTGADRMLTQRCDKKLNALAISVMNQPGV 121

Qy 121 KLRVTEGWDGDGHSESHYEGRAVDTTSDRSKYGMALARVEAGFDWVYYESKAH 180
 Db 122 KLRVTEGWDGDGHSESHYEGRAVDTTSDRSKYGMALARVEAGFDWVYYESKAH 181

Qy 123 KLRVTEGWDGDGHSESHYEGRAVDTTSDRSKYGMALARVEAGFDWVYYESKAH 182

Qy 181 IHCSTKAENSVAAKSGGCPGSATVHLSEGGTKLVKDLSPGDRVLAAHLLFVAPHDNSATEPEASSGSGPPSGALG 300
 Db 182 IHCSTKAENSVAAKSGGCPGSATVHLSEGGTKLVKDLSPGDRVLAAHLLFVAPHDNSATEPEASSGSGPPSGALG 301

Qy 241 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 300
 Db 242 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 301

Qy 243 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 302

Db 244 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 303

Db 245 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 304

Db 246 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 305

Db 247 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 306

Db 248 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 307

Db 249 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 308

Db 250 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 309

Db 251 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 310

Db 252 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 311

Db 253 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 312

Db 254 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 313

Db 255 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 314

Db 256 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 315

Db 257 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 316

Db 258 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 317

Db 259 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 318

Db 260 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 319

Db 261 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 320

Db 262 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 321

Db 263 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 322

Db 264 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 323

Db 265 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 324

Db 266 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 325

Db 267 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 326

Db 268 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 327

Db 269 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 328

Db 270 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 329

Db 271 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 330

Db 272 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 331

Db 273 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 332

Db 274 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 333

Db 275 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 334

Db 276 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 335

Db 277 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 336

Db 278 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 337

Db 279 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 338

Db 280 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 339

Db 281 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 340

Db 282 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 341

Db 283 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 342

Db 284 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 343

Db 285 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 344

Db 286 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 345

Db 287 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 346

Db 288 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 347

Db 289 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 348

Db 290 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 349

Db 291 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 350

Db 292 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 351

Db 293 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 352

Db 294 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 353

Db 295 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 354

Db 296 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 355

Db 297 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 356

Db 298 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 357

Db 299 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 358

Db 300 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 359

Db 301 FLDRDGAKKVKPYIETREPRLLTAAHLLFVAPHDNSATEPEASSGSGPPSGALG 360

RESULT 35
 Sequence 3, Application US/09969520A
 Patent No. US2002017163A1
 GENERAL INFORMATION:
 APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
 APPLICANT: BEACHY, Philip A.
 TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED FILE REFERENCE: JHU1670-1
 CURRENT APPLICATION NUMBER: US/09/969, 520A
 CURRENT FILING DATE: 2002-06-04
 PRIOR APPLICATION NUMBER: US 60/235, 153
 PRIOR FILING DATE: 2000-09-22
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 3
 LENGTH: 437
 TYPE: PRT

RESULT 36
 Sequence 2, Application US/10411927
 Publication No. US20040005602A1
 GENERAL INFORMATION:
 APPLICANT: Jessel, L., Thomas M.
 APPLICANT: Dodd, Jane
 APPLICANT: Roelink, Henk
 APPLICANT: Edlund, Thomas
 TITLE OF INVENTION: DNA ENCODING A VERTEBRATE HOMOLOG OF HEDGEHOG, VH-1
 FILE REFERENCE: 45375seq
 CURRENT APPLICATION NUMBER: US/10/411, 927
 CURRENT FILING DATE: 2003-04-11
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: PatentIn Ver. 2.0 - beta
 SEQ ID NO: 2
 LENGTH: 437
 TYPE: PRT
 ORGANISM: RAT
 US-10-411-927-2

Query Match Score 83.4%; Best Local Similarity 87.5%; Pred. No. 8.7e-12; Matches 405; Conservative 8; Mismatches 22; Indels 28; Gaps 4;
 OTHER INFORMATION: Artificial sequence
 US-10-411-927-2

Qy 1 MILLARCLLIVLSSLLVCSGLACPGGFGKRRPKKLTPLAYKQIPVNAEKTIGASG 60
 Db 2 LILLARCLFLVILASSLLVCPGLACPGGFGKRRPKKLTPLAYKQIPVNAEKTIGASG 61

Qy 61 RYEKGKISRNSRERFELTPYNPDIIKFDDEENTGADRMLTQRCDKKLNALAISVMNQPGV 120
 Db 62 RYEKGKTRNSRERFELTPYNPDIIKFDDEENTGADRMLTQRCDKKLNALAISVMNQPGV 121

RESULT 39
US-09-969-520A-2
Sequence 2, Application US/09969520A
Patent No. US2002017163A1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED FILE REFERENCE: JHU1670-1
CURRENT APPLICATION NUMBER: US/09/969,520A
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: US 60/235,153
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 2
LENGTH: 437
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Altered sonic hedgehog protein

Query Match 83.4%; Score 2058; DB 9; Length 437;
Best Local Similarity 87.2%; Pred. No. 1..3e-17;
Matches 403; Conservative 8; Mismatches 25; Indels 26; Gaps 3;

Qy 1 MILLARCLLIVLVLVSSGLAGPGRGFGKRHKPLTPLAYKQFIPNVAEKTLGASC 60
Db 2 LILLARCFVLASSLLVCPGLACGPGRGFGKRHKPLTPLAYKQFIPNVAEKTLGASC 61

Qy 61 RYEGKISRSRNSERFELTPNPDIFKDENTGADRINTQRCDKLNALAISWNQPGV 120
Db 62 RYEGKTRNSRNSERFELTPNPDIFKDENTGADRINTQRCDKLNALAISWNQPGV 121

Qy 121 KLRVTEGWDGDGHSESHLYGEAVDITTSDRSKYGLMLARLAVEAGFDWVYYESKAH 180
Db 122 KLRVTEGWDGDGHSESHLYGEAVDITTSDRSKYGLMLARLAVEAGFDWVYYESKAH 181

Qy 181 IHCSYKAENSAVAKSGCPFGSATVHLBQGGTKLVKDLSPGDRVLAQDGRLYSDFLT 240
Db 182 IHCSYKAENSAVAKSGCPFGSATVHLBQGGTKLVKDLSPGDRVLAQDGRLYSDFLT 241

Qy 241 FLDRDDGAKVYVETLERERLITTAHLLVAPHD-----SGPTPG 286
Db 242 FLDRDGAKVYVETLERERLITTAHLLVAPHD-----SGPTPG 286

Qy 301 PRALFASRVPRGQRTVVAERDGDRLLPAAVHSVTLSPEAAAGAYPLTAQGTILINRVL 360
Db 287 PSALFASRVPRGQRTVVAERGDDRLLPAAVHSVTLSPEAAAGAYPLTAQGTILINRVL 346

Qy 361 ASCYAVIEEWSWAFAFAPPRLAALALAPARTDGDGGDRGGGRVALTAQGA 420
Db 347 ASCYAVIEEWSWAFAFAPPRLAALALAPARTDGGGGS1P-AQSA 395

Qy 421 ADAPGAGATAGIHWYSQLYQIGTWLDSPLAHPLGMAVKSS 462
Db 396 TEARGAEPTAGIHWYSQLYQIGTWLDSPLAHPLGMAVKSS 437

RESULT 41
US-09-969-520A-4
Sequence 4, Application US/09969520A
SEQ ID NO 4
Patent No. US20020177163A1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED FILE REFERENCE: JHU1670-1
CURRENT APPLICATION NUMBER: US 60/235,153
CURRENT FILING DATE: 2002-06-04

Query Match 83.1%; Score 2052; DB 9; Length 437;

Best Local Similarity 87.0%; Prcd. No. 4.4e-171; Matches 402; Conservative 8; Mismatches 26; Indels 26; Gaps 3;

Qy	1 MILLARCLLIVSLLIVSGLACGPGRGKRRHKPLTPLAYQFIPVNAEKTIGASG 60	Db	122 KERVTEGWDEGHSESHESLHGEAVDITTSDRSKYGMARLAVEAGFDWVYESKAH 181
Qy	2 LILLARCFVLASSLLIVCPGLACGPGRGKRRHKPLTPLAYQFIPVNAEKTIGASG 61	Qy	181 IHC5VKAENSYAAKS5GCCPFSATVHLEQGCTKLVKDLSPDRVLAAADDQGRLLYSDFLT 240
Qy	61 RYEKGKSRNSERFELTPNYPDIIKFDENTGADRMLTQCKXKLNALAISVMNQPGV 120	Db	182 IHC5VKAENSYAAKS5GCCPFSATVHLEQGCTKLVKDLSPDRVLAAADDQGRLLYSDFLT 241
Qy	62 RYEKGKTRNSERFELTPNYPDIIKFDENTGADRMLTQCKXKLNALAISVMNQPGV 121	Qy	181 FLDRDGAKKVFYVIETRPERRLILTAALHLFVAPHNDSATGEPASSGGPPGGGALG 300
Db	121 KLRVTEGWDEGHSESHESLHGEAVDITTSDRSKYGMARLAVEAGFDWVYESKAH 180	Db	182 FLDRDGAKKVFYVIETRPERRLILTAALHLFVAPHNDSATGEPASSGGPPGGGALG 300
Db	122 KLRVTEGWDEGHSESHESLHGEAVDITTSDRSKYGMARLAVEAGFDWVYESKAH 181	Qy	241 FLDRDGAKKVFYVIETRPERRLILTAALHLFVAPHNDSATGEPASSGGPPGGGALG 300
Db	181 IHC5VKAENSYAAKS5GCCPFSATVHLEQGCTKLVKDLSPDRVLAAADDQGRLLYSDFLT 240	Db	242 FLDRDGAKKVFYVIETRPERRLILTAALHLFVAPHNDSATGEPASSGGPPGGGALG 300
Qy	182 IHC5VKAENSYAAKS5GCCPFSATVHLEQGCTKLVKDLSPDRVLAAADDQGRLLYSDFLT 241	Qy	241 FLDRDGAKKVFYVIETRPERRLILTAALHLFVAPHNDSATGEPASSGGPPGGGALG 300
Db	242 FLDRDGAKKVFYVIETRPERRLILTAALHLFVAPHNDSATGEPASSGGPPGGGALG 300	Db	242 FLDRDGAKKVFYVIETRPERRLILTAALHLFVAPHNDSATGEPASSGGPPGGGALG 300
Qy	301 PRALFASRVRGQRVYVVAEEDGDRLLPAVNHSTLSEEAGAYAPLTIQGTILINRVL 360	Db	287 F5ALFASRVRGQRVYVVAEEDGDRLLPAVNHSTLSEEAGAYAPLTIQGTILINRVL 346
Db	287 F5ALFASRVRGQRVYVVAEEDGDRLLPAVNHSTLSEEAGAYAPLTIQGTILINRVL 346	Qy	361 ASCYAVIEEHSAHRAFAPEFLAHALLAALAPARTDRGSGGGDRGGGSRVALTAGA 420
Db	347 ASCYAVIEEHSAHRAFAPEFLAHALLAALAPARTDRGSGGGDRGGGSRVALTAGA 420	Db	347 ASCYAVIEEHSAHRAFAPEFLAHALLAALAPARTDRGSGGGDRGGGSRVALTAGA 420
Qy	421 ADAPGAGATACTIHWYSQLQIGTWILDSEALHPICGMVAKSS 462	Qy	421 ADAPGAGATACTIHWYSQLQIGTWILDSEALHPICGMVAKSS 462
Db	396 TEARGAEPTAGIHWYSQLQIGTWILDSEALHPICGMVAKSS 437	Db	396 TEARGAEPTAGIHWYSQLQIGTWILDSEALHPICGMVAKSS 437
Db	RESULT 43	Db	RESULT 43
Qy	US-09-969-520A-6	Qy	US-09-969-520A-6
Db	Sequence 6, Application US/09969520A	Db	Sequence 6, Application US/09969520A
Db	Patent No. US202017113A1	Db	Patent No. US202017113A1
Db	GENERAL INFORMATION:	Db	GENERAL INFORMATION:
Db	APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE	Db	APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
Db	APPLICANT: BEACHY, Philip A.	Db	APPLICANT: BEACHY, Philip A.
Db	TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED	Db	TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED
Db	FILE REFERENCE: JHU16010-1	Db	FILE REFERENCE: JHU16010-1
Db	CURRENT APPLICATION NUMBER: US/09/969,520A	Db	CURRENT APPLICATION NUMBER: US/09/969,520A
Db	PRIOR APPLICATION NUMBER: US 60/235,153	Db	PRIOR APPLICATION NUMBER: US 60/235,153
Db	PRIOR FILING DATE: 2000-09-22	Db	PRIOR FILING DATE: 2000-09-22
Db	NUMBER OF SEQ ID NOS: 17	Db	NUMBER OF SEQ ID NOS: 17
Db	SEQ ID NO 6	Db	SEQ ID NO 6
Db	SOFTWARE: PatentIn version 3.1	Db	SOFTWARE: PatentIn version 3.1
Db	OTHER INFORMATION: Altered sonic hedgehog protein	Db	OTHER INFORMATION: Altered sonic hedgehog protein
Db	US-09-969-520A-6	Db	US-09-969-520A-6
Db	Query Match 82.8%; Score 2045; DB 9; Length 437;	Db	Query Match 82.8%; Score 2045; DB 9; Length 437;
Db	Best Local Similarity 86.6%; Pred. No. 1.8e-170; Matches 400; Gaps 3;	Db	Best Local Similarity 86.6%; Pred. No. 1.8e-170; Matches 400; Gaps 3;
Db	LENGTH: 437	Db	LENGTH: 437
Db	TYPE: PRT	Db	TYPE: PRT
Db	ORGANISM: Artificial sequence	Db	ORGANISM: Artificial sequence
Db	FEATURE: Other information	Db	FEATURE: Other information
Db	OTHER INFORMATION: Altered sonic hedgehog protein	Db	OTHER INFORMATION: Altered sonic hedgehog protein
Db	US-09-969-520A-6	Db	US-09-969-520A-6
Db	Query Match 82.8%; Score 2048; DB 9; Length 437;	Db	Query Match 82.8%; Score 2048; DB 9; Length 437;
Db	Best Local Similarity 86.8%; Pred. No. 9.e-171; Matches 27; Indels 26; Gaps 3;	Db	Best Local Similarity 86.8%; Pred. No. 9.e-171; Matches 27; Indels 26; Gaps 3;
Db	Matches 401; Conservative 8; Mismatches 27; Indels 26; Gaps 3;	Db	Matches 401; Conservative 8; Mismatches 27; Indels 26; Gaps 3;
Db	1 MILLARCLLIVSLLIVSGLACGPGRGKRRHKPLTPLAYQFIPVNAEKTIGASG 60	Qy	181 IHC5VKAENSYAAKS5GCCPFSATVHLEQGCTKLVKDLSPDRVLAAADDQGRLLYSDFLT 240
Db	2 LILLARCFVLASSLLIVCPGLACGPGRGKRRHKPLTPLAYQFIPVNAEKTIGASG 61	Db	182 IHC5VKAENSYAAKS5GCCPFSATVHLEQGCTKLVKDLSPDRVLAAADDQGRLLYSDFLT 241
Qy	61 RYEKGKSRNSERFELTPNYPDIIKFDENTGADRMLTQCKXKLNALAISVMNQPGV 120	Qy	241 FLDRDGAKKVFYVIETRPERRLILTAALHLFVAPHNDSATGEPASSGGPPGGGALG 300
Db	62 RYEKGKTRNSERFELTPNYPDIIKFDENTGADRMLTQCKXKLNALAISVMNQPGV 121	Db	242 FLDRDGAKKVFYVIETRPERRLILTAALHLFVAPHNDSATGEPASSGGPPGGGALG 300
Qy	121 KLRVTEGWDEGHSESHESLHGEAVDITTSDRSKYGMARLAVEAGFDWVYESKAH 180	Qy	301 PRALFASRVRGQRVYVVAEEDGDRLLPAVNHSTLSEEAGAYAPLTIQGTILINRVL 360
Db	61 RYEKGKSRNSERFELTPNYPDIIKFDENTGADRMLTQCKXKLNALAISVMNQPGV 120	Db	302 PRALFASRVRGQRVYVVAEEDGDRLLPAVNHSTLSEEAGAYAPLTIQGTILINRVL 346
Db	62 RYEKGKTRNSERFELTPNYPDIIKFDENTGADRMLTQCKXKLNALAISVMNQPGV 121	Qy	287 PSALFASVRPGQRVYVVAEEDGDRLLPAVNHSTLSEEAGAYAPLTIQGTILINRVL 346
Qy	121 KLRVTEGWDEGHSESHESLHGEAVDITTSDRSKYGMARLAVEAGFDWVYESKAH 180	Db	242 PSALFASVRPGQRVYVVAEEDGDRLLPAVNHSTLSEEAGAYAPLTIQGTILINRVL 346

RESULT 44
 US 09-969-520A-7
 Sequence 7, Application US/09969520A
 PRIORITY NUMBER: US 2002017163A1
 GENERAL INFORMATION:
 APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
 TITLE OF INVENTION: METHOD OF USE OF SONIC HEDGEHOG PROTEIN AS A LIGAND FOR PATCHED FILE REFERENCE: JHU1670-1
 CURRENT FILING DATE: 2002-06-04
 PRIORITY NUMBER: US 09/969,520A
 NUMBER OF SEQ ID NOS: 17
 SEQ ID NO 7
 LENGTH: 437
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Altered sonic hedgehog protein
 US-09-969-520A-5

Query Match Score 2036; DB 9; Length 437;
 Best Local Similarity 86.1%; Prod. No. 3.4e-18;
 Matches 398; Conservative 10; Mismatches 28; Indels 26; Gaps 3;

Qy 1 MLLIARCLLVLVSSLLVYSGIACPGFGRGRRHPKKLTPLAYKOFITPIVNAEKTIGASG 60
 Db 2 LLLIARCLVILVASSLLVYSGIACPGFGRGRRHPKKLTPLAYKOFITPIVNAEKTIGASG 61

Qy 61 RYEKGKISRNSRERPFELTPNYPDIIKFDEBENTGADRINTQRCKDNLALATSMVNQNPVG 120
 Db 62 RYEKGKTRNSRERPFALITPNYPDIIKFDEBENTGADRINTQRCKDNLALATSMVNQNPVG 121

Qy 121 KLRVTEGWDDEGHSESHYEGRAVDTTSDRSKYGMALARVEAGFDWVYYESKAH 180
 Db 122 KLRVTEGWDDEGHSESHYEGRAVDTTSDRSKYGMALARVEAGFDWVYYESKAH 181

Qy 181 IHCSYKAENSAVAKSGCCPGSATVHLEQGGTTLKVLSPGDRVLADDQGRLLYSDFLT 240
 Db 182 IHCSYKTAANSAVAAAGCPCPGSATVHLEQGGTTLKVLSPGDRVLADDQGRLLYSDFLT 241

Qy 241 FLDRDGAKKVFTYITERPRLLTIAHHLLVAPNDSATGEPEASSGSGPPSGCALG 300
 Db 242 FLDRDGAKKVFTYITERPRLLTIAHHLLVAPND-----SGPTPG 286

Qy 301 PRALFASRVPGQRYVVAERDGDRRLPAAVESVTLSSEAAGAYAPITAQGTILINRVL 360
 Db 302 PSALFASRVPGQRYVVAERGDGRRLPAAVHSVTLSSEAAGAYAPITAHTGTLINRVL 346

Qy 361 ASCYAVIEEHSAWAHAFAPRLAHALLAALAPARTDGSGGDRGGGRVALTAPGA 420
 Db 347 ASCYAVIEEHSAWAHAFAPRLAHALLAALAPARTDGSGGSIP-AQSA 395

Qy 421 ADAPGAGATAGIHWYSQQLYQIGTWLSEALHPIGMATKSS 462
 Db 396 TEARGAEPAFPAGIHWYSQQLYHGTWLDSETMPLGMATKSS 437

RESULT 45
 US 09-969-520A-10
 Sequence 10, Application US/08900220C
 Publication No. US 00-0045206A1
 GENERAL INFORMATION:
 APPLICANT: Miao, Ningning
 Wang, Monica
 Mahanthappa, Nagesh K.
 Pang, Kevin
 Jin, Ping
 TITLE OF INVENTION: Method of Treating Dopaminergic and GABA-nergic Disorders
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESS: FOLLY, HOAG & ELLIOT LLP
 STREET: ONE POST OFFICE SQUARE

RESULT 46
 US 09-900-220C-10
 Sequence 10, Application US/08900220C
 Publication No. US 00-0045206A1
 GENERAL INFORMATION:
 APPLICANT: Miao, Ningning
 Wang, Monica
 Mahanthappa, Nagesh K.
 Pang, Kevin
 Jin, Ping
 TITLE OF INVENTION: Method of Treating Dopaminergic and GABA-nergic Disorders
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESS: FOLLY, HOAG & ELLIOT LLP
 STREET: ONE POST OFFICE SQUARE

RESULT 45
 US 09-969-520A-5
 Sequence 5, Application US/09969520A

CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII (text)

CURRENT APPLICATION DATA:
 FILING DATE: 24-Jul-1997
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent. Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE DOCKET NUMBER: ONV-044.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 832-1000
 TELEFAX: (617) 832-7000
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 425 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-08-900-220C-10

Query Match 73.2%; Score 1807; DB 8; Length 425;
 Best Local Similarity 77.8%; Pred. No. 1.2e-149;
 Matches 361; Conservative 37; Indels 44; Gaps 6;

Db 1 MLLARLLVLYSSLIVCSLAGFGIGRKRRPKKLTPLAYKOFINVAETLGASG 60
 Db 4 MLLTRILVGFLCIALVSSSLTCGPGRIGKRHKPKCLTPLAYQFINTVAETLGASG 63

Qy 61 RYEKGTSRNSERFKELTPNPDIFKDDEENTGADRIMTORCKDNALAISYMNONPCV 120
 Db 64 RYEKGTRNSERFKELTPNPDIFKDDEENTGADRIMTORCKDNALAISYMNONPCV 123

Qy 121 KLRVTEGWDDEGHHSSELHVEGRADITTSDRSKYGMRLARAVEAGFDWYYYESKAH 180
 Db 124 KLRVTEGWDDEGHHSSELHVEGRADITTSDRSKYGMRLARAVEAGFDWYYYESKAH 183

Qy 181 IHCVKTAENSYAKSGCGFPGSATVHLEQSGTKLKDLSGDRYLAAADDQGRILYSDFLT 240
 Db 184 IHCVKTAENSYAKSGCFPSATVHLEQSGTKLKDLSGDRYLAAADDQGRILYSDFLT 243

Qy 241 FLDRDDGAKVYFYIETREPERLITTAHILLFVAP-HNDS-ATGEPEASSGSGPPSGCA 298
 Db 244 FLDRMSSRKFYFYIETRQPARRLITTAHILLFVAP-QNHNEAT----STSG---- 292

Qy 299 LGPRALFASRVRPGQRYVVAERGDDRLLPAVSVTSLBEANGAYAPITAQGTILINR 358
 Db 293 --QALPASNYKPGQRYVVLGE-GQQQLLPASVHSVSLREASAYAPITAQGTILINR 347

Qy 359 VLASCYAVIEBSWAIRAFAPRLLAHALLAALAPARTDRGSDGGDRGGGRVALTP 418
 Db 348 VLASCYAVIEBSWAIRAFAPRLLAHALLAALAPARTDRGSDGGDRGGGRVALTP 418
 -CP 381

Qy 419 GAADAPGAGATAGIHNYSQLYQIGTWLDSBAILPHGLMAVKSS 462
 Db 382 DGAIPTAATTGIRVSRLLRIGSVWLDALPHGLMAVKSS 425

RESULT 47
 US-08-954-771-B
 Sequence 8, Application US/08954771
 Publication No. US2003054437A1
 General Information:
 Applicant: Ingham, Phillip W.
 Applicant: McMahon, Andrew P.

Qy 359 VLASCYAVIEEHSWAHRAFAPEERLAHALLAALAPARTDRGGDGGDRGGGRVALTAP 418
 Db 348 VLASCYAVIEEHSWAHRAFAPEERLAQCLLAA-----CP 381

Qy 419 GADAPAGATAGIHWYQOLLYQIGTMWLDSEAHLPGMVKSS 462
 Db 382 DGAIPTAATTGIGHWSRLLYRIGSMWLDGHALHPGMVAPAS 425

RESULT 48
 US-08-462-386D-8
 Sequence 8, Application US/08462386D
 GENERAL INFORMATION:
 APPLICANT: Ingham, Phillip W.
 PUBLICATION NO. US20030186357A1
 APPLICANT: McMahon, Andrew P.
 APPLICANT: Tabin, Clifford J.
 TITLE OF INVENTION: Vertebrate Tissue Pattern-Inducing
 TITLE OF INVENTION: Proteins and Uses Related Thereto
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESS: LAHIVE & COCKFIELD
 STREET: 60 State Street, Suite 510
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII (text)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/462,386D
 FILING DATE: 5-JUNE-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/435,093
 FILING DATE: 4-MAY-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/356,060
 FILING DATE: 14-DEC-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/176,427
 FILING DATE: 30-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: HMI-006CP3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 8:
 SEQENCE CHARACTERISTICS:
 LENGTH: 425 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-462-386D-8

Db 124 KLRVTEGWDGHSEESLHYEGRAVDTITSDRDSKYGMLARLAVEAGFDWVYYESKAH 183
 Qy 181 IHCSYKAENSAAKSGCFCPGSATVHLBQGTTKLVKLDSPGDRVLAADDQGRLLYSDPLT 240
 Db 184 IHCSYKAENSAAKSGCFCPGSATVHLHGTTKLVKLDSPGDRVLAADDQGRLLYSDPLT 243
 Qy 241 FLDRDGAKKVYVIEPRERLTAAHLLFVAP-HNDS-ATGPEAASSGSOPSGGA 298
 Db 244 FLDRMDSRKLFVYIETRQPRARLLTAAHLLFVAP-QCHNOSEATG----STSG---- 292

Qy 299 LGPRLAFASRVRPGORYVVAERDGERLPPAVHSTVLSEAGAYAPLTQAGTILINR 358
 Db 293 --QALFAASNVKEGQTVLGE-GGQQLPASVSYLREEASGAYAPLTQAGTILINR 347

Qy 359 VLASCYAVIEEHSWAHRAFAPEERLAHALLAALAPARTDRGGDGGGRVALTAP 418
 Db 348 VLASCYAVIEEHSWAHRAFAPEERLAQCLLAA-----CP 381

Qy 419 GAADAPAGATAGIHWYSQIYQIGTWWILDSEALPHPMVGMVKSS 462
 Db 382 DGATPTAAITTGHWYSRLLYRIGSMWLDGHALHPGMVAPAS 425

RESLT 49
 US-09-021-660A-34
 ; Sequence 34, Application US/09021660A
 ; Patent No. US2001041668A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baron, M.
 ; APPLICANT: Barrington, S.
 ; APPLICANT: Belauhoff, M.
 ; TITLE OF INVENTION: METHODS FOR MODULATING HEMATOPOIESIS AND VASCULAR
 ; GROWTH
 ; FILE REFERENCE: HU1-P01-060
 ; CURRENT APPLICATION NUMBER: US/09/021,660A
 ; CURRENT FILING DATE: 2001-08-27
 ; PRIOR APPLICATION NUMBER: 01/037,513
 ; PRIOR FILING DATE: 1997-02-10
 ; PRIOR APPLICATION NUMBER: 60/049,763
 ; PRIOR FILING DATE: 1997-06-16
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 34
 ; LENGTH: 425
 ; TYPE: PRT
 ; ORGANISM: Gallus gallus
 ; US-09-021-660A-34

Query Match Score 1807; DB 9; Length 425;
 Best Local Similarity 73.2%; Pred. No. 1.2e-149;
 Matches 361; Conservative 22; Mismatches 37; Indels 44; Gaps 6;

Qy 1 MLLARCLLIVSSLLVCGSLACGPGRGFGRHRPKLTPPLAYKFIPVNAEKTGLGSG 60
 Db 4 MLLTRILLVFGFICLVLVSSGLTCGPGRGFGRHRPKLTPPLAYKFIPVNAEKTGLGSG 63

Qy 61 RYEKGKSRNSERFKELTBYNPDPDIFKDENTGADRMTQCDKLNALAISVMNQPGV 120
 Db 64 RYEKGKTRNSERFKELTBYNPDPDIFKDENTGADRMTQCDKLNALAISVMNQPGV 123

Qy 121 KLRVTEGWDGHSEESLHYEGRAVDTITSDRDSKYGMLARLAVEAGFDWVYYESKAH 180
 Db 124 KLRVTEGWDGHSEESLHYEGRAVDTITSDRDSKYGMLARLAVEAGFDWVYYESKAH 183

Qy 1 MLLARCLLIVSSLLVCGSLACGPGRGFGRHRPKLTPPLAYKFIPVNAEKTGLGSG 60
 Db 4 MLLTRILLVFGFICLVLVSSGLTCGPGRGFGRHRPKLTPPLAYKFIPVNAEKTGLGSG 63

Qy 61 RYEKGKSRNSERFKELTBYNPDPDIFKDENTGADRMTQCDKLNALAISVMNQPGV 120
 Db 64 RYEKGKTRNSERFKELTBYNPDPDIFKDENTGADRMTQCDKLNALAISVMNQPGV 123

Qy 121 KLRVTEGWDGHSEESLHYEGRAVDTITSDRDSKYGMLARLAVEAGFDWVYYESKAH 180

Qy 299 LGPRALFAASRVPGGORYVVAERDGDRLLLPAAYHSVTISEEAGAYAAPLTAQGTILINR 358
 Db 293 --QALFASNYKPGQRYVGE-- GQQQLIPASVHSVREESGATAFLPQGTILINR 347
 Qy 359 VLASCYAVIEEWSWAHRAAFPLAHALLAALAPARTDRGGSDGGDRGGGRVALTAP 418
 Db 348 VLASCYAVIEEWSWAHRAAFPLAQGLLAAL-----CP 381
 Qy 419 GAADAPGAGATAGIHWYSQLYQITWLJUDSEATHPLGMAVKSS 462
 Db 382 DGAIDPTAAATTGIGHWYSRLLYRGSWVJDGDALHPGMVAPAS 425

RESULT 50
 US-09-151-999-10
 Sequence 10, Application US/09151999
 GENERAL INFORMATION:
 APPLICANT: Wang, Elizabeth
 TITLE OF INVENTION: REGULATION OF EPITHELIAL TISSUE BY HEDGEHOG-LIKE
 FILE REFERENCE: ONV-031.02
 CURRENT APPLICATION NUMBER: US/09/151,999
 EARLIER APPLICATION NUMBER: 08/955,552
 NUMBER OF SEQ ID NOS: 28
 SEQ ID NO 10
 LENGTH: 425
 TYPE: PRT
 ORGANISM: chicken Shh
 US-09-151-999-10

Query Match 73.2%; Score 1807; DB 9; Length 425;
 Best Local Similarity 77.8%; Pred. No. 1_2e-149; Gaps 6;
 Matches 361; Conservative 22; Mismatches 44; Indels 44; Gaps 6;
 Qy 1 MLLARCLLIVLYSSILVCSGLACGPGRGFGRHKPKLTLPLAYQFIPNVAKTKLGSG 60
 Db 4 MLLTRLLVFCIALVLSGLTCPGRGIGKRHKPKLTLPLAYQFIPNVAEKTGSG 63
 Qy 61 RYEKGKISRSNTERFKELTPYNPD1IFKDENTGADRLMQRCKDKLNALAISYMNONPGV 120
 Db 64 RYEKGKISTRFERFKELTPYNPD1IFKDENTGADRLMQRCKDKLNALAIYMNONPGV 123
 Qy 121 KLRVTEGWDDEGHSESLHYEGRAVDITSDRRSKYMNLARIAVEGFDWVYESKAH 180
 Db 124 KLRVTEGWDDEGHSESLHYEGRAVDITSDRRSKYMNLARIAVEGFDWVYESKAH 183
 Qy 181 IHCSYKAENSYAAKSGCFFPSATVHLEQGTLVLDLSFGDRYLAADDQGRLLYSDPLT 240
 Db 184 IHCSYKAENSYAAKSGCFFPSATVHLEQGTLVLDLSFGDRYLAADDGRLLYSDPLT 243
 Qy 241 FLDRDGAKKVFYVIETREPRLILTAAILLFVAP-HNDS -ATGEPEASSGSGPPSGCA 298
 Db 244 FLDRMDSRKLYVIETRQPRLILTAAILLFVAPQHQSEATG---STSG---- 292
 Qy 299 LGPRALFAASRVPGGORYVVAERDGDRLLLPAAYHSVTISEEAGAYAAPLTAQGTILINR 358
 Db 293 --QALFASNYKPGQRYVGE-- GQQQLIPASVHSVREESGATAFLPQGTILINR 347
 Qy 359 VLASCYAVIEEWSWAHRAAFPLAHALLAALAPARTDRGGSDGGDRGGGRVALTAP 418
 Db 348 VLASCYAVIEEWSWAHRAAFPLAQGLLAAL-----CP 381
 Qy 419 GAADAPGAGATAGIHWYSQLYQITWLJUDSEATHPLGMAVKSS 462
 Db 382 DGAIDPTAAATTGIGHWYSRLLYRGSWVJDGDALHPGMVAPAS 425

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OM protein - protein search, using sw model.

Run on: March 29, 2004, 18:28:04 ; Search time 20 Seconds
(without alignments)

2284.549 Million cell updates/sec

Title: US-09-883-848A-15
Perfect score: 2469
Sequence: 1 MLLARCLLVLVSSILVCS GMAYKSSXSXRGAGGGAREGA 475

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 150 summaries

Database : PIR7B:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.62	83.5	437	2 A49425	Sonic hedgehog protein homolog v patterning protein hedgehog homolog v morphogen Xhh Prec sonic hedgehog protein Desert hedgehog protein Indian hedgehog protein segment polarity protein hedgehog - desert hedgehog - hypothetical prote myosin heavy chain hypothetical prote hypothetical prote fibroin - Chinese fibroin hypothetical prote probable secreted T-box protein 2 - hypothetical glyci [protein-PII] urid hypothetical prote hypothetical glyci hypothetical protein sarcalumenin precursor hydroxy-tRNA synthase related to spore C integrin alpha-7 C probable polypeptide conserved hypothetical subtilisin-like protein sarcolumenin
2	20.60	83.4	437	2 B53193	76.5
3	18.07	73.2	425	2 A49424	76.5
4	15.06	61.0	418	2 A53193	77.5
5	14.98	60.7	444	2 S56765	78.5
6	14.59	59.1	415	2 A49426	79.5
7	11.83	47.9	396	2 B49425	80.5
8	10.75	41.6	336	2 C49425	81.5
9	8.90	36.0	471	2 A46400	82.5
10	4.49	18.2	94	2 G02735	83.5
11	15.95	6.5	615	2 T29550	84.5
12	12.49	6.0	1207	2 T23754	85.5
13	13.85	5.6	1226	2 T31328	86.5
14	13.55	5.5	484	2 T34504	87.5
15	13.45	5.4	481	2 T27665	88.5
16	5.2	1147	1 MWAXIB		89.5
17	12.28	5.2	629	2 T19563	90.5
18	12.65	5.1	1021	2 T23252	91.5
19	123.5	5.0	2639	2 T31328	92.5
20	12.1	4.9	868	2 T22288	93.5
21	11.19	4.8	318	2 T35213	94.5
22	11.85	4.8	702	2 G01840	95.5
23	11.16	4.7	1329	2 E70917	96.5
24	115.5	4.7	940	2 E87250	97.5
25	11.15	4.7	486	2 H87311	98.5
26	11.14	4.6	741	2 G70917	99.5
27	11.11	4.5	333	2 A31065	100.5
28	11.11	4.5	1298	1 EDBB75	101.5
29	11.0	4.5	462	2 T35852	102.5

103	95	904	2	C70559	Score 83.5%; Best Local Similarity 87.0%; Pred. No. 3; 5e-147; Matches 40;	DB-2; Length 437; Conservative	
104	95	974	1	A40213	10; Mismatches 24;	Indels 26; Gaps 3;	
105	95	1122	2	G64987	1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60		
106	94.5	3.8	269	2	T37073	2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61	
107	94.5	3.8	384	2	E70637	61 RYEKGKISRNSERKELTNPYNNPDLIFKOFENTGADRLTQRCKDKUNALAI5VNQPGV 120	
108	94.5	3.8	454	2	B70632	62 RYEKGKISTRNSERKELTNPYNNPDLIFKOFENTGADRLTQRCKDKUNALAI5VNQPGV 121	
109	94.5	3.8	660	2	G83612	121 KLRVTEGMDEDGHSESELHYEGRAVDITTSDRSKYGMMLARAVAGEDFVVYESKAH 180	
110	94.5	3.8	716	2	T34191	122 KLRVTEGMDEDGHSESELHYEGRAVDITTSDRSKYGMMLARAVAGEDFVVYESKAH 181	
111	94	3.8	1216	2	T37054	122 KLRVTEGMDEDGHSESELHYEGRAVDITTSDRSKYGMMLARAVAGEDFVVYESKAH 181	
112	94	3.8	453	2	T51274	122 KLRVTEGMDEDGHSESELHYEGRAVDITTSDRSKYGMMLARAVAGEDFVVYESKAH 181	
113	94	3.8	478	2	B87598	122 KLRVTEGMDEDGHSESELHYEGRAVDITTSDRSKYGMMLARAVAGEDFVVYESKAH 181	
114	94	3.8	526	2	T36033	122 KLRVTEGMDEDGHSESELHYEGRAVDITTSDRSKYGMMLARAVAGEDFVVYESKAH 181	
115	94	3.8	672	2	T02411	122 KLRVTEGMDEDGHSESELHYEGRAVDITTSDRSKYGMMLARAVAGEDFVVYESKAH 181	
116	94	3.8	1454	2	A12057	122 KLRVTEGMDEDGHSESELHYEGRAVDITTSDRSKYGMMLARAVAGEDFVVYESKAH 181	
117	94	3.8	1654	2	T02844	122 KLRVTEGMDEDGHSESELHYEGRAVDITTSDRSKYGMMLARAVAGEDFVVYESKAH 181	
118	94	3.8	1784	2	T02844	181 IHCSYKAENSVAAKSGGCPPGSATVHLLEGGTKLVKDOLSPGDRVLAADDQGRLLYSDFLT 240	
119	94	3.8	2183	2	T37218	182 IHCSYKAENSVAAKSGGCPPGSATVHLLEGGTKLVKDOLSPGDRVLAADDQGRLLYSDFLT 241	
120	93.5	3.8	342	2	S18639	182 IHCSYKAENSVAAKSGGCPPGSATVHLLEGGTKLVKDOLSPGDRVLAADDQGRLLYSDFLT 241	
121	93.5	3.8	347	2	T35013	241 FLDRDGAKKVYYIETRPREPLILTAHLLLEVAPINDSARGEPEASSGSGPPSGALG 300	
122	93.5	3.8	376	2	C87481	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
123	93.5	3.8	383	2	T34871	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
124	93.5	3.8	509	2	E70756	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
125	93.5	3.8	558	2	T37056	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
126	93.5	3.8	615	2	H87569	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
127	93.5	3.8	641	1	QQB21	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
128	93.5	3.8	1252	2	T31119	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
129	93.5	3.8	1733	2	B45344	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
130	93	3.8	328	2	G88459	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
131	93	3.8	451	2	D88295	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
132	93	3.8	506	2	S55786	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
133	93	3.8	880	2	H87562	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
134	93	3.8	13056	2	A70934	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
135	93	3.8	1407	2	T28702	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
136	93	3.8	2723	2	T03221	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
137	93	3.8	13055	2	T16580	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
138	92.5	3.7	1227	2	T35236	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
139	92.5	3.7	532	2	E87343	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
140	92.5	3.7	625	2	H98148	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
141	92.5	3.7	651	2	AD3119	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
142	92.5	3.7	1683	2	S38103	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
143	92	3.7	339	2	S20880	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
144	92	3.7	600	2	D8326	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
145	92	3.7	1237	2	A56764	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
146	92	3.7	1616	2	T17884	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
147	92	3.7	1690	2	T35694	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
148	91.5	3.7	4735	2	T17463	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
149	91.5	3.7	170	2	JC2213	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
150	91.5	3.7	354	2	T35380	242 FLDRDEGAKKVYYIEPLRERILTAHLLFVAPINDSARGEPEASSGSGPPSGALG 300	
ALIGNMENTS							
RESULT 1							
A49425	Sonic hedgehog protein precursor - mouse						
C;Species: Mus musculus (house mouse)							
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999							
R;Accession: A49425							
R;Echelard, Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohler, J.; McMahon, J.A.; McManamy, C.; Cell 75, 1417-1430, 1993							
A;Title: Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the induction of the sonic hedgehog gene by sonic hedgehog protein.							
A;Reference number: A49425; PMID:7916661							
A;Accession: A49425							
A;Molecule type: mRNA							
A;Residues: 1-437 <ROE>							
A;Cross-references: GB-L227340; PIDN:AAA20999.1; PID:G452123							
C;Superfamily: sonic hedgehog protein							
RESULT 2							
A;Species: Rattus norvegicus (Norway rat)							
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 10-Dec-1999							
C;Accession: B53193							
R;Roelink, H.; Augsburg, A.; Heemskerk, J.; Korzh, V.; Ruiz i Altada, A.; Cell 76, 761-775, 1994							
A;Title: Floor plate and motor neuron induction by vhh-1, a vertebrate homolog of hedgehog homolog vhh-1 - rat							
A;Reference number: A53193; PMID:8124714							
A;Accession: B53193							
A;Status: preliminary							
A;Molecule type: mRNA							
A;Residue: 1-437 <ROE>							
A;Cross-references: GB-L227340; PIDN:AAA20999.1; PID:G452123							
Query Match 83.4%; Best Local Similarity 87.5%; Matches 405; Conservative							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							
Db 2 LLLIARCLVLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 61							
Query Match 83.4%; Best Local Similarity 87.5%; Pred. No. 4; 9e-147; Matches 22; Indels 28; Gaps 4;							
Qy 1 MLLIARCLLIVLVLVSSGLACPGPRGFGRHRPKRLTPLAYQFIPVNAEKTIGASG 60							

Qy	241	FLDRDGAKKVFYVIETREPRERLLTAHHLFVAPHNSATGEPEASSGSGPPSGGALG	300		RESULT 4
Db	242	FLDEDEGAKRKFVVIETREPRERLLTAHHLFVAPND	286		A53193 hedgehog homolog vhh-1 - zebra fish
Qy	301	PRAFLASVRPGQRVYVVAERGDDRRLIPPAVHSVTLSEAAAGAYAALTAQGTILINRL	360		C;Species: Brachydanio rerio (zebra fish)
Db	287	PSPLFASRTRPGQRVYVVAERGDDRRLIPPAVHSVTLREAAAGAYAALTAQGTILINRL	346		C;Sequence_revision 06-Jan-1995 #text_change 10-Dec-1999
Qy	361	ASCVAVIEHSHWAHRAAFRLAHALLAALAPARTDRGGDSGGDRCGGGRRVALTAP-G	419		C;Accession: A53193
Db	347	ASCVAVIEHSHWAHRAAFRLAHALLAALAPARTD-----GGGG-SIPAPQS	394		R;Roelink, H.; Augerburger, A.; Heemskerk, J.; Korzh, V.; Norlin, S.; Ruiz i Altaba, A.; Title: Floor Plate and motor neuron induction by vhh-1, a vertebrate homolog of hedgehog
Qy	420	AADAPGAGTAGAHHWYSQQLYQIGTWLIDSEALHPLGMNAVKSS	462		A;Reference number: A53193
Db	395	VAEARGGCPPGTHWYSQILLYHIGTWLIDSETLHPLGMNAVKSS	437		A;Accession: A53193
Qy					A;Status: preliminary
Db					A;Molecule type: mRNA
Qy					A;Residue: 1-418 <R0E>
Db					A;Cross-references: GB:L27585; NID:9452159; PID:9452160
					C;Superfamily: sonic hedgehog protein
					Query Match 61.0%; Score 1506; DB 2; Length 418;
					Best Local Similarity 61.5%; Pred. No. 1-96-105;
					Matches 300; Conservative 47; Mismatches 68; Indels 50; Gaps 5;
					1 MLLARCLLIVVSGLAGCPGRGKRPKKTPLAYKOFIPNVAEKTICAGS 60
					1 MRLTRVLLVLSLTVLISLVSGLACGPGRGKRPKKTPLAYKOFIPNVAEKTICAGS 60
					61 RYEKGKISRNSERFRKELTTPNPNPDIKFKDENTGADRLTQRCKDKNLALAI5VNQWQGV 120
					61 RYEKGKTRNSERFRKELTTPNPNPDIKFKDENTGADRLTQRCKDKNLALAI5VNQWQGV 120
					121 KLRVTEGWDDEGHHSSEESLHYEGRADVTTSDRRSKYGMLARLAVAEAGFDWVYYESKAH 180
					121 KLRVTEGWDDEGHHSSEESLHYEGRADVTTSDRRSKYGMLARLAVAEAGFDWVYYESKAH 180
					181 IHCSYKAENSAAKSGCFFGSATVHLEQGGTKLVDKDLSPGDRVLAADDQGRILYSDFLT 240
					181 IHCSYKAENSAAKSGCFFGSATVHLEQGGTKLVDKDLSPGDRVLAADDQGRILYSDFLT 240
					Qy 241 FLDRDGAKKVFYVIETREPRERLLTAHHLFVAPHNSATGEPEASSGSGPPSGGALG 300
					Db 241 FTDRDSTTRFVYETOEPEKTTAAHLFVL---DNSTEDHTVM-----286
Qy					Qy 1 MLLARCLLIVVSGLAGCPGRGKRPKKTPLAYKOFIPNVAEKTICAGS 60
Db					Db 4 MLLTRVLLVLSLTVLISLVSGLACGPGRGKRPKKTPLAYKOFIPNVAEKTICAGS 63
Qy					Qy 61 RYEKGKISRNSERFRKELTTPNPNPDIKFKDENTGADRLTQRCKDKNLALAI5VNQWQGV 120
Db					Db 64 RYEKGKTRNSERFRKELTTPNPNPDIKFKDENTGADRLTQRCKDKNLALAI5VNQWQGV 123
Qy					Qy 121 KLRVTEGWDDEGHHSSEESLHYEGRADVTTSDRRSKYGMLARLAVAEAGFDWVYYESKAH 180
Db					Db 124 KLRVTEGWDDEGHHSSEESLHYEGRADVTTSDRRSKYGMLARLAVAEAGFDWVYYESKAH 183
Qy					Qy 181 IHCSYKAENSAAKSGCFFGSATVHLEQGGTKLVDKDLSPGDRVLAADDQGRILYSDFLT 240
Db					Db 184 IHCSYKAENSAAKSGCFFGSATVHLEQGGTKLVDKDLSPGDRVLAADDQGRILYSDFLT 243
Qy					RESULT 5
Db					S56765 morphogen Xhh precursor - African clawed frog
Qy					C;Species: Xenopus laevis (African clawed frog)
Db					C;Date: 10-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
Qy					C;Accession: S56765
Db					R;Stolow, M.A.; Shi, Y.B.
Qy					Nucleic Acids Res. 22, 2555-2562, 1995
Db					A;Title: Xenopus sonic hedgehog as a potential morphogen during embryogenesis and thymo-
Qy					A;Reference number: S56765; PMID:9335719; NID:9790937
Db					A;Status: Preliminary; nucleic acid sequence not shown
Qy					A;Molecule type: mRNA
Db					A;Residues: 1-444 <STO>
Qy					C;Cross-references: EMBL:L39213; NID:9790937; PIDN: AAC42227.1; PID:9790938
Db					C;Superfamily: sonic hedgehog protein
Qy					Query Match 60.7%; Score 149B; DB 2; Length 444;
Db					Best Local Similarity 64.1%; Pred. No. B.2e-05;

RESULT 6

A4 9426 sonic hedgehog gene shh protein - zebra fish
N; alternate names: local cell-cell interaction signaling protein
C; species: Brachydanio rerio (zebra fish)
C; accession: A49426
R; Krauss, S.; Concoeder, J. P.; Ingham, P. W.
Cell 75, 143-144, 1993
A; Title: A functionally conserved homolog of the Drosophila segment polarity gene hh is
A; Reference number: A49426; PMID: 826519
A; Accession: A49426; MUID: 9404335; PMID: 9404335
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Residues: 1-415 (KRAA)
A; Experimental source: embryo
A; Note: sequence extracted from NCBI backbone (NCBIP:142459)
C; Superfamily: sonic hedgehog protein

Query Match Score 59.1%; Length 415;
Best Local Similarity 64.3%; Pred. No. 6.4e-10;
Matches 295; Conservative 47; Mismatches 73; Indels 44; Gaps 6;

Qy 1 MLLIARCLLIVLSSLLIVSGLACGGTGGFKRRPKKLTPLAYKOFIPVNAEKTIGASG 60
Db 1 MRLJTRVLLVSLLTLSSLLIVSGLACGGTGGFKRRPKKLTPLAYKOFIPVNAEKTIGASG 60
Qy 60 RYEGKISRSNTERFKELTTPNYPDIFKDEENTGADRMLTORCKDKLNALAIYSMNQPGV 120
Db 61 RYEGKISRSNTERFKELTTPNYPDIFKDEENTGADRMLTORCKDKLNALAIYSMNQPGV 120
Db 120 KLRVTEGMDGHSEESHYEGRAVDITTSDRDSKYGMLARLAVEAGFDWVYYYESKA 179
Qy 121 KLRVTEGMDGHSEESHYEGRAVDITTSDRDSKYGMLGRLAVEAGFDWVYYYESKA 180
Qy 180 HTHCSVKAAENSYBAKSGCCFPGSATVLEOGGTLYKDLSPGDRVLAADPOGRLLYSDFL 239
Db 181 HTHCSVKAAENSYVAAKSGCCFPGARVNVEFGTKAVKDLSPGDRVLSDPGNLILYSDFL 240
Qy 240 TELDRDGAKKVYVIEPREPRERLITAHHHLVEPHNDSATGEPEASSSGGPPSGGAL 299
Db 241 MFIDQERDVKLPVVIETISQ--RKIRUTAHHLFVAQ----TWNIGTR 282
Qy 300 GPRALFAVRPQRQVTVAAERGDRRLPAAVHSVTLSSEAAGAYAPLTAQGTILINRY 359
Db 283 SFKSVFAASNIQPEBLVITADPK--TMTLKVAVKVEKVDL-EEDPTGAAPLTAHGTIVIDQV 339
Qy 360 LASCYAVIEEHSWAHRAAPFLAHALLAALAPARTDGGDGGGGGGG-----411
Db 344 LASCYAVIEEHTWAHLAPAPLRFGMSSLYSPR-----DSSPSPGLQPHHQVD 388
Qy 412 -----RVALTAGAAGATAAGIHWY SOLIYQITWLSDSEALHPLGAHKSS 462
Db 389 LQSHHQVDLQSHHQVDLQSHHQLEGIHWY SOLIYQITWLSDNSLHPLGMATKSS 444
Qy 241 FLDRDGAKKVYVIEPREPRERLITAHHHLVEPHNDSATGEPEASSSGGPP-SGGAL 299
Db 242 FLDRDGAKKVYVIEPREPRERLITAHHHLVEPHNDSATGEPEASSSGGPP-SGGAL 299
Qy 241 IHC SYKAENSYVAAKSGCCFPGSATVLEOGGTLYKLVQDRLSPGDRVLAADQGRLLYSDFL 240
Db 182 IHVSYRADSLAVRAGFCFGNATVRSLSGERGLREHRGDWLALAAGRVPPTVLU 241
Qy 241 FLDRDGAKKVYVIEPREPRERLITAHHHLVEPHNDSATGEPEASSSGGPP-SGGAL 299
Db 242 FLDRDGAKKVYVIEPREPRERLITAHHHLVEPHNDSATGEPEASSSGGPP-SGGAL 299
Qy 300 GPRAFLASRVRPQRQVYVAAERGDRRLPAATHSVTLSSEAAGAYAPLTAQGTILINRV 359
Db 287 AP--VFAARRLRAQDSVLA---PGDDALQFARVARA-REEAVGVFAPLTAHGTLLNDV 339
Qy 360 LASCYAVIEEHSWAHRAAPFLAHALLAALAPARTDGGDGGGRVALTARG 419
Db 340 LASCYAVIEEHSWAHRAAPFLAHALLAALAPARTDGGDGGGRVALTARG 419
Qy 420 AADAPAGATAGIHWY SOLIYQITWLSDSEALHPLGAHKSS 447
Db 373 GAVQP----TGMHNTSRLLYRABELM 395

RESULT 8
 Indian hedgehog protein - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: C49425
 C;Accession: C49425
 R;Echelard, Y.; Epstein, D.J.; St-Jacques, B.; Shen, L.; Mohier, J.; McMahon, J.A.; McMahon, R.; Lees, J.J.; von Kessler, D.P.; Parks, S.; Beachy, P.A.
 A;Title: Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the regulation of limb development by regulating the expression of genes encoding sonic hedgehog and other proteins.
 A;Reference number: A49425; MUID:94094334; PMID:7916661
 A;Accession: C49425
 A;Status: preliminary
 A;Residues: 1-336 <ECH>
 A;Cross-references: GB:X76291
 C;Superfamily: sonic hedgehog protein
 A;Molecule type: mRNA
 A;Cross-references: 1-471 <EEB>
 A;Note: sequence extracted from NCBI backbone (NCBIP:115418)

A;Accession: JN0501
 A;Molecule type: mRNA
 A;Cross-references: 1-471 <TAS>
 A;Note: it is uncertain whether Met-1 or Met-51 is the initiator
 A;Note: intron positions were determined from partial DNA sequence
 R;Lee, J.J.; von Kessler, D.P.; Parks, S.; Beachy, P.A.
 Cell 71, 33-50, 1992
 A;Title: Secreted and localized transcription suggest a role in positional signaling for sonic hedgehog protein.
 A;Reference number: A43480; MUID:93008241; PMID:1394430
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: DNA
 A;Cross-references: GB:L02793; NID:9157609; PID:9157610
 A;Residues: 1-471 <EEB>
 A;Note: sequence extracted from NCBI backbone (NCBIP:115418)

A;Gene: hh
 A;Cross-references: FlyBase:FBgn0004644
 A;Introns: 160/3; 248/1
 C;Superfamily: sonic hedgehog protein
 C;Keywords: transmembrane protein
 F;62-82/Domain: transmembrane #status predicted <TMM>

Query Match	Score	Length	DB	DB 2	Length	471:
Best Local Similarity	41.6%	DB 2;				
Matches	54.6%	Pred. No.	1.2e-69;			
218: Conservative	39;	Mismatches	77;	Indels	65;	Gaps 8;
Qy	71	ERFKELTPNPYNDIIFKDEENTGADRILMQRCKDKLNLALISMWNQPGKLRVTEGWD	130			
Db	1	ERFKELTPNPYNDIIFKDEENTGADRILMQRCKDKLNLALISMWNQPGKLRVTEGRD	60			
Qy	131	DGHHSSESHLEHYEGRAVDITTSDRDSESKYGMALARAVEAGFDWNTYESKAHISSVZENS	190			
Db	61	DGHHSSESHLEHYEGRAVDITTSDRDSESKYGMALARAVEAGFDWNTYESKAHISSVZENS	120			
Qy	191	VAAKSGGCFFPSATVHLEQGTLVLDLGDRVLAADDQGRLLYSDPFLTFDLDDGAKK	250			
Db	121	AAAKTGGCPAGAQVRLENGervalSAVPGDVRVLAGEDGTPTFSVDLJIFDREPNRLR	180			
Qy	251	VFVVIETREPERLILITAHHLFVAPHNDTSATGEPEAASSGSPGSSGAIGPRAFLASRVR	310			
Db	181	AFQVIETQDPPLRLLTAHHLFIA---DNHT-EPAAHF---RATFASHVQ	224			
Qy	311	PQGRVYVAERDGDRRLPAVHSTVLSERAAGAYAPLTAQGTTILINVLASYAVIEEH	370			
Db	225	PQGYVIV---SGVPOLQPARVAAS-TYHALGSAPLPRHGTVIVEDVASCRAAVADH	279			
Qy	371	SWAHRFAFPFLAHALL-AALAPATDRCGDDSGGGDRGGGGRVALTAGAADAAPGAGAT	429			
Db	280	HIAQLAFAWPFLRFPSLAWGSMTPSE-----	304			
Qy	430	AGIHWYSQLYQIGWMLLSEALHLMGMVKSSXSRGAG	468			
Db	305	-GVHSTPQMLYRLGRULLEESTFHPLGMS-----GAG	335			

RESULT 9
 segment polarity protein hedgehog - fruit fly (Drosophila melanogaster)
 N;Alternate names: hh protein
 C;Species: Drosophila melanogaster
 C;Accession: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 10-Dec-1999
 C;Accession: A46400; JN0501; A43480
 R;Tabata, T.; Baton, S.; Kornberg, T.B.
 Genes Dev. 6, 2635-2645, 1993
 A;Title: The Drosophila hedgehog gene is expressed specifically in posterior compartment
 A;Reference number: A46400; MUID:94040725; PMID:1340474
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-471 <TAB>
 A;Cross-references: GB:866384; NID:9435848; PID:9435849
 A;Experimental source: Oregon-R
 A;Note: sequence extracted from NCBI backbone (NCBIN:138996; NCBIP:138997)
 R;Tashiro, S.; Michiue, T.; Higashijima, S.; Zenno, S.; Ishimaru, S.; Takahashi, F.; Ori Gene 124, 183-189, 1993
 A;Title: Structure and expression of hedgehog, a Drosophila segment-polarity gene require
 A;Reference number: JN0501; MUID:93185922; PMID:8166882
 A;Status: preliminary; translated from GB/EMBL/DDJB

RESULT 10

G02735

desert hedgehog - human (Fragment)

C;Species: Homo sapiens (man)

C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 11-Jan-2000

C;Accession: G02735

R;Drummond, I.A.

submitted to the EMBL Data Library, June 1996

A;Reference number: H01643

A;Accession: G02735

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Cross-references: 1-471 <EEB>

A;Note: sequence extracted from NCBI backbone (NCBIP:115418)

C;Comment: This protein is required for cell-cell communication.

C;Genetics:

A;Gene: hh

A;Cross-references: FlyBase:FBgn0004644

A;Introns: 160/3; 248/1

C;Keywords: transmembrane protein

F;62-82/Domain: transmembrane #status predicted <TMM>

A;Molecule type: mRNA
A;Residues: 1-94 <DRU>
A;Cross-references: ENBL:U59748; NID:91401271; PID:91401271
C;Genetics:
A;Gene: hdhh
C;Superfamily: sonic hedgehog protein

Query Match 18.2%; Score 449; DB 2; Length 94;
Best Local Similarity 84.0%; Pred. No. 6 9e-21; Indels 0; Gaps 0;
Matches 79; Conservative 13; Mismatches 2;

Qy 84 IIFKDEENTGADRIMTOKDKUNALISVMNQWPGYKLRYTEGWDGDGHSEESLHYEG 143
Db 1 IIFRDEENSGADRIMTERRKNGYKLLARLAVEAGFDNWVYGS 94

RESULT 11

T2550 Hypothetical protein ZK377.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T29550
R;Hahn, M.; Hawkins, J.
Submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid ZK377.
A;Reference number: Z26639
A;Accession: P29550
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-615 <NHA>
A;Cross-references: ENBL:U88183; PIDN:AAB52656.1; GSPDB:GN00028; CBSP:ZK377.1
A;Experimental source: strain Bristol N2; clone ZK377
C;Genetics:
A;Gene: CBSP:ZK377.1
A;Map position: X
A;Introns: 46/1; 70/3; 157/2; 176/1; 245/2; 314/3; 402/3; 499/2

RESULT 13

T2405 hypothetical protein R08B4.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T24045
R;White, S.
Submitted to the EMBL Data Library, November 1995
A;Accession: T24045
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-126 <WIL>
A;Cross-references: ENBL:Z268008; PIDN:CAA92000.1; GSPDB:GN00028; CBSP:R08B4.1
C;Genetics:
A;Map Position: X
A;Introns: 53/2; 113/1; 152/3; 204/3; 272/1; 354/1; 389/3; 714/3; 839/3; 877/1; 960/3; 1

Query Match 5.6%; Score 138.5; DB 2; Length 1226;
Best Local Similarity 24.4%; Pred. No. 0 041; Indels 49; Gaps 8;
Matches 50; Conservative 38; Mismatches 68;

Qy 189 NSVAKGCCFPGSATVHLQEGGTXLVKDLSPGDRVLAADDQGRLLYSDFLTFLRDGCA 248
Db 1012 SALVATGACSLD1WV-TTPTGKRMQDQIDIGYVLTADL-KTYFTITLWHRPEK 1069

RESULT 12

T23754 hypothetical protein T05C12.10 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T23754; T2513
R;Thomas, K.
Submitted to the EMBL Data Library, June 1995
A;Reference number: Z19793
A;Accession: T23754
A;Status: preliminary; translated from GB/EMBL/DDBJ

Query Match 6.0%; Score 149; DB 2; Length 1207;
Best Local Similarity 26.5%; Pred. No. 0 0065; Indels 36; Gaps 9;
Matches 55; Conservative 37; Mismatches 82;

Qy 184 SVKAENSVAAKSGG ---CPFGSATVHLQEGGTXLVKDLSPGDRVLAADDQGRLLYSDF 238
Db 942 AVLADTPGAGAACGGRSNCSFASDLSLV-TTIVTGQRNDLQLGTDYVLYPSSGNVLKVEV 1000

Query Match 299 LGPR ALFAASVRVRGQRVTVVAERGDRLRLLPAAVHSVTLSEBA-----AGAYAALT 349
Db 1001 EMFYTHEPPTTRTNVVLVYTKSGR-KLSUTGRHLPPVACGS-----CVEQTMMNPQD 1052

Query Match 1053 VAMRESKYAAEKARKECYCLSIDE SG-----VIADEIVRVGRMTMVGYPSMT 1100
Db 1101 VEGSLIVDGWLSSCFSHLESHS-AHKLIFDF 1130

Db	1114 -----AIFASDIEVGDDCVVLYRKYRQQKIBETITRSV-----RTGIYSPLTNNGRII 1161	Qy	198 CFPGSATVHLEGGTKLVKDLSPGDRVLADDQGRLLYSDFLFLD----RDDGAKKVF 252
Qy	356 INRVIAASCXAVIEEHS-----WAH 374	Db	314 CFPNDAVVNYKEKAVMDLEIGWWEALDEN-----EDITELPVKYWLHRPEOEAE 368
Db	1162 VNDMLASCYSEICQNTLQTTEFFWAY 1186	Qy	253 YVIEETREPPLLTAHHLLVFAPHNDSATGEPEASSSGPPSGGALPRAFSVRG 312
RESULT 14	T34504 hypothetical protein ZK1290.12 - Caenorhabditis elegans	Db	369 PLEFSLDNGETFTLKEHLVY-----TTECRONS-----SELKISWESISAGKVNAG 415
C;Species: Caenorhabditis elegans	C;Accession: T34504	Qy	313 QVRYVVAERDGDRILLPAAYHSVTLSE-----EAAGAYAPLTAQGTILINRVLASCYA 365
C;Accession: T34504	R;Taich, A.	Db	416 DCFYLQSE-----ALTKYRLVEILDIKRVKKTGIVAPMTSQGHLLVNLKHTSCHS 466
Submitted to the EMBL Data Library, July 1995	A;Description: The sequence of <i>C. elegans</i> cosmid ZK1290.	Qy	366 VIEEH 370
A;Accession number: Z23535	A;Accession: T34504	Db	467 EVDH 471
A;Status: Preliminary; translated from GB/EMBL/DDBj	A;Status: Preliminary; translated from GB/EMBL/DDBj	RESULT 16	MWAXTB
A;Residues: 1-84 <TA>	A;Cross-references: EMBL:U21308; PIDN:AAB93321.1; GSDB:GR00020; CBSP:ZK1290.12	Qy	myosin heavy chain IB - Acanthamoeba castellanii
A;Experimental source: strain Bristol N2; Clone ZK1290	C;Species: myosin ATPase (EC 3.6.4.1)	Db	N;Contains: myosin ATPase (EC 3.6.4.1)
C;Genetics:	C;Cross-references: GB: M30780	Qy	C;Sequence revision 30-Sep-1990 #text_change_19-Apr-2002
A;Gene: CBSP:ZK1290.12	C;Accession: JQ0095; B34448	Db	C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change_19-Apr-2002
A;Map position: 2	A;Title: Gene 82; 269-280; 1889	Qy	R;Jung, G.; Schmidt, C.J.; Hammer III, J.A.
A;Introns: 66/3; 124/2; 181/2; 392/1	A;Reference number: JQ0095; PMID:9060816; PMID:251109	Db	Gene 82; 269-280; 1889
Query Match 5.5%; Score 135.5; DB 2; Length 484;	A;Accession: JQ0095	Qy	A;Title: Myosin I heavy-chain genes of <i>Acanthamoeba castellanii</i> : cloning of a second gene
Best Local Similarity 24.5%; Pred. No. 0.021; Mismatches 42; Conservative 46; Indels 35; Gaps 8;	A;Molecule type: DNA	Db	A;Reference number: JQ0095; PMID:9060816; PMID:251109
Matches 46; Cross-references: EMBL:U21308; PIDN:AAB93321.1; GSDB:GR00020; CBSP:ZK1290.12	A;Residues: 1-114 <JUN>	Qy	A;Cross-references: GB: M30780
A;Experimental source: strain Bristol N2; Clone ZK1290	C;Keywords: actin binding; ATP; hydrolase; nucleotide binding; P-loop; phosphoprotein;	Db	A;Note: this organism expresses at least three isoforms of myosin I heavy-chain, encode gene MIB, whereas the protein previously identified as MIB is the product of gene MI
C;Genetics:	F:12-664/Domain: myosin motor domain homology <MMOT>	Qy	R;Brzeska, H.; Lynch, T.J.; Martin, B.; Korn, E.D.
A;Gene: CBSP:ZK1290.12	F:103-110/Region: nucleotide-binding motif A (P-loop)	Db	J. Biol. Chem. 264: 19340-19348, 1989
A;Map position: 2	F:552-573/Region: actin binding #status Predicted	Qy	A;Title: The localization and sequence of the phosphorylation sites of <i>Acanthamoeba</i> myo
A;Introns: 66/3; 124/2; 181/2; 392/1	F:698-714/Region: carboxyl-terminal <CD>	Db	A;Reference number: A34448; PMID:9037074; PMID:2530230
Query Match 5.5%; Score 135.5; DB 2; Length 484;	A;Gene: MIB	Qy	A;Title: In this protein, the coiled-coil rod-like region found in many myosin heavy
Best Local Similarity 24.5%; Pred. No. 0.021; Mismatches 42; Conservative 46; Indels 35; Gaps 8;	A;Introns: 1/3; 39/3; 102/2; 135/3; 183/3; 212/1; 291/3; 379/3; 492/3; 617/2; 649/3; 78	Db	protein is globular and does not self-assemble into filaments.
Matches 46; Cross-references: EMBL:U21308; PIDN:AAB93321.1; GSDB:GR00020; CBSP:ZK1290.12	C;Super-family: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 homolog	Qy	C;Genetics: SH3 homology <SH3>
A;Experimental source: strain Bristol N2; Clone ZK1290	C;Keywords: actin binding; ATP; hydrolase; nucleotide binding; P-loop; phosphoprotein;	Db	F:910-1094/Region: basic
C;Genetics:	F:1097-114/Region: SH3 homology <SH3>	Qy	F:910-1094/Region: alanine/glycine/proline-rich
A;Gene: CBSP:ZK1290.12	F:109/Binding site: ATP (Lys) #status Predicted	Db	F:1097-114/Domain: SH3 homology <SH3>
A;Map position: 2	F:315/Binding site: phosphate (Ser) (covalent) #status Predicted	Qy	F:315/Binding site: phosphate (Ser) (covalent) #status Predicted
A;Introns: 66/3; 124/2; 181/2; 392/1	Query Match 5.2%; Score 129; DB 1; Length 1147;	Db	Query Match 5.2%; Score 129; DB 1; Length 1147;
Query Match 5.5%; Score 135.5; DB 2; Length 484;	Best Local Similarity 21.3%; Pred. No. 0.19; Mismatches 55; Indels 150; Gaps 21;	Qy	Best Local Similarity 21.3%; Pred. No. 0.19; Mismatches 55; Indels 150; Gaps 21;
Best Local Similarity 24.5%; Pred. No. 0.021; Mismatches 42; Conservative 46; Indels 35; Gaps 8;	Matches 104; Conservative 99	Db	Matches 104; Conservative 99
Matches 46; Cross-references: EMBL:U21308; PIDN:AAB93321.1; GSDB:GR00020; CBSP:ZK1290.12	C;Keywords: actin binding; ATP; hydrolase; nucleotide binding; P-loop; phosphoprotein;	Qy	44 YKQFIPNVAEKTLGASGRYEGKISRNSERFEKLTNPYNPDIFKD---EERTGADRMLT 99
A;Experimental source: clone ZK1037	F:552-573/Region: actin binding #status Predicted	Db	591 YGLILEENVRVRAFGA-----YRAEFDRLRYYKLSP-----KTRWINGEWMSGARK--- 637
A;Accession: T27665	F:698-714/Region: basic	Qy	100 QRCKDKUNALAISVMNQWPGYKLRYTEGWDEGHSSEESL-----HYEG 143
A;Status: Preliminary; translated from GB/EMBL/DDBj	C;Genetics: CESP:ZK1037.10	Db	638 DGCQTLINDLGGLT-SWQLGSKSVFPRYPTLFHEECLDRKDYCTLRQKANFHWS 696
A;Molecule type: DNA	A;Map Position: 5 <WIL>	Qy	144 R-----AUDITSDRDRSKYMLARLAVEAGDWYYESKAIIHCYSAAK 194
A;Residues: 1-41 <WIL>	A;Experimental source: clone ZK1037	Db	697 RXHOLEQRKMAADLILKSRKERORHYSNRKYE----FDYINTDANYDLDQDCVR--SSGRDK 750
A;Introns: 37/3; 75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3	C;Genetics: CESP:ZK1037.10	Qy	Best Local Similarity 24.3%; Pred. No. 0.024; Mismatches 34; Indels 39; Gaps 6;
Submitted to the EMBL Data Library, October 1996	A;Accession: T27665	Db	Matches 45; Conservative 45; Mismatches 34; Indels 39; Gaps 6;
A;Reference number: Z20401	A;Status: Preliminary; translated from GB/EMBL/DDBj	Qy	Query Match 5.2%; Score 129; DB 1; Length 1147;
A;Accession: T27665	A;Molecule type: DNA	Db	Best Local Similarity 21.3%; Pred. No. 0.19; Mismatches 55; Indels 150; Gaps 21;
A;Status: Preliminary; translated from GB/EMBL/DDBj	A;Cross-references: EMBL:Z81142; PIDN:CA03509.1; GSDB:GR00023; CESP:ZK1037.10	Qy	44 YKQFIPNVAEKTLGASGRYEGKISRNSERFEKLTNPYNPDIFKD---EERTGADRMLT 99
A;Molecule type: DNA	C;Keywords: actin binding; ATP; hydrolase; nucleotide binding; P-loop; phosphoprotein;	Db	591 YGLILEENVRVRAFGA-----YRAEFDRLRYYKLSP-----KTRWINGEWMSGARK--- 637
A;Map Position: 5 <WIL>	F:552-573/Region: actin binding #status Predicted	Qy	100 QRCKDKUNALAISVMNQWPGYKLRYTEGWDEGHSSEESL-----HYEG 143
A;Experimental source: clone ZK1037	C;Genetics: CESP:ZK1037.10	Db	638 DGCQTLINDLGGLT-SWQLGSKSVFPRYPTLFHEECLDRKDYCTLRQKANFHWS 696
A;Accession: T27665	A;Introns: 1-41 <WIL>	Qy	144 R-----AUDITSDRDRSKYMLARLAVEAGDWYYESKAIIHCYSAAK 194
A;Status: Preliminary; translated from GB/EMBL/DDBj	A;Experimental source: clone ZK1037	Db	697 RXHOLEQRKMAADLILKSRKERORHYSNRKYE----FDYINTDANYDLDQDCVR--SSGRDK 750
A;Molecule type: DNA	A;Introns: 37/3; 75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3	Qy	Best Local Similarity 24.3%; Pred. No. 0.024; Mismatches 34; Indels 39; Gaps 6;
A;Cross-references: EMBL:Z81142; PIDN:CA03509.1; GSDB:GR00023; CESP:ZK1037.10	C;Genetics: CESP:ZK1037.10	Db	Matches 45; Conservative 45; Mismatches 34; Indels 39; Gaps 6;
C;Accession: T27665	A;Introns: 37/3; 75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3	Qy	Query Match 5.2%; Score 129; DB 1; Length 1147;
R;Baslam, V.	A;Experimental source: clone ZK1037	Db	Best Local Similarity 21.3%; Pred. No. 0.19; Mismatches 55; Indels 150; Gaps 21;
Submitted to the EMBL Data Library, October 1996	A;Accession: T27665	Qy	44 YKQFIPNVAEKTLGASGRYEGKISRNSERFEKLTNPYNPDIFKD---EERTGADRMLT 99
A;Reference number: Z20401	A;Status: Preliminary; translated from GB/EMBL/DDBj	Db	591 YGLILEENVRVRAFGA-----YRAEFDRLRYYKLSP-----KTRWINGEWMSGARK--- 637
A;Accession: T27665	A;Molecule type: DNA	Qy	100 QRCKDKUNALAISVMNQWPGYKLRYTEGWDEGHSSEESL-----HYEG 143
A;Status: Preliminary; translated from GB/EMBL/DDBj	A;Cross-references: EMBL:Z81142; PIDN:CA03509.1; GSDB:GR00023; CESP:ZK1037.10	Db	638 DGCQTLINDLGGLT-SWQLGSKSVFPRYPTLFHEECLDRKDYCTLRQKANFHWS 696
A;Molecule type: DNA	C;Keywords: actin binding; ATP; hydrolase; nucleotide binding; P-loop; phosphoprotein;	Qy	144 R-----AUDITSDRDRSKYMLARLAVEAGDWYYESKAIIHCYSAAK 194
A;Cross-references: EMBL:Z81142; PIDN:CA03509.1; GSDB:GR00023; CESP:ZK1037.10	A;Introns: 1-41 <WIL>	Db	697 RXHOLEQRKMAADLILKSRKERORHYSNRKYE----FDYINTDANYDLDQDCVR--SSGRDK 750
C;Accession: T27665	A;Experimental source: clone ZK1037	Qy	Best Local Similarity 24.3%; Pred. No. 0.024; Mismatches 34; Indels 39; Gaps 6;
A;Status: Preliminary; translated from GB/EMBL/DDBj	A;Introns: 37/3; 75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3	Db	Matches 45; Conservative 45; Mismatches 34; Indels 39; Gaps 6;
A;Molecule type: DNA	C;Genetics: CESP:ZK1037.10	Qy	Query Match 5.2%; Score 129; DB 1; Length 1147;
A;Cross-references: EMBL:Z81142; PIDN:CA03509.1; GSDB:GR00023; CESP:ZK1037.10	A;Map Position: 5 <WIL>	Db	Best Local Similarity 21.3%; Pred. No. 0.19; Mismatches 55; Indels 150; Gaps 21;
C;Accession: T27665	A;Experimental source: clone ZK1037	Qy	44 YKQFIPNVAEKTLGASGRYEGKISRNSERFEKLTNPYNPDIFKD---EERTGADRMLT 99
A;Status: Preliminary; translated from GB/EMBL/DDBj	A;Introns: 37/3; 75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3	Db	591 YGLILEENVRVRAFGA-----YRAEFDRLRYYKLSP-----KTRWINGEWMSGARK--- 637
A;Molecule type: DNA	C;Genetics: CESP:ZK1037.10	Qy	100 QRCKDKUNALAISVMNQWPGYKLRYTEGWDEGHSSEESL-----HYEG 143
A;Cross-references: EMBL:Z81142; PIDN:CA03509.1; GSDB:GR00023; CESP:ZK1037.10	A;Map Position: 5 <WIL>	Db	638 DGCQTLINDLGGLT-SWQLGSKSVFPRYPTLFHEECLDRKDYCTLRQKANFHWS 696
C;Accession: T27665	A;Experimental source: clone ZK1037	Qy	144 R-----AUDITSDRDRSKYMLARLAVEAGDWYYESKAIIHCYSAAK 194
A;Status: Preliminary; translated from GB/EMBL/DDBj	A;Introns: 37/3; 75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3	Db	697 RXHOLEQRKMAADLILKSRKERORHYSNRKYE----FDYINTDANYDLDQDCVR--SSGRDK 750
A;Molecule type: DNA	C;Genetics: CESP:ZK1037.10	Qy	Best Local Similarity 24.3%; Pred. No. 0.024; Mismatches 34; Indels 39; Gaps 6;
A;Cross-references: EMBL:Z81142; PIDN:CA03509.1; GSDB:GR00023; CESP:ZK1037.10	A;Map Position: 5 <WIL>	Db	Matches 45; Conservative 45; Mismatches 34; Indels 39; Gaps 6;
C;Accession: T27665	A;Experimental source: clone ZK1037	Qy	Query Match 5.2%; Score 129; DB 1; Length 1147;
A;Status: Preliminary; translated from GB/EMBL/DDBj	A;Introns: 37/3; 75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3	Db	Best Local Similarity 21.3%; Pred. No. 0.19; Mismatches 55; Indels 150; Gaps 21;
A;Molecule type: DNA	C;Genetics: CESP:ZK1037.10	Qy	44 YKQFIPNVAEKTLGASGRYEGKISRNSERFEKLTNPYNPDIFKD---EERTGADRMLT 99
A;Cross-references: EMBL:Z81142; PIDN:CA03509.1; GSDB:GR00023; CESP:ZK1037.10	A;Map Position: 5 <WIL>	Db	591 YGLILEENVRVRAFGA-----YRAEFDRLRYYKLSP-----KTRWINGEWMSGARK--- 637
C;Accession: T27665	A;Experimental source: clone ZK1037	Qy	100 QRCKDKUNALAISVMNQWPGYKLRYTEGWDEGHSSEESL-----HYEG 143
A;Status: Preliminary; translated from GB/EMBL/DDBj	A;Introns: 37/3; 75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3	Db	638 DGCQTLINDLGGLT-SWQLGSKSVFPRYPTLFHEECLDRKDYCTLRQKANFHWS 696
A;Molecule type: DNA	C;Genetics: CESP:ZK1037.10	Qy	144 R-----AUDITSDRDRSKYMLARLAVEAGDWYYESKAIIHCYSAAK 194
A;Cross-references: EMBL:Z81142; PIDN:CA03509.1; GSDB:GR00023; CESP:ZK1037.10	A;Map Position: 5 <WIL>	Db	697 RXHOLEQRKMAADLILKSRKERORHYSNRKYE----FDYINTDANYDLDQDCVR--SSGRDK 750
C;Accession: T27665	A;Experimental source: clone ZK1037	Qy	Best Local Similarity 24.3%; Pred. No. 0.024; Mismatches 34; Indels 39; Gaps 6;
A;Status: Preliminary; translated from GB/EMBL/DDBj	A;Introns: 37/3; 75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3	Db	Matches 45; Conservative 45; Mismatches 34; Indels 39; Gaps 6;
A;Molecule type: DNA	C;Genetics: CESP:ZK1037.10	Qy	Query Match 5.2%; Score 129; DB 1; Length 1147;
A;Cross-references: EMBL:Z81142; PIDN:CA03509.1; GSDB:GR00023; CESP:ZK1037.10	A;Map Position: 5 <WIL>	Db	Best Local Similarity 21.3%; Pred. No. 0.19; Mismatches 55; Indels 150; Gaps 21;
C;Accession: T27665	A;Experimental source: clone ZK1037	Qy	44 YKQFIPNVAEKTLGASGRYEGKISRNSERFEKLTNPYNPDIFKD---EERTGADRMLT 99
A;Status: Preliminary; translated from GB/EMBL/DDBj	A;Introns: 37/3; 75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3	Db	591 YGLILEENVRVRAFGA-----YRAEFDRLRYYKLSP-----KTRWINGEWMSGARK--- 637
A;Molecule type: DNA	C;Genetics: CESP:ZK1037.10	Qy	100 QRCKDKUNALAISVMNQWPGYKLRYTEGWDEGHSSEESL-----HYEG 143
A;Cross-references: EMBL:Z81142; PIDN:CA03509.1; GSDB:GR00023; CESP:ZK1037.10	A;Map Position: 5 <WIL>	Db	638 DGCQTLINDLGGLT-SWQLGSKSVFPRYPTLFHEECLDRKDYCTLRQKANFHWS 696
C;Accession: T27665	A;Experimental source: clone ZK1037	Qy	144 R-----AUDITSDRDRSKYMLARLAVEAGDWYYESKAIIHCYSAAK 194
A;Status: Preliminary; translated from GB/EMBL/DDBj	A;Introns: 37/3; 75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3	Db	697 RXHOLEQRKMAADLILKSRKERORHYSNRKYE----FDYINTDANYDLDQDCVR--SSGRDK 750
A;Molecule type: DNA	C;Genetics: CESP:ZK1037.10	Qy	Best Local Similarity 24.3%; Pred. No. 0.024; Mismatches 34; Indels 39; Gaps 6;
A;Cross-references: EMBL:Z81142; PIDN:CA03509.1; GSDB:GR00023; CESP:ZK1037.10	A;Map Position: 5 <WIL>	Db	Matches 45; Conservative 45; Mismatches 34; Indels 39; Gaps 6;
C;Accession: T27665	A;Experimental source: clone ZK1037	Qy	Query Match 5.2%; Score 129; DB 1; Length 1147;
A;Status: Preliminary; translated from GB/EMBL/DDBj	A;Introns: 37/3; 75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3	Db	Best Local Similarity 21.3%; Pred. No. 0.19; Mismatches 55; Indels 150; Gaps 21;
A;Molecule type: DNA	C;Genetics: CESP:ZK1037.10	Qy	44 YKQFIPNVAEKTLGASGRYEGKISRNSERFEKLTNPYNPDIFKD---EERTGADRMLT 99
A;Cross-references: EMBL:Z81142; PIDN:CA03509.1; GSDB:GR00023; CESP:ZK1037.10	A;Map Position: 5 <WIL>	Db	591 YGLILEENVRVRAFGA-----YRAEFDRLRYYKLSP-----KTRWINGEWMSGARK--- 637
C;Accession: T27665	A;Experimental source: clone ZK1037	Qy	100 QRCKDKUNALAISVMNQWPGYKLRYTEGWDEGHSSEESL-----HYEG 143
A;Status: Preliminary; translated from GB/EMBL/DDBj	A;Introns: 37/3; 75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3	Db	638 DGCQTLINDLGGLT-SWQLGSKSVFPRYPTLFHEECLDRKDYCTLRQKANFHWS 696
A;Molecule type: DNA	C;Genetics: CESP:ZK1037.10	Qy	144 R-----AUDITSDRDRSKYMLARLAVEAGDWYYESKAIIHCYSAAK 194
A;Cross-references: EMBL:Z81142; PIDN:CA03509.1; GSDB:GR00023; CESP:ZK1037.10	A;Map Position: 5 <WIL>	Db	697 RXHOLEQRKMAADLILKSRKERORHYSNRKYE----FDYINTDANYDLDQDCVR--SSGRDK 750
C;Accession: T27665	A;Experimental source: clone ZK1037	Qy	Best Local Similarity 24.3%; Pred. No. 0.024; Mismatches 34; Indels 39; Gaps 6;
A;Status: Preliminary; translated from GB/EMBL/DDBj	A;Introns: 37/3; 75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3	Db	Matches 45; Conservative 45; Mismatches 34; Indels 39; Gaps 6;
A;Molecule type: DNA	C;Genetics: CESP:ZK1037.10	Qy	Query Match 5.2%; Score 129; DB 1; Length 1147;
A;Cross-references: EMBL:Z81142; PIDN:CA03509.1; GSDB:GR00023; CESP:ZK1037.10	A;Map Position: 5 <WIL>	Db	Best Local Similarity 21.3%; Pred. No. 0.19; Mismatches 55; Indels 150; Gaps 21;
C;Accession: T27665	A;Experimental source: clone ZK1037	Qy	44 YKQFIPNVAEKTLGASGRYEGKISRNSERFEKLTNPYNPDIFKD---EERTGADRMLT 99
A;Status: Preliminary; translated from GB/EMBL/DDBj	A;Introns: 37/3; 75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3	Db	591 YGLILEENVRVRAFGA-----YRAEFDRLRYYKLSP-----KTRWINGEWMSGARK--- 637
A;Molecule type: DNA	C;Genetics: CESP:ZK1037.10	Qy	100 QRCKDKUNALAISVMNQWPGYKLRYTEGWDEGHSSEESL-----HYEG 143
A;Cross-references: EMBL:Z81142; PIDN:CA03509.1; GSDB:GR00023; CESP:ZK1037.10	A;Map Position: 5 <WIL>	Db	638 DGCQTLINDLGGLT-SWQLGSKSVFPRYPTLFHEECLDRKDYCTLRQKANFHWS 696
C;Accession: T27665	A;Experimental source: clone ZK1037	Qy	144 R-----AUDITSDRDRSKYMLARLAVEAGDWYYESKAIIHCYSAAK 194
A;Status: Preliminary; translated from GB/EMBL/DDBj	A;Introns: 37/3; 75/3; 141/3; 173/2; 253/1; 298/3; 310/1; 371/2; 424/3	Db	697 RXHOLEQRKMAADLILKSRKERORHYSNRKYE----FDYINTDANYDLDQDCVR--SSGRDK 750
A;Molecule type: DNA	C;Genetics: CESP:ZK1037.10	Qy	Best Local Similarity 24.3%; Pred. No. 0.024; Mismatches 34; Indels 39; Gaps 6;
A;Cross-references: EMBL:Z81142; PIDN:CA03509.1; GSDB:GR00023; CESP:ZK103			

RESULT 15

Qy 195 SGCCPPGSATVHLEQGGTKLVKDLSPGDRVLAAADDQGR-----LIYSDFLTFLDRDGA 248
 Db 751 EATAFT-----DQVYLNRERGKPERDLIVNEATEYFAIRKKCS 789

Qy 249 KKVYVIETREPERLLTAHIL---FVAPH-----NDSATGEPBASSGGCOPSG 296
 Db 790 QGVVYNLKRIPIGEIASLSLSTLQDNVYVTHNQYDMVIFENDKTEIVTLMENYKMSG 849

Qy 297 GALGPRLFASTRVRPGQEVYVAERGDRILLPAAVHSVTIUSEAAGAYAPLTAQCTIL 356
 Db 850 GRDLP-----VNENDNTYKAASNGAQRL-----TFSKNEASASQPSIKS---- 890

Qy 357 NRVLASCYAVIEEHSWAHRAFAPRFLAHALLAALAPARTDR-----GGDSGGDR 406
 Db 891 -----RANTOIGIATGL-----PKETDSSPPNTPSGGGGGGGRRG 927

Qy 407 GGGGRVALTAPGADAPAGATAGIHWYSOLLYQIGTWTWLLSEALRPLGMVAKSSXSRG 466
 Db 928 GGGGRGA---AGGRRGGFGGGGG---ysQPvAQ----AOVPAQVQPQVAAVPSAGRG 977

Qy 467 AGGGAREGA 475
 Db 978 GPNGGGPGA 986

RESULT 17

T10563 hypothetical protein C29F3.2 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Accession: T10563 ; sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T19563 ; T23034
 R;Matthews, L.
 Submitted to the EMBL Data Library, October 1996
 A;Reference number: 219142
 A;Accession: T19563
 A;Molecule type: DNA
 A;Residues: 1-629 <WIL>
 A;Cross-references: EMBL:Z81043; PIDN:CABO2804.1; GSPDB:GN00023; CESP:C29F3.2
 A;Experimental source: clone C29F3
 R;White, S.
 Submitted to the EMBL Data Library, June 1998
 A;Reference number: Z19657
 A;Accession: T23034
 A;Status: Preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-629 <WIL>
 A;Cross-references: EMBL:AL023813; PIDN:CAA19424.1; GSPDB:GN00023 ; CESP:C29F3.2
 A;Experimental source: clone H02K04
 C;Genetics:
 A;Gene: CESP:C29F3.2
 A;Map position: 5
 A;Introns: 23/1; 111/3; 177/3; 207/2; 287/1; 381/3; 399/3; 417/1; 476/2; 528/3; 537/2; 5

Query Match 5.2%; Score 128; DB 2; Length 629;
 Matches 43; Conservative 35; Mismatches 75; Indels 22; Gaps 7;

Best Local Similarity 24.6%; Pred. No. 0.11; Length 629;

A;Text _change 15-Oct-1999 #text_change 15-Oct-1999

RESULT 18

T31328 fibroin - Chinese oak silkmoth
 C;Species: Antheraea pernyi (Chinese oak silkmoth)
 C;Accession: T31328
 R;Sezutsu, H.; Tamura, T.; Yukuiiro, K.
 Submitted to the EMBL Data Library, August 1998
 A;Description: Characterization of the full length fibroin gene of a wild silkmoth, Ant: A;Reference number: Z20995
 A;Accession: T31328
 A;Status: Preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-2639 <SEZ>
 A;Cross-references: EMBL:AF083334; NID:93450882; PID:93450883; PIDN:AAC32606.1
 C;Genetics:
 A;Introns: 14/3

Query Match 5.0%; Score 123.5; DB 2; Length 2639;
 Matches 55; Conservative 10; Mismatches 101; Indels 27; Gaps 6;

Qy 198 CPPGSATVHLEQGGTKLVKDLSPGDRVLAAADDQGRILYSDFLTFLDRD 255
 Db 421 CFPADAEVNTYERGVYKRMDELEVGDWVQALHGK-ETTYSFVKWHLRDEQSAEVFBFL 479

Qy 256 ETREPERLLTAHILFVAPHNSATGDPPEASSGGPSSGGALGPRAFLAFAVRVPGQR 315
 Db 480 EN---GESFRTEKHLVPAVHSVTIUSEAAGAYAPLTAQGTTLINVLASCYAVIEEH 521

Qy 316 YVVAEVDGRILLPAVHSVTIUSEAAGAYAPLTAQGTTLINVLASCYAVIEEH 370
 Db 522 FFMQOPENASKPQYQILDIQVRK-TGUYAPMTSLGHILVNQHTSCHSEIDHH 575

Qy 400 DSGGGRRGGCG - GIVVLTAPGANDAPGAGATQIHYGQIQTWILDSEALHPLGM 457
 Db 2266 SGGYGGGGVGSDSAAAAAAAAGACGAGGGYGYG---GXYGSYGSDSAARAAA 2321

RESULT 18

Qy	458 AVKSSXSRGAGGG 470	390 LAPARTDREGDSGGGDRGGGRVALTAPGAADAPGAGAT---AGTHWSQL-LYQI 442
Db	2322 AANGGAGCvGGG 2334	146 RPPADTTDG---GATDEGAANPSEGATPGSATDPGTATDGPSSATEGWAEYGDAEAA 203
Qy		443 G-TWILDSEALHPLG-----MAYKSSXSRGAGGAREGA 475
Db		204 GDDWTVDGACPDASGGEGDPWSATMSVPEESGAGAGAAQFA 247
RESULT 20	T2281	
	hypothetical protein F46B3.5 - Caenorhabditis elegans	
C;Species:	Ceenorhabditis elegans	
C;Date:	15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999	
C;Accession:	T2281	
R;Ainscough, R.		
submitted to the EMBL Data Library, November 1996		
A;Reference number: Z10541		
A;Accession: T2281		
A;Status: preliminary; translated from GB/EMBL/DDJB		
A;Molecule type: DNA		
A;Residues: 1-868 <WIL>		
A;Cross-references: EMBL:Z81540; PIDN:CA00405.1; GSPDB:GN00023; CESP:F46B3.5		
A;Experimental source: clone F46B3		
C;Genetics:		
A;Gene: CESP:F46B3.5		
A;Map position: 5		
A;Map position: 200/1: 235/3; 436/3; 561/3; 581/3; 696/3; 742/1; 826/3; 846/3		
A;Introns: 45/3; 200/1: 235/3; 436/3; 561/3; 581/3; 696/3; 742/1; 826/3; 846/3		
Query Match	4.9%	Score 121; DB 2; Length 868;
Best Local Similarity	26.7%	Pred. No. 0 54; Indels 24; Gaps 8;
Matches 47; Conservative 32; Mismatches 73; DB		
Qy	195 GGCFFPGSATVHLLEQGGTKVLDGLSPGDVIAADDQGRLLSDFLTDLDRDGARKVYYI 255	4.9%; Score 118.5; DB 2; Length 702;
Db	662 GGCFF-SSTDIVTTBEGKRNDEIDVGDTLTA-NRVKFHFTPTVLWIRESEKLEELTI 719	A;Cross-references: GDB:568496; OMIM:600747
Qy	256 ETREPERLILTAHHLYFAPHNDSATG---EPRASSGGPPSGGALGPRLPASRYRFG 312	A;Map Position: 17Q11-17q22
Db	720 -TTERGSTLQQTPLHEMYTKCNESSEFTRKLP-----NEHTALASYLEIG 765	C;Superfamily: mouse transcription factor tbx2; T-box homology <TBX>
Qy	313 QRYVVAERGDRRLPAATHSVTILSEEAGAYAPITAGTILINRVIASCYAVIE 368	F;104-285/Domain: T-box homology
Db	766 DCV-1LTENTKFRQ---EXTINOTRGLK-TGIYSPLTKNGRITVNMDLASCYSEVO 816	
Qy		
Db		
RESULT 21	T35213	
	probable secreted protein - Streptomyces coelicolor	
C;Species:	Streptomyces coelicolor	
C;Date:	05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999	
R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.		
submitted to the EMBL Data Library, September 1998		
A;Reference number: Z21572		
A;Accession: T35213		
A;Status: preliminary; translated from GB/EMBL/DDJB		
A;Molecule type: DNA		
A;Residues: 1-318 <SSE>		
A;Cross-references: EMBL:AL031515; PIDN:CAA20618.1; GSPDB:GN00070; SCOEDB:SC5C7.06		
A;Experimental source: Strain A3 (2)		
C;Genetics:		
A;Gene: SC0DB:SC5C7.06		
Query Match	4.8%	Score 119; DB 2; Length 318;
Best Local Similarity	26.3%	Pred. No. 0 21; Mismatches 19; Indels 46; Gaps 9;
Matches 59; Conservative 19; DB		
Qy	276 PINDSATGEPEASSGGCPGSSGALGPRLFASPRVRPGQRVYVVAERDGDRLLPDAVHSY 335	
Db	46 PADDSAAVPPSAEEAPPSCAQAAAR-VPSDAGFDTIV-----SV 88	
Qy	336 TSEEAGAYAIDLTA----QGTILINRVIASCYAVIEHSWAIRAFAPRLAHALLA 389	
Db	89 SCGPTGGSSAPASLDATSAFAEFGTVALKVADDAGTA---SGPATRGTRIAAAEDFAE 145	
Qy		
Db		
RESULT 22	G01840	
	T-box Protein 2 - human	
C;Species:	Homo sapiens (man)	
C;Date:	21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 23-Jul-1999	
R;Campbell, C.E.		
C;Accession: G01840		
A;Reference number: G08632		
A;Accession: G01840		
A;Status: preliminary; translated from GB/EMBL/DDJB		
A;Molecule type: mRNA		
A;Residues: 1-702 <CAM>		
A;Cross-references: EMBL:U28049; NID:9924927; PIDN:AAA73861.1; PID:9924928		
C;Genetics:		
A;Gene: GDB:TBX2		
A;Map position: 17Q11-17q22		
Query Match	4.8%	Score 118.5; DB 2; Length 702;
Best Local Similarity	19.3%	Pred. No. 0 63; Mismatches 46; Indels 295; Gaps 23;
Matches 116; Conservative 144; DB		
Qy	118 PGVKLRVTEGMDEDGHSEBSLHYEGRAVIDTTSDR-----DRSKYGMILR 163	
Db	95 PKVTLAKELMDQ-----FHKLGUTEMVTKSGRMFPFKYRVSGIDKKARYILL-- 144	
Qy	164 LAVEAGFDWVYYYESKAIHICSVKAENS---VAAKSGCFCFGSATVLEQGGT-----	
Db	145 DIVAAD-----CRYKFHNISRWVNTAGADPEWKMYTHDPSATGEOWMAKP 193	
Qy	213 -----KLVKDLS-----PGDRVLAADDQGRLLSDFLTFL-----242	
Db	194 VAFHKLRLTNNISDKIGFTLINSMKYQPREFHVANDILKPLYSTRTVVFETDFIAV 253	
Qy	243 -----DRDGAKKYVYTETREPRLITAHLI--FVAFHND 279	
Db	254 TAYQNDRKIQKIDNNPFAGKFRDNGR-----REKERQKLTPLSLRLEYERKPERD 306	
Qy	280 SATGEPBASSGGGPS-----GGALGPRLPALPSRV-----309	
Db	307 GA-EPSASSCDPPPARPEPPTSPGAPSPLRLRAREEKSCAADSDEPEPLSBERARA 364	
Qy	310 -----FPGQRVYVVAERDGD-----RR---326	
Db	365 PLGRSPARDASASPTRLTPEPARERCPERGKEPAESGGDGPFGLRSLERKEPARKDE 424	
Qy	327 -----LLPRAVHSVTLSEBAG-----AVAPLTAQGTILINRV-----359	
Db	425 GRKEAECKEQGLAPLVQTDASASPQAGHPLGLAFFFSLHQQFFGQLGQPLFLHP- 483	
Qy	360 LASCYAVIEEHSWAHRAPPLAHALLAALAPARTDRGDSGGGRGGGRVALATPG 419	
Db	484 -----GQFTNGPQGFSAMGMH-LIASVA-----GGNGGG-GGPDTAAGIDAGG 526	
Qy	420 AADAPGAGTAG---IHWSQL-----439	
Db	527 LGPAAASAASTAAAPPFLHSQMLNLASQTPIMPTEGGFPPYPTYMANAAAASALPSTSAA 586	
Qy	440 -----YQIGTWLILSEALHPLGMVAKSSXSRGAGGAR 472	
Db	587 AAAAAAGSLSRSPRFGLGSARPRLRFSPYQIPVTPSTSLTTGLA-SEGSKAAGNSR 644	

Qy	473 E 473	Matches	82;	Conservative	39;	Mismatches	15;	Indels	77;	Gaps	14;										
Db	645 E 645	Qy	90 ENTGADLMTQRCKDKUNALAIISVNRQWPGKYLRLRVTEGWDDEGHHSFESIHYEGRAVIDT 149	Db	610 ENPERJRLILLVITVADTRAVGPGVNNCKWGQLR-----ELYNATEAVFRGGGRGSDAA 662																
RESULT 23																					
ET0917	hypothetical Glycine-rich protein Rv1450c - Mycobacterium tuberculosis (strain H37RV)	Qy	150 TS-DRDRSKYGMILARLAVEAGFDWVTTYSRKAHICSYKAENSAAKSGCPGSAT--- 204	Db	663 ANYQRHQUESTBARAHL-----LETDAPKKWWVAAMENAYNSAFSODDLF 708																
C;Species: Mycobacterium tuberculosis	C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000	Qy	205 VHLP-----OGGTKLXKDLSGDR---VIAADDGGRLLYSDFL----- 239	Db	709 HHAELARRAAIQCQAAEQQVRPGSNAAEVVAFAKER-RGLFDALLAISIIGGNTVGAR 767																
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.	R;Connor, R.; Davies, R.; Feltwell, K.; Gentle, S.; Hamlin, N.; Holroyd, S.	Qy	240 TFLRDGKAKVYVIE-TREP---RERLILTAAHHLFAPHNDSATGDPBASSGPP 294	Db	768 VFTSRQGQDLDVFVQDVYTGAFFGCENPRLAERLADLEAAKGKDALAVERGSEOTRA 827																
Rajandream, M.A./Rogers, J.; Rutter, S.; Seeger, K.; Skellon, S.; Squares, S.	Nature 393, 537-544, 1998	Qy	295 SGGLGPRALF-----ASRVPGCORYVVAERDGRRLPAATHSVTLSEE 341	Db	828 AAFIAFAPSYTIDNDASINDATVVEASGDRP-LHAAIATLADSLAISIQSAHIDYGERA 886																
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.	A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome	Qy	342 AGAYAPLTAQG----TIIINRVLASCYAVIBEHSHWRAFAP-FRIAHALLA 388	Db	887 VDAFYVQFTEGGKVTDTRKLNALKADDLIAALEQNEASAPAARPGLRRARASYA 939																
A;Reference number: A05000; PMID:98295987;	A;Status: Preliminary; nucleic acid sequence not shown; translation not shown	Db	828 AAFIAFAPSYTIDNDASINDATVVEASGDRP-LHAAIATLADSLAISIQSAHIDYGERA 886																		
A;Molecule type: DNA	A;Cross-references: GB:AL123456; NID:93250713; PIDN:CAB09271.1; PMID:9634230	Qy	342 AGAYAPLTAQG----TIIINRVLASCYAVIBEHSHWRAFAP-FRIAHALLA 388	Db	887 VDAFYVQFTEGGKVTDTRKLNALKADDLIAALEQNEASAPAARPGLRRARASYA 939																
A;Experimental source: Strain H37Rv	C;Genetics:	Db	828 AAFIAFAPSYTIDNDASINDATVVEASGDRP-LHAAIATLADSLAISIQSAHIDYGERA 886																		
A;Gene: Rv1450c	C;superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology	RESULT 25																			
Query Match	4.7%; Score 116; DB 2; Length 1329;	H87311	hypothetical protein CC0505 [imported] - Caulobacter crescentus	C;Species: Caulobacter crescentus	C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001	C;Accession: H87311	R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.	B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon	N. J.; Embley, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.	Proc. Natl. Acad. Sci. U.S.A. 98, 4126-4141, 2001	A;Title: Complete Genome Sequence of Caulobacter crescentus.	A;Reference number: A87249; PMID:21173698; PMID:11259647	A;Accession: H87311	A;Status: preliminary	A;Molecule type: DNA	A;Cross-references: GB:AB005673; NID:913421686; PIDN:AAK22492.1; GSPDB:GN00148	C;Genetics:	A;Gene: CC0505			
Best Local Similarity	28.3%; Pred. No. 2.2;	Matches	68;	Conservative	18;	Mismatches	90;	Indels	64;	Gaps	12;	Query Match	4.7%; Score 115; DB 2; Length 486;	Best Local Similarity	21.7%; Prod. No. 0.71;	Mismatches	50;	Indels	86;	Gaps	17;
Db	3 IVIVAPETAAALDVARIGSSIGAAAAGSTTSVLAAGADEVSAAIALLEGSHAREY 62	Qy	271 LLVPAPHNDSDATEPEAAGS-GPPSGACGP-----RADFASVVRPG 312	Db	63 QATSTQVAFERHDPAQTLSAVSY-WGAERTNA-APLATHEENVNLNAPQNL--- 116																
Qy	117 -----LGRLPLGGAAGAPG-TGQAAGGGLIWNGAGGSGAP-QVGVGGAGA 164	Qy	313 QRV--YVVAERDGRRLPAVHSVTLSSEAAGAYAPLTAGCTTILNRLASCYAVIEEH 370	Db	371 SWAHRAFAFERLAAHLL--AAALAPARTDRGGDGSGG---CDRGCGGGGRV 413																
Db	165 GLPCTGGACAGGAAAGAG-----GSGCWTLNGGGVGAGGCGSLLGEATGGAGNA 217	Qy	414 ALTAP-GRADAPGAGATAGIHMYSQLIQITWLDSEALHLI-CHAYAKSSXSRSRGGGGA 471	Db	118 GQPAYGLAATGPGRK-----DTIGSRAITAADSDPDRPVWSVMGANTLQAL 166																
Qy	277 HNDSATGEPEASSGSGPSSGGALGPRALFASRVPGGORYVVAERDGD---RRLIPAAV 332	Qy	111 ISVNQNQWPGVKLRLVTEGMDDEGHHS-ERSLSHYEGRAV--DIRTSDDRSKYGMЛАLAV 166	Db	116 KTLEAT-RPAE-----VQLJISKRVYTISDQDDAGAWRKTYSLF 208																
Db	167 -----IADDGGRLLYSDELFLDRDGAKKFWYVETREPRERLILT-AAHLIFVAP 276	Qy	167 EAGFDWVWYYESKAHICSYKAEN-SVAKSGCCFPSSATVLEQGGTKLVRKDLSPEGDRV 224	Db	225 -----EIDIEALVATTSTMREIHPSTIRLVLIGQVRP--NLVLUHANGYPTAESLSARIRA 117																
Qy	226 -----DTIGSRAITAADSDPDRPVWSVMGANTLQAL 166	Db	61 EIDIEALVATTSTMREIHPSTIRLVLIGQVRP--NLVLUHANGYPTAESLSARIRA 117	Db	118 GQPAYGLAATGPGRK-----DTIGSRAITAADSDPDRPVWSVMGANTLQAL 166																
Db	277 HNDSATGEPEASSGSGPSSGGALGPRALFASRVPGGORYVVAERDGD---RRLIPAAV 332	Qy	209 YIV----SPGGYGAATWNGIFQAVDGDNTTVSNALAQNTIOQGRGPGLGAAYPDVAGM 263	Db	333 HSVTLSSEAGAYAPLTAQTI-----AVIEERSWAH 374																
Qy	375 RAFAPERLAAHALAPARTDRGDSGGDRGGGGVALTAGAAGPAGATAGTHW 434	Db	375 RAFAPERLAAHALAPARTDRGDSGGDRGGGGVALTAGAAGPAGATAGTHW 434																		
Db	375 RAFAPERLAAHALAPARTDRGDSGGDRGGGGVALTAGAAGPAGATAGTHW 434	Qy	375 RAFAPERLAAHALAPARTDRGDSGGDRGGGGVALTAGAAGPAGATAGTHW 434																		

Db	264 EGDTPAFL-NLIPGLA-----DPERPDWGGWGRYALYTPNLADTDPKGFTGGVPI 314	Query Match 4.5%; Score 111; DB 2; Length 333;
Qy	415 YSQLIQYQIGTMLIDSEALTH--.bLGMAYRSS 462	Best Local Similarity 23.2%; Pred. No. 0 87; Matches 74; Conservative 27; Mismatches 116; Indels 102; Gaps 12;
Db	315 EPE-TRPINTNAIDTVAPHEPAFFGRAVKVS 344	Qy 184 SVKAENSYVAKSGCCFPGSATVHLEQQGETKLVRKDLSPGDRVIAADDQGRLLYSDFLFP 243 Db 4 SGSAAGTTTASGS--.GLGSLRHGSGG--SGSSAALGGSGSADQVRRYRAFT 53
RESULT 26	G70917 hypothetical glycine-rich protein Rv1452c - Mycobacterium tuberculosis (strain H37RV)	Qy 244 RDDGAK- -KVFY----VIET----REPRERLJLTAAH-- 270 Db 54 REQFARLXEFYRENYVSRPRCELAALNLPETIKWFQNRMKDGRQLAMSWPHPA 113
C;Species: Mycobacterium tuberculosis	C;Accession: G70917	Qy 271 --.LIFVAPHNDSATGE----PEASSSGGPSSGALGPRAFLPSR 308
C;Text_change: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 07-Mar-2003	R;Connor, S.T.; Broich, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Relman, D.; Gentle, S.; Hamlin, N.; Holroyd, S.; RaJandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Shelton, S.; Squares, S.	Db 114 DPSFTYTMTH-AAATGSLSPYPFFSHVPFLHYHPVGUTAAAASGAAAAAASSPFAT 172
Nature 393, 537-544, 1998	A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.	Qy 309 VRPGORVYVVAERDGDRLPLPAVHSVTISEEAGAY-APLTAQGTILINRVLASCYAVI 367
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome	A;Reference number: A70500; MUID:98295987; PMID:9634230	Db 173 IRPLDFTRALSPYSPRELLJCSPFH----.FGLYQRPAAAGLNSAASAASAAAAAA 224
A;Accession: G70917	A;Status: preliminary; nucleic acid sequence not shown; translation not shown	Qy 368 EERHWAHRAP----.FRLAHALLAALAPARTDGRGDSGGDRGGGGR 412
A;Cross-references: 1-741 <COL>	A;Molecule type: DNA	Db 225 AAASSAAARAAAPPSCGGSAPSCSCLSSHQSAAAAAAALGSRGGGGGGGGGGG- 283
A;Cross-references: GB:295844; GB:123456; NID:93250713; PIDN:CA09269.1; PID:92131044	A;Genetics:	Qy 413 VALTAGAADAAGAGATAG 431
C;Uncharacterized protein, PE motif containing elastin related uncharacterized glycine-rich protein, PE motif containing	C;Superfamily: elastin	Db 284 ----.GGAGAGGG 291
RESULT 28	EDBE75	Query Match 4.5%; Score 111; DB 1; Length 1298;
		EDBE75 immediate-early protein IE175 - human herpesvirus 1
		C;Species: human herpesvirus 1
		C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1998 #text_change 16-Jun-2000
		C;Accession: A23510
		R;McGeoch, D.J.; Dolan, A.; Donald, S.; Brauer, D.H.K.
		B;McGeoch, D.J.; Dolan, A.; Donald, S.; Brauer, D.H.K.
		Nucleic Acids Res. 14, 1727-1745, 1996
		A;Title: Complete DNA sequence of the short repeat region in the genome of herpes simplex virus type I
		A;Reference number: A23510; PMID:3005930
		A;Accession: A23510
		A;Molecule type: DNA
		A;Cross-references: 1-1298 <MCG>
		C;Comment: This protein acts at the transcriptional regulatory level and is required th-
		C;Genetics:
		A;Gene: IE3;
		A;Map Position: short repeat region (IRS)
		C;Superfamily: herpesvirus immediate-early protein IE175
		C;Keywords: DNA binding; early protein; transcription regulation
Db	271 LLFVAPHNDSATGEPEASSGS--GPPSGCALGP-----RALFAFSRVRPG 312	Query Match 4.5%; Score 111; DB 1; Length 1298;
Qy	3 LVIVTPETAAASPVARYGSSICVANSAAAGTSVLAAGADEVSAAITALFGSHAREY 62	Best Local Similarity 25.3%; Pred. No. 5.1;
Db	313 QRV--YVVAERDGDRLPLPAVHSVTISEEAGAYAPLTAQGTILINRVLASCYAIEEH 370	Matches 96; Conservative 34; Mismatches 134; Indels 108; Gaps 20;
Qy	63 QAISTQVAAFHDPRAQTLSAVGYY-VSELEATVA-APLITLHNVLNANAPIQAL-- 116	Qy 148 ITTSDRDRSKY--GMALAR----LVEAG-FDWVYYESKAIHKS----- 184
Db	371 SWAHAFAPPRLAHALL---.AALPARTDGRGDSGG----.GDRGGGGGRV 413	Db 410 ISGAANNSSSPTGSVARAVPHLGYMAAGREGFNGIHAIAAAAVAMSRRYDRAQOKGFLITS 469
Qy	117 ----.LGRLHIGDAAGAPG-TGQAGGAGLWLQNGGAGGSGAPGQVGGGACAA 164	Qy 185 -----VKAANSVAKSGCCFPGATVHLEQGENKLVDLSPDR-----VLA 226
Db	414 ALTAP-GAADAPEGASATAGTHWYSSLQYQITWLJLDSEALHPL-GMAVKSNSXRSRAGGA 471	Db 470 LRRAYAPLLARENAAALTGAAAS-PGIGA--DDEGWVAAVAAAPGERAVPGYGAAGILA 525
Qy	165 GLFGTCGAGGGAGGAGAGGAG----.GSGGWLQNGGAGGQSLUGGATGGAGNA 217	Qy 227 ADDQGRLLYS-----DFLTFLDRDDGAKK-----VFVYIETTEPRERL---- 264
Db	RESULT 27	Db 526 A--LGRISAAPASPGGDDPAAHADDDAGRAQAGRVAVECLAACTGILEAEGF 583
A39065	homeotic protein EVX2 - human (fragment)	C;Species: Homo sapiens (man)
	C;Accession: A39065	C;Text_change: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 17-Oct-1997
	R;DeRaposo, M.; Morelli, F.; Acampora, D.; Migliaccio, E.; Simeone, A.; Boncinelli, E.	C;Cross-references: GDB:1227528; OMIM:142991
	Genomics 10, 43-50, 1991	A;Title: EVX2, a human homeobox gene homologous to the even-skipped segmentation gene,
	A;Reference number: A39065; MUID:91257849; PMID:1675198	A;Map Position: 2q24.3-2q31
	A;Accession: A39065	C;Superfamily: unassigned homeobox proteins; homeobox homology
	A;Status: preliminary; not compared with conceptual translation	C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
	A;Molecule type: DNA	F;46-102/Domain: homeobox homology <HOX>
	C;Genetics:	
	A;Gene: GDB:EVX2	
	A;Cross-references: GDB:1227528; OMIM:142991	
	A;Map Position: 2q24.3-2q31	
	C;Superfamily: unassigned homeobox proteins; homeobox homology	
	F;46-102/Domain: homeobox homology <HOX>	

Qy	368	EEHS-----WAHRFAPFRLAHLAAALAPA--RTDGGPSGGSDR--GGGGRVALTAP 418	Qy	164	LAVEAGFDWVYYESKAHICSVKAENS--VAAKSGGCPGSGATVHLEOGGT----- 212			
Db	692	FDNQSIRPLAAAASAP-DAADALLAAAASAAPREGRKRKSPGPARPPGGPRPKTKK 750	Db	145	MDIVAARD-----CRYKFINSRMWVAGRADEMPKRMTHPDSPATGEQWMAKP 193			
Qy	419	GAADAPCGAGATA 430	Qy	213	-----XLVKDL-----PDRVLAAADQGRLLKSDFLTL----- 242			
Db	751	SGADAPGSDDARA 762	Db	194	VAFHKLKLTTNNISDKEGFTILNSMVKYQPRFHIVTRANDILKLPYSTRTYFPETDFIAV 253			
RESULT 29								
Db	T35852	probable UDP-N-acetyl-muramoyl-L-alanine ligase - Streptomyces coelicolor	Qy	243	-----DRDDGAKKYYVIEPRERPLLTAAHLI-FVAPHND 279			
C;Species:	Streptomyces coelicolor		Qy	254	TAVQNDDKITQLKIDNNNEFAKGRFDTGNGR-----RERKQKLTPRLYYEHHCKPERD 306			
C;Date:	05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000		Db	280	SATGEPEASS-----GGPPPSGGALGRALFASRYRGQYVYV--AERDGDRRLLP 329			
C;Accession:	T35852		Qy	307	GA-EIASSCDPPBPEPPPSAAPSPLRRAAEKEENGAASDPEPERTGER-- 361			
A;Cross-references:	DBTBS:1049727 ; PIDN: CAB41553.2 ; GSDB:GN00070 ; SCOECD:SC9B1.07		Db	330	AAYHTSVTSEEAGAYAPLTAQGTILINRVLASCYAVIEEWSWAHPAFAFRLAHLA- 388			
A;Submitted to:	the EMBL Data Library, April 1999		Db	362	-----SAPLRCRSPS-----RDASPARLTPEPRS 386			
A;Reference number:	Z21591		Qy	389	-AIAAPARTDRCGDSSGCD-----RGGGGSGRVAITAP----- 418			
A;Status:	Preliminary; translated from GB/EMBL/DDJB		Qy	387	ERSPERCSKEPIEGCGGPFLRSLSKERPEARRKDEGRDVGEOREKPSL----- 446			
A;Molecule type:	DNA		Db	419	---GAADAPGAGATAIGHWY-----SOLLYQITWLDSSEAHPLGM----- 458			
A;Residues:	1462 <SAU>		Qy	447	ASPIGAGHPUCAFASHGQHGCQFFGPGACQPLHEQOFANGPGAFSAMONGHLLASVA 506			
A;Cross-references:	ENBIL:AL049727 ; PIDN: CAB41553.2 ; GSDB:GN00070 ; SCOECD:SC9B1.07		Db	459	VKSXXSRSGGGGREG 474			
A;Experimental source:	strain A3 (2)		Qy	507	GGGGSSGGAGPGTAAG 522			
C;Generics:			RESULT 31					
A;Gene:	SCOECD:SC9B1.07		Db	EDBE1	EDBE1 immediate-early protein IE110 - human herpesvirus 1 (strain 17)			
C;Superfamily:	UDP-N-acetyl-imuramate-alanine ligase		Qy	207	FAKIVPGCTLVITAADHEGARELTRRIAGRVTVTYGESEDADVRVLSVVOGLKSETV 266			
Query Match:	4.5%	Score 110; DB 2; Length 462;	Db	C;Species:	human herpesvirus 1			
Best Local Similarity:	26.3%	Pred. No. 1..6;	Qy	355	C;Sequence_revision 31-Mar-1988 #text_change 17-Mar-2000			
Matches:	47;	Mismatches 21; Indels 71; Gaps 6;	Db	C;Date:	31-Mar-1988			
C;Conservative:			Qy	267	C;Accession:	A29152		
Score:			Db	R;Perry, L.J.; Rixon, F.J.; Everett, R.D.; Frame, M.C.; McGeoch, D.J.				
Pred. No.:			Qy	415	J Gen. Virol. 67, 2365-2380, 1986			
Pred. No.:			Db	A;Title:	Characterization of the IE110 gene of herpes simplex virus type 1.			
Pred. No.:			Qy	298	A;Reference number:	A29152; PMID:87059760; PMID:303529		
Pred. No.:			Db	A;Accession:	A29152.			
Pred. No.:			Qy	305	A;Molecule type:	DNA		
Pred. No.:			Db	A;Residues:	1-775 <PER>			
Pred. No.:			Qy	306	A;Cross-references:	GB:X04614; NID:g59832; PID:CAA28285.1; PID:959833		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	307	A;Introns:	19/3; 242/1		
Pred. No.:			Db	C;Superfamily:	herpesvirus immediate-early protein IE110; RING finger homology			
Pred. No.:			Qy	308	C;Keyword:	protein; transcription regulation; zinc finger		
Pred. No.:			Db	F;112-162:Domain:	RING finger homology <RNG>			
Pred. No.:			Qy	309	F;116-156:Region:	Zinc finger C3HC4 motif		
Pred. No.:			Db	Query Match	4.3%; Score 107; DB 1; Length 775;			
Pred. No.:			Qy	310	Best Local Similarity 24.7%; Pred. No. 5..2;			
Pred. No.:			Db	Matches 68; Conservative 18; Mismatches 89; Indels 80; Gaps 12;				
Pred. No.:			Qy	375	A;Residues:	1-775 <PER>		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	376	A;Cross-references:	GB:U15566; NID:g5558875; PID: AAC52697.1; PID:9558876		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	377	A;Gene:	Tbx2		
Pred. No.:			Db	C;Superfamily:	mouse transcription factor tbx2; T-box homology			
Pred. No.:			Qy	378	F;104-285:Domain:	t-box homology <TBX>		
Pred. No.:			Db	Query Match	4.4%; Score 107.5; DB 1; Length 701;			
Pred. No.:			Qy	379	Best Local Similarity 20.0%; Pred. No. 4..2;			
Pred. No.:			Db	Matches 99; Conservative 40; Mismatches 150; Indels 207; Gaps 20;				
Pred. No.:			Qy	380	A;Residues:	116-163		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	381	A;Cross-references:	ENBIL:AL049727 ; PIDN: CAB41553.2 ; GSDB:GN00070 ; PMID:87059760		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	382	A;Gene:	Tbx2		
Pred. No.:			Db	C;Superfamily:	mouse transcription factor tbx2; T-box homology			
Pred. No.:			Qy	383	F;104-285:Domain:	t-box homology <TBX>		
Pred. No.:			Db	Query Match	4.4%; Score 107.5; DB 1; Length 701;			
Pred. No.:			Qy	384	Best Local Similarity 20.0%; Pred. No. 4..2;			
Pred. No.:			Db	Matches 99; Conservative 40; Mismatches 150; Indels 207; Gaps 20;				
Pred. No.:			Qy	385	A;Residues:	116-163		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	386	A;Cross-references:	ENBIL:AL049727 ; PIDN: CAB41553.2 ; GSDB:GN00070 ; PMID:87059760		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	387	A;Gene:	Tbx2		
Pred. No.:			Db	C;Superfamily:	mouse transcription factor tbx2; T-box homology			
Pred. No.:			Qy	388	F;104-285:Domain:	t-box homology <TBX>		
Pred. No.:			Db	Query Match	4.4%; Score 107.5; DB 1; Length 701;			
Pred. No.:			Qy	389	Best Local Similarity 20.0%; Pred. No. 4..2;			
Pred. No.:			Db	Matches 99; Conservative 40; Mismatches 150; Indels 207; Gaps 20;				
Pred. No.:			Qy	390	A;Residues:	116-163		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	391	A;Cross-references:	ENBIL:AL049727 ; PIDN: CAB41553.2 ; GSDB:GN00070 ; PMID:87059760		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	392	A;Gene:	Tbx2		
Pred. No.:			Db	C;Superfamily:	mouse transcription factor tbx2; T-box homology			
Pred. No.:			Qy	393	F;104-285:Domain:	t-box homology <TBX>		
Pred. No.:			Db	Query Match	4.4%; Score 107.5; DB 1; Length 701;			
Pred. No.:			Qy	394	Best Local Similarity 20.0%; Pred. No. 4..2;			
Pred. No.:			Db	Matches 99; Conservative 40; Mismatches 150; Indels 207; Gaps 20;				
Pred. No.:			Qy	395	A;Residues:	116-163		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	396	A;Cross-references:	ENBIL:AL049727 ; PIDN: CAB41553.2 ; GSDB:GN00070 ; PMID:87059760		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	397	A;Gene:	Tbx2		
Pred. No.:			Db	C;Superfamily:	mouse transcription factor tbx2; T-box homology			
Pred. No.:			Qy	398	F;104-285:Domain:	t-box homology <TBX>		
Pred. No.:			Db	Query Match	4.4%; Score 107.5; DB 1; Length 701;			
Pred. No.:			Qy	399	Best Local Similarity 20.0%; Pred. No. 4..2;			
Pred. No.:			Db	Matches 99; Conservative 40; Mismatches 150; Indels 207; Gaps 20;				
Pred. No.:			Qy	400	A;Residues:	116-163		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	401	A;Cross-references:	ENBIL:AL049727 ; PIDN: CAB41553.2 ; GSDB:GN00070 ; PMID:87059760		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	402	A;Gene:	Tbx2		
Pred. No.:			Db	C;Superfamily:	mouse transcription factor tbx2; T-box homology			
Pred. No.:			Qy	403	F;104-285:Domain:	t-box homology <TBX>		
Pred. No.:			Db	Query Match	4.4%; Score 107.5; DB 1; Length 701;			
Pred. No.:			Qy	404	Best Local Similarity 20.0%; Pred. No. 4..2;			
Pred. No.:			Db	Matches 99; Conservative 40; Mismatches 150; Indels 207; Gaps 20;				
Pred. No.:			Qy	405	A;Residues:	116-163		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	406	A;Cross-references:	ENBIL:AL049727 ; PIDN: CAB41553.2 ; GSDB:GN00070 ; PMID:87059760		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	407	A;Gene:	Tbx2		
Pred. No.:			Db	C;Superfamily:	mouse transcription factor tbx2; T-box homology			
Pred. No.:			Qy	408	F;104-285:Domain:	t-box homology <TBX>		
Pred. No.:			Db	Query Match	4.4%; Score 107.5; DB 1; Length 701;			
Pred. No.:			Qy	409	Best Local Similarity 20.0%; Pred. No. 4..2;			
Pred. No.:			Db	Matches 99; Conservative 40; Mismatches 150; Indels 207; Gaps 20;				
Pred. No.:			Qy	410	A;Residues:	116-163		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	411	A;Cross-references:	ENBIL:AL049727 ; PIDN: CAB41553.2 ; GSDB:GN00070 ; PMID:87059760		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	412	A;Gene:	Tbx2		
Pred. No.:			Db	C;Superfamily:	mouse transcription factor tbx2; T-box homology			
Pred. No.:			Qy	413	F;104-285:Domain:	t-box homology <TBX>		
Pred. No.:			Db	Query Match	4.4%; Score 107.5; DB 1; Length 701;			
Pred. No.:			Qy	414	Best Local Similarity 20.0%; Pred. No. 4..2;			
Pred. No.:			Db	Matches 99; Conservative 40; Mismatches 150; Indels 207; Gaps 20;				
Pred. No.:			Qy	415	A;Residues:	116-163		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	416	A;Cross-references:	ENBIL:AL049727 ; PIDN: CAB41553.2 ; GSDB:GN00070 ; PMID:87059760		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	417	A;Gene:	Tbx2		
Pred. No.:			Db	C;Superfamily:	mouse transcription factor tbx2; T-box homology			
Pred. No.:			Qy	418	F;104-285:Domain:	t-box homology <TBX>		
Pred. No.:			Db	Query Match	4.4%; Score 107.5; DB 1; Length 701;			
Pred. No.:			Qy	419	Best Local Similarity 20.0%; Pred. No. 4..2;			
Pred. No.:			Db	Matches 99; Conservative 40; Mismatches 150; Indels 207; Gaps 20;				
Pred. No.:			Qy	420	A;Residues:	116-163		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	421	A;Cross-references:	ENBIL:AL049727 ; PIDN: CAB41553.2 ; GSDB:GN00070 ; PMID:87059760		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	422	A;Gene:	Tbx2		
Pred. No.:			Db	C;Superfamily:	mouse transcription factor tbx2; T-box homology			
Pred. No.:			Qy	423	F;104-285:Domain:	t-box homology <TBX>		
Pred. No.:			Db	Query Match	4.4%; Score 107.5; DB 1; Length 701;			
Pred. No.:			Qy	424	Best Local Similarity 20.0%; Pred. No. 4..2;			
Pred. No.:			Db	Matches 99; Conservative 40; Mismatches 150; Indels 207; Gaps 20;				
Pred. No.:			Qy	425	A;Residues:	116-163		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	426	A;Cross-references:	ENBIL:AL049727 ; PIDN: CAB41553.2 ; GSDB:GN00070 ; PMID:87059760		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	427	A;Gene:	Tbx2		
Pred. No.:			Db	C;Superfamily:	mouse transcription factor tbx2; T-box homology			
Pred. No.:			Qy	428	F;104-285:Domain:	t-box homology <TBX>		
Pred. No.:			Db	Query Match	4.4%; Score 107.5; DB 1; Length 701;			
Pred. No.:			Qy	429	Best Local Similarity 20.0%; Pred. No. 4..2;			
Pred. No.:			Db	Matches 99; Conservative 40; Mismatches 150; Indels 207; Gaps 20;				
Pred. No.:			Qy	430	A;Residues:	116-163		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	431	A;Cross-references:	ENBIL:AL049727 ; PIDN: CAB41553.2 ; GSDB:GN00070 ; PMID:87059760		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	432	A;Gene:	Tbx2		
Pred. No.:			Db	C;Superfamily:	mouse transcription factor tbx2; T-box homology			
Pred. No.:			Qy	433	F;104-285:Domain:	t-box homology <TBX>		
Pred. No.:			Db	Query Match	4.4%; Score 107.5; DB 1; Length 701;			
Pred. No.:			Qy	434	Best Local Similarity 20.0%; Pred. No. 4..2;			
Pred. No.:			Db	Matches 99; Conservative 40; Mismatches 150; Indels 207; Gaps 20;				
Pred. No.:			Qy	435	A;Residues:	116-163		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	436	A;Cross-references:	ENBIL:AL049727 ; PIDN: CAB41553.2 ; GSDB:GN00070 ; PMID:87059760		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	437	A;Gene:	Tbx2		
Pred. No.:			Db	C;Superfamily:	mouse transcription factor tbx2; T-box homology			
Pred. No.:			Qy	438	F;104-285:Domain:	t-box homology <TBX>		
Pred. No.:			Db	Query Match	4.4%; Score 107.5; DB 1; Length 701;			
Pred. No.:			Qy	439	Best Local Similarity 20.0%; Pred. No. 4..2;			
Pred. No.:			Db	Matches 99; Conservative 40; Mismatches 150; Indels 207; Gaps 20;				
Pred. No.:			Qy	440	A;Residues:	116-163		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	441	A;Cross-references:	ENBIL:AL049727 ; PIDN: CAB41553.2 ; GSDB:GN00070 ; PMID:87059760		
Pred. No.:			Db	C;Genetics:				
Pred. No.:			Qy	442	A;Gene:	Tbx2		
Pred. No.:			Db	C;Superfamily:	mouse transcription factor tbx2; T-box homology			
Pred. No.:			Qy	443	F;104-285:Domain:	t-box homology <TBX>		
Pred. No.:			Db	Query Match	4.4%; Score 107.5; DB 1; Length 701;			
Pred. No.:			Qy	444	Best Local			

RESULT 32

E70554 Hypothetical protein Rv148C - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;ID: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: E70554 R;Role: S.T.; Broich, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Raaijmakers, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-541, 1998 A;Authors: Scarves, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; PMID: 963430 A;Status: Preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residue: 1-482 <COL> A;Cross-references: GB:295584; GB:AL123456; PIDN: CAB09036..1; PID: g2117186 A;Experimental source: strain H37RV C;Genetics:

A;Gene: Rv148C C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1945

Query Match Score 4.3%; Best Local Similarity 24.7%; Pred. No. 3.4%; Matches 77; Conservative 21; Mismatches 94; Indels 120; Gaps 16;

Qy 204 TVHLEGGTAKVLDKDLSPGDRVLAADDQGRIL-LYSDFELTFLDRDGAKPVYVI--ETR 258 Db 100 TALTEQHQKIA-LONGERSLKSPIOSDIFSGFQTC---AKEVLOVLSRFREW 152

Qy 259 EPRLPLLTAAHLFVA---PHDSDATEPEAHSGGPPS-GQALCPRALPASRVPB 311 Db 153 TPREPCRVQLINHLHAVALQFLPTPOLIQQVPLSKGTAPSAGSAAP---CLEPA 207

Qy 312 GQRV---YVV----AERD-----AVVISVTLSE 339 Db 208 GKLEPLAYCVPVIRTOPSAAELAENDDDSGYGEAFARPDEKGAGASRTVHQ 267

Qy 340 EAAGAYAPLAPLQAGTTILNRASCYAVIEEHSWAHRAFAPFLRHALLAALAPARTDRGG 399 Db 268 EPPGEPSP-----APKRM-----KLDSSRG 287

Qy 400 DSGGGDBGGGGGRVALTAAGAADAAGAGATAGIHWYSCULYQIGTWLLSEALHPLGMAY 459 Db 288 GSGGGCGG-----ARAAAALLGDPAAAL-----LRPDALL 323

Qy 460 KSSXSXSGAGGA 471 Db 324 SSLVAVGGCGA 335

RESULT 34

T09084 phosphatidylinositol 3-kinase - Chlamydomonas reinhardtii (fragment) C;Species: Chlamydomonas reinhardtii C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 C;Accession: T09084 R.Molendijk, A.J.; Irvine, R.F. Plant Mol. Biol. 37, 53-66, 1998 Article: Inositol signalling in Chlamydomonas: Characterization of a phosphatidylinositol kinase. PMID: 9620264 A;Status: Preliminary; translated from GB/EMBL/DBJ A;Molecule type: DNA A;Residues: 1-490 <COL> A;Cross-references: EMBL:U97663; NID: g2109290; PIDN: AAC50018..1; PID: g2109291 A;Experimental source: strain cw-15 C;Genetics: C;Introns: 265/3; 331/3; 370/3; 455/1; 481/3

Query Match Score 4.3%; Best Local Similarity 25.1%; Pred. No. 3.7%; Matches 23; Mismatches 123; Indels 81; Gaps 15;

Db 191 VAAKSGGGFPFGATAVHLEQGTTKLVDLSPGDRVLADDQGRILYSDFLTL---DRDD 246 C;Species: Homo sapiens (man) Db 234 LAAGGG---GGG-----GGG-----SPDGSTAR-----MBWLAFCVKYFDLP 271

C;Accession: JCT583 R;Fujimoto, K.; Shen, M.; Matsubara, K.; Shingu, S.; Honda, K.; Yoshida, E. Biochem. Biophys. Res. Commun. 280, 164-171, 2001 A;Title: Molecular cloning and characterization of DEC2, a new member of basic helix-loop-helix protein, DEC2 - human C;Species: Homo sapiens (man) Db 272 DAQLVLLVEAEGRREALVGSSVTPLFSKRGRLKTSQRLAVWEAAP-----PCTQFP 325 A;Reference number: JCT583; PMID: 11162494

C;Species: Streptomyces fradiae
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000
C;Accession: T14070
R;Hosted, T.J.; Baller, R.H.
A;Molecule type: DNA
A;Residues: 1-124 <HOS>
A;Cross-references: EMBL:AF016696; NID:92738764; PID:g2738765; PTDN: AAC01566.1
C;Genetics:
A;Note: cps-1
C;Superfamily: Mycobacterium tuberculosis mbtE Protein/ acetate-CoA ligase homolog
C;Keywords: carrier protein; phosphopantetheine; phosphoprotein
F;188-612/Domain: acetate-CoA ligase homology <ACP>
F;559-727/Domain: acyl carrier protein homology <ACP>
F;691/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match	Score 4.3%	Length 1324;
Best Local Similarity	22.2%	DB 2;
Matches	108;	Pred. No. 14;
Conservative	52;	Mismatches 188;
Matches	108;	Indels 139;
		Gaps 21;

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Qy      52 AEKTLGASG-RYEKGKISRNRNSEEFK-----ELTPNNNPDIIFKDEENTGAABLMT 99
Db      46 AVSAGHGLR EGGSGRTTNHEPLSLYALPQPAHLRLDRPDAV-----DDVTT 96
Qy      100 QRCKDKL-----NLAISYMWNPFGVKLRVTEGWDGEHHSE 136
Db      97 RHAADLLERBLTAHVHSAPATPTAAATAATPATARAAPAPRAAGEGAPATIVDAFEARVRATP 156
Qy      137 ESLHYEGRAVDITTSDRSKYGMIAALAVEAGFDWVYTESAHIIROSVAENSYA--- 193
Db      157 EAPAVLAGEEBELTYAED-AARANLRLBEGG-----TGPESRATVSRNAMLPVAVLGI 212
Qy      194 -KSGCF-PGSATVHLEQGGTKLVKDLSPGDRVLAADDQGRLLYSDFLTLDRGAKKV 251
Db      213 LKGGCYYPVGATPLPR-AARTLREPAPVCLLTDPAEAARTTAAAPTGDQRDEA--- 268
Qy      252 FYYVIEETREPR--ERLLIITAHLLEFV--APHNSATGEP-----EASGGSPBSGG 297
Db      269 -----PGGVERVLTGALLAAFDPAPPTDAERAAGLPLPGHLAVYLHTSSSGRSRKGV 320
Qy      298 ALGRPAFLFASRVEPREGQRTYVAERDGERLPPAVHSTSEAAQGYAPLTAQGTI--- 354
Db      321 AVEHQVTALLSWAGTV-----GADPLHRTVASTSESFDVSVEDTIVPLTGRIEIV 374
Qy      355 -----LINVRLASCYAVIE----HSL-AHRAFAFPRLAHALLALA 391
Db      375 ENTIAVADRTGEGEPSLNIAVPSALQALLERGEDIAVHFLCAGEPF-DAPLRSLRRAFP 433
Qy      392 PAR-----TDRGDSGGGDRGGGGRVVALTAFGAADAP---GA 426
Db      434 RARVANLYGPTETTVFVTAHFLDDGAPPVG--RPLPGVRVHILDPWLRPVFDGVVGE 491
Qy      427 GATAGH 433
Db      492 LYLAGEH 498

```

RESULT 37
T36248 CDA Peptide synthetase I - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 01-Dec-2000
C;Accession: T36248
R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajand
A;Reference number: Z21602
A;Accession: T36248
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-7463 <SAU>

A;Cross-references: EMBL:AL035640; PIDN:CARB38518.1; GSPDB:GN00070; SCOEDB:SCE63.03c
 A;Experimental source: strain A3 (2)
 C;Gene: cdaps1; SCOEDB:SCB63.03c
 C;Superfamily: acetate-CoA ligase homology; acyl carrier protein homology
 C;Keywords: carrier protein; phosphonate; phosphoprotein
 F;16-10/4:Domain: acetate-CoA ligase homology #status atypical <AC11>
 F;1090-15/1:Domain: acyl carrier protein homology <ACP1>
 F;115-2184/7:Domain: acetyl-CoA ligase homology <AC12>
 F;1200-2268/7:Domain: acetyl carrier protein homology <ACP2>
 F;3265-3329/7:Domain: acetyl carrier protein homology <ACP3>
 F;1323-4746/7:Domain: acetyl carrier protein homology <ACP4>
 F;1762-4830/7:Domain: acetyl carrier protein homology <ACP5>
 F;5163-5786/7:Domain: acetate-CoA ligase homology <AC15>
 F;5102-5870/7:Domain: acetyl carrier protein homology <ACP6>
 F;1122-2232-2297-4794-5834-6916/Binding site: phosphopantetheine (Ser) (covalent) #status
 F;118 PGVRLRVTCWDEGHH-----SERSLHYEGRADTTSD--RDRSK 157
 Db 450 PDEBERVLQWNDTAHEVDETTLPFLPARAARTPGHBAVVEGSTSLTYAELDARAERLA 509
 Qy 158 YGMLARLAVAEAGFDWVYYSKSAHTHCSYTAENSAAKSGCF----- 199
 Db 510 GALTARGAQPFRFVAVRSAAELVALLA---VLSKGAAVPVDPGYPADRIAHILRD 565
 Qy 200 -----PGSATVHL----- 207
 Db 566 AGAMLVLTTRDTAERLPGCSTPRLLDEAAAGTAAAGAAPPGTLPFLAPFGHPAYVI 625
 Qy 208 -EQGTTKLK-----DLSPGDRVLAADD-----QG 231
 Db 626 YTSGSGTGRPGVVISHRA1VNRLAWMDQYGLPSDRVLYQTKTPSGFDVSVWEFWPLVQG 685
 Qy 232 RLL-----YSD---FLTFIDRDDGAKKFYV----TETREPERPLI-LTAAHLIF- 273
 Db 686 ATLVVAPRGHTDPAYLAGTVVRREGCVTTLHFVPSMLDFVRRFCG 745
 Qy 274 -----VAPHNDSATGPBEPA-----SGSGP----- 293
 Db 74 6 GEALPAELRARFRAYSDVPLHN--LYGPEAAVDVTYWWCAEDTGDPPIGRPVWNTTRM 803
 Qy 294 -----PSG-----GAIKPRLFAASRY-----RPQRYVVAE-- 320
 Db 804 YVLDAAIRPVBAAGVPGELYTAGVQLARGLTGRPLASAERTADPHGAPSMTRTGDLAR 863
 Qy 321 -RDGDERRLPLPAEVSVTL-----SEBAAGAYAPLTAQGTTILINRLASCYAVIEEH 370
 Db 864 WNHDGSLDYLGRADIHQVKLRGFRFIELGEAALYRQEPAIAQAAVVLR-----EDR 913
 Qy 371 SWAHRFA--PFRLNAHLLAALAPARTDGG-----GDSGGGRGGGGGVRAIT 416
 Db 914 PGDQRQLVAYTYPARDATLTCPPABGTHCPGAAPDTDAFGTAAGTSGPGS-----T 969
 Qy 417 AFGAAADAPGAGATAGTHWYSLLYQIGTWILDSEALHPL--GMAVKSSXSRGNGGARE 473
 Db 970 GSGTGSSGTGSCARPG----PDGTATHTVAGAGPAAAGGETAAGDAGTC 1014
 Qy 474 G 474
 Db 1015 G 1015
 RESULT 38
 T33110 hypothetical protein C18H7.3 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
 C;Accession: T33110
 R;Tin-Wallam, A.; Fronick, W.
 Submitted to the EMBL Data Library, May 1998
 A;Description: The sequence of *C. elegans* cosmid C18H7.
 A;Reference number: Z21284
 A;Accession: T33110
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-460 <TIN>
 A;Cross-references: EMBL:AF067607; PIDN:AXC17641.1; GSPDB:GN00022; CESP:C18H7.3
 A;Experimental source: strain Bristol N2; clone C18H7
 C;Genetics:
 A;Gene: CESP:C18H7.3
 A;Map position: 4
 A;Map: C18H7.3
 C;Superfamily: Phaeosolus glycine-rich cell wall protein 1.8
 C;Introns: 84/1
 Query Match 4.3%; Score 105.5; DB 2; Length 460;
 Best Local Similarity 28.9%; Pred. No. 3 8; Mismatches 100; Indels 56; Gaps 11;
 Matches 67; Conservative 9; MisMatches 100; Indels 56; Gaps 11;
 Qy 275 APHNDSATGEP-----EASSGSGP-PSC-GALGPRALFAASRVPGORVYVVAERDG- 323
 Db 207 AGEPPAGPAGPFPGPNGAGGSGGPFPGPAGPFPGPNGKDGEEAGAPG-----KDG 258
 Qy 324 -----DRLIIPAVHSVTL---SREAAAGAYAPLTAQGTTILINRLASCYAVIEEH 370
 Db 259 AGADGAPGTDAAYCOPPRSAALGAGGEPAGA-APEA-----AAAPPAAPEA 308
 Qy 371 SWAH-----RAFAPFLLAHALAALAPARTDGGDSGGGDRGGGGRVALTAGAA 421
 Db 309 PAEAGGGAEPAAGAAPDAAAAPEAEEAAPAEEAAPAEGAGGAAPAARPDAAAAPPEA 368
 RESULT 39
 A55207 glycerol-3-phosphate dehydrogenase glpD (EC 1.1.1.-) - *Pseudomonas aeruginosa*
 C;Species: *Pseudomonas aeruginosa*
 C;Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change 11-Jun-1999
 R.Schweizer, H.P.; Po, C.
 A;Accession: A55207
 J. Bacteriol. 176, 2184-2193, 1994
 A;Title: Cloning and nucleotide sequence of the glpD gene encoding sn-glycerol-3-phosphoglycerate kinase
 A;Reference number: A55207; PMID:94209216; PMID:8157588
 A;Accession: A55207
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-510 <SCH>
 A;Cross-references: GB:L06231; NID:9450177; PIDN:AAA81584.1; PID:9450378
 C;Genetics:
 A;Gene: glpD
 C;Superfamily: glycerol-3-phosphate dehydrogenase (aerobic)
 C;Keywords: oxidoreductase
 Query Match 4.2%; Score 104.5; DB 2; Length 510;
 Best Local Similarity 23.5%; Pred. No. 4.7; Mismatches 35; MisMatches 123; Indels 139; Gaps 20;
 Matches 91; Conservative 91; MisMatches 123; Indels 139; Gaps 20;
 Qy 103 KDKLNALAIISVNNQWPGVYLRLTEGNDDEGHSEESLHYEGRAVDTTSDRSKYGMAL 162
 Db 125 REGLPASACVQRQQP-LKAEIQRGGF-----YSDCAVDD-----A 159
 Qy 163 RLAVEAGEDWVYYESKAIHHCYSVKAENSVAK-SGCCFPGSAT----- 204
 Db 160 RLVVLNAIS--AREGAAVHTAPAAASPVAARDSGCTWSATAACIRSARALVNAGPW 217
 Qy 205 -----VHLEQGGTKLVKD1SPGDRVLAADDGRLI-----YSDFITFL- 242
 C;Species: *Caenorhabditis elegans*

RESULT 40

S23077

moresonin polyketide beta-ketoacyl synthase (EC 2.3.1.-) chain 2 - Streptomyces cinnamoneus

C:Species: Streptomyces cinnamoneus

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S23077; S16168

C:Keywords: nucleic acid repeat

P:arrowsmith, T. J.; Sherman, D. H.; Birch, A.; Hopwood, D. A.; Robinson, J.

Mol. Gen. Genet. 234, 254-264, 1992

A:Title: Characterisation of actI-homologous DNA encoding polyketide synthase genes from P:22-398:Domains: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

A:Accession: S23077

A:Molecule type: DNA

A:Residues: 1-402 <ARR>

A:Cross-references: EMBL:211511; NID:946799; PID:CAA77597.1; PID:946801

C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-protein] synthase: acyltransferase

F:22-398:Domains: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Query Match Score 104; DB 1; Length 402; Best Local Similarity 24.1%; Pred. No. 3.7; Mismatches 33; Indels 126; Gaps 21; Matches 95; Conservative

Qy 140 HYEGRAVDITTSBDRSKYGMALARLAVAGFDWYYESKAHICSYKAENSY--AAKSGG 197

Db 60 HLPGRLVPT---DR---VTRSLAAL-A-DVALADAGVEAAFDDLMGVVTASHAGG 109

Qy 198 CFPSSATVHEGGTKLKVDSLSPDRVLADDGRLYSDFLTLDGAKKVPY--- 253

Db 110 -----FEFGDELQLKLGGCQPVLSA-----YQSFAMFYANNSQISIRGMKG 153

Qy 254 -----VIETREPERLILTAAHILFVAPHNDSATGEPEASSGSPPGGAGLGP 302

Db 154 PSGVVPSDQGGLALAQQRRLVKGTPLIV-----CGAVERPRAQAGSSSPRGG-- 205

Qy 303 ALFASRVRPQRYVVAERDGDRLLPAHVSYTLESEAAGAYAPLTAQGTILINRYLAS 362

Db 206 ---MSDSDEPNRAVLPFDGD-RGYVPGGCRGVVPPFLRBEA AP--ARGA---- 249

Qy 363 CYATTEHHWAHRAPAFP----BLAHALLAALAPARTRG----GDSGG--GDRGG 408

Db 250 --EVYGEAGFLARLPAPHSGRGSTRAHTAATLADDACTGDPDTRVFDGGGRYNPDBAE 307

Qy 409 -----GGGRVIALTAP-----GAADAPGAGA----TAGI-----HW 435

Db 308 AEAISEVFRGPVTPCPRMTGRLHSGAFLDVACALIAMSAGVIPPTVHDPCPEIDL 367

Qy 436 SQQLYQIGTWWILDSEALHPIGMAYKSSXSRGAGG 469

Db 368 DLVLLQV-----RPAALRTALGGARGHGG 391

Qy 465 RGAGGGAREGA 475

Db 988 TWASGEENGKA 998

N:Alternate names: Protein YM9571.08; protein YML010w

C:Species: Saccharomyces cerevisiae

C:Accession: A4053; S55109

R:Swanson, M.S.; Malone, E.A.; Winston, F.

R:Gentles, S.; Bowman, S.

A:Title: SPTS, an essential gene important for normal transcription in *Saccharomyces cerevisiae*

A:Reference number: A40253; MUID:91246167; PMID:1840633

A:Accession: A40552

A:Molecule type: DNA

A:Residues: 1-1063 <SWA>

A:Cross-references: GB: M62882; NID:9172679; PID:AAA35085.1; PID:9172680

R:Cross-references: P:148-216/Region: aspartic acid/glutamic acid-rich

submitted to the EMBL Data Library, June 1995

A:Reference number: S55109

A:Accession: S55102

A:Molecule type: DNA

A:Residues: 1-1063 <GEN>

A:Cross-references: EMBL:Z49810; NID:9854472; PID:CAA89942.1; PID:9854480; MIPS:YML010w

A:Experimental source: strain AB972

C:Genetics:

A:Gene: SGD:SPT5

A:Cross-references: SGD:S0004470; MIPS:YML010w

A:MD Position: 13L

C:Keywords: tandem repeat

P:148-216/Region: 6-residue repeats

F:931-1053/Region: 6-residue repeats

Query Match Score 104; DB 2; Length 1063; Best Local Similarity 21.6%; Prd. No. 13; Mismatches 61; Indels 168; Gaps 29; Matches 119; Conservative

Qy 45 KQFIPNVAEKTIGRSGRYEG-----KTSRNSERFKEUTPNTNPDI-TIKFDEBENTGADR 97

Db 496 KNIQITVVE--LAIFGSKEGAVDLTSYQSIIKQAQKRVTFQGDR-BLVNLSEQRGKG 553

Qy 98 MTQRKD---KINALA-----ISVANIQ--WPGVKLRLVTEGWDGHSHSESL----- 139

Db 554 VTRTRKDIATIKUNGFTPLEFPSTLRKTFQGDHTVING---BHQDGAGLVNEQ 609

Qy 140 -----HYEGRAVDITTSBDRSKYGMALARLAVAGFDWYYESKAHICSYKAENSV- 191

Db 610 GQVTFEMSTSREVTTIANLSK--IDTTATSEYALHDIVELSAK-NVACITIQAGDIF 667

Qy 192 -----AKSGCFEPGSATVHLQEGTTLVQDKLPSGDRVLAADD-----QGRLLYSD 237

Db 668 KVIDETGKYSTITOSILEKINTARAYARISSVTDANGNEIKIGDTIVEKGSRREGVLYIQ 727

Qy 238 FLTFLDRDGAKKYVIFTREPREPLILTAHILFVAPHN-----DSAT 282

Db 728 -----TQQIFV-----SKVIVENAGFVNVPNSNVEAVASKDNMLSNKMDLSK 770

Qy 283 GEPEASGSGPS-----GG--ALGPRALFASRVRGQRVYVAERDGDRLL 328

Db 771 MNPEITSKMGPSSXTFQQPIQSQQGREGVALKTVTFRSAGYKGQ-LGIVKDVGNDKATV 829

Qy 329 PAATIS-----VTLSEBAAAGAYAPLTAQGTI--LINRVLASCYAVIEEHSWAHRAFAFR 381

Db 830 --ELHSKNKHITIDKHLTYNNREGEGEGITYDELVNR -- RGRVPARMGPSPYVSARN 883

Db 382 LAHALIAALA-----PARTDRGGDSGGG-----PARTDRGGDSGGG 411

Db 884 MATGGIAAGAAATSSGSGGMMTPGWSFDCGKTPAVNAHGGSGGGVSSWGASTWGSQG 943

Qy 412 RVALTPGAAADAPGAGATAJLHWSQLLQIGWLDSALHPLGMV---KSS--XS 464

Db 944 NGGASWNGGA---GGGASA---WGSQGTGATSTW-----GGASWGNKSSWGSAS 987

RESULT 41

A40253 acidic nuclear protein SPTS - yeast (*Saccharomyces cerevisiae*)

RESULT 42						
T30342	protein HMWP1 - Yersinia enterocolitica					
C;Species: Yersinia enterocolitica						
C;Accession: T30342						
C;Accesion: T30342	22-Oct-1998 #sequence_revision 22-Oct-1999 #text_change 01-Dec-2000					
R;R;Belouat, C.; Schubert, S.; Heesemann, J.						
J;Title: The Yersinia enterocolitica gene cluster of Yersinia enterocolitica: organization, structure, and expression of the yersiniabactin biosynthetic genes						
A;Reference number: 220833; MUID:98117033; PMID:9457855						
A;Accession: T30342						
A;Status: preliminary; translated from GB/EMBL/DBJU						
A;Cross-references: EMBL:Y12527; NID:e1228641; PID:e1228642; PIDN:CAA73127.1						
A;Residues: 1-3161 <PEL>						
A;Molecule type: DNA						
C;Geneticloc:						
A;Gene: irp1						
C;Superfamily: 3-oxoacyl-1-fatty-acid-carrier-protein synthase I homology: acyl carrier protein						
C;Keywords: carrier protein; phosphopantetheine; phosphoprotein						
C;Domain: 3-oxoacyl-1-acyl-carrier-protein synthase I homology <OAS>						
F;FE:8116-887/Domain: acyl carrier protein homology <ACP1>						
F;FE:2855-2892/Domain: acyl carrier protein homology <ACP2>						
Banding site: phosphopantetheine (Ser) (covalent) #status predicted						
Query Match Score 4.2%; Score 104; DB 2; Length 3161;						
Best Local Similarity 20.9%; Pred. No. 54; Mismatches 51;保守性 Matches 106; Gaps 24;						
Matches 106; Conservatory 51; Mismatches 142; Indels 208; Gaps 24;						
Qy 105 KLNALAISYMNONQGVK-LRVTE-----GWDDE--GHHSEBSLHYEGRAYDITI 150						
Db 137 KTGFASSRMSTVYGRREALNYTEAQVKGQLCSUMGNDIDYIATRAAYKLNLHGPALSQV 196						
Qy 151 SDRDRSKYGMALARAVEAGFDWVYESXAHHS-SVRAENSAVAKSNSG---CFPGSATVH 206						
Db 197 A---CSSSLVA-----VHLACESLRAAGESDMAVAVGVALSFPPQQAGYR 236						
Qy 207 LEQG-----GTVKVDLSPGDRLTAADQGRILYSDPLTF 241						
Db 237 YQPQMIFSPDGHCAPPFDASAEGTAGNGLGVRLRLR-DAILSQDP---IISVTLSS 290						
Qy 242 LDRRDGAKKYVVFYVLETRPREPLILTRABHLFVAPNHDSATGEPEASSGSGPSSGGALGP 301						
Db 291 AVNDGNRKYGYTFPSVSAQAVBEA---LMLAIDDRQVGYE-THGIGPLGDAIEI 346						
Qy 302 RALFASRVRPGQRTYVVAERDGDRLPAVHS-----						
Db 347 EAL-----RNYY-APRPODQRCLGSKVRSNMGHLDTAAGIAGLKTIVLAVSRQIP 396						
Qy 335 -----VTLSEEANGA 344						
Db 397 PLINFHPTPNBALKLEESPFTIPVSAQAWQDEMERYAGVSSFGIGGTNCMHIVASLPDLNA 456						
Qy 345 YAPLTAQG----TILIN-----RVLASCYA-VIEEHs-----WAHRAFAFRL 382						
Db 457 RLPTNDSGRKSTALLLSAADSARLDRLLTADLAGLRENTDASLAAFTALHARRLDLPRL 516						
Qy 383 AHALLAALAALPARTDRGGDSGG---GDRCGGGGARYVALTAPGAADAPGAGATAICHW-Y 436						
Db 517 AAPLNRETAAALSDWAGEKSGLTYSGHGSKGQZWLF-----GOGS---HWRTMG 565						
Qy 437 QLIWQGTWLD-----SENHP 454						
Db 566 QTMYQHGSTAFADMLDRCFSSACSEMLTP 592						
RESULT 43						
S33121	homoeotic protein CDP - dog (fragment)					
N;Alternate names: CCAAT displacement protein; homeotic protein C-Dox						
C;Species: Canis lupus familiaris (dog)						
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999						
C;Accession: S33121						
P;Andersson, V.; Nadai-Ginard, B.; Mahdavi, V.						

Clox, a mammalian homeobox gene related to *Drosophila cut*, encodes DNA-binding protein. *Development* 116, 321-334, 1992
A1: Reference number: S33121; MUID: 9316194; PMID: 163085

A	Accession:	S33121
A	Status:	preliminary
A	Molecule type:	mrNA
A	Residues:	1-975 <ANP>
C	Cross-references:	EMBL:X69017; PIDN:CAA48782.1; PID:G2202
C	Superfamily:	homeotic protein CDP; cut repeat homology; homeobox homology
C	Keywords:	DNA binding; duplication; homeobox; nucleus; transcription regulation
F	1-67/Domain:	cut repeat homology (fragment) <CU1>
F	183-455/Domain:	cut repeat homology <CU2>
F	566-638/Domain:	cut repeat homology <CU3>
F	685-741/Domain:	homeobox homology <HOX>
Query Match	4.2%	Score 103.5; DB 2; Length 975;
Best Local Similarity	23.8%	Pred. No. 13;
Matches	71;	Conservative
QY	166	VEAGFDWVYYEYKAKHICGSKRAENSAVARSGGGFPGSATRVHUGQGTLVKDLSJPQGDVVL 225
DB	635	VEILMDMVERMKTAY---MRRHHSSVYNSDQPCEPPSUGIDYSQGASDOPQHLKKPFRV 690
QY	226	AADDQGRLL-----YSDFLTFLD-RDDGAKKVFYVIETREPREPLLTTAAH 270
DB	691	LAPEKEALKRAYCQQKPPSPSKTIEELAQLNKRTSTINWFENYRSIRRE----- 742
QY	271	LLFV-----AHNDSDATGEPAASSGGPPSGS-----ALGPRLFASRYR 310
DB	743	-LFFEEIIQAGSQCGAAGHSPSA----RSSGAAPSSRGDSCDGVEAEGPGADA---- 792
QY	311	PGQRVYVVAERDGDRLIPAAVHSVTLSBEAAAGAYAPLTAQGTITLINVLASCYAVIIEH 370
DB	793	-----ESAAADAAAGSQQGP----- 807
QY	371	SWAHRFAPEFLAHALLAALAPARTDGGDSGGDRGGGGRVALTAGAADDAGAGA 428
DB	808	-AEAIAVADBEREBAPRAEKRSRPRGPQGPGRGGG----PAPGAPARAAAA 858
RESULT 44		
E70661	probable PE protein - Mycobacterium tuberculosis (strain H37RV)	
C	Species:	Mycobacterium tuberculosis
C	Date:	17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C	Author:	E70661
R	; Brosh, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Cole, S.T.; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holst, I.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skeates, S.; Squares, S.	
Nature	393, 537-544, 1198	
A	Authors:	Spokes, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A	Title:	Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence
A	Reference number:	A70500; MUID:98295987; PMID:9634230
A	Accession:	E70661
A	Status:	preliminary; nucleic acid sequence not shown; translation not shown
A	Molecule type:	DNA
A	Residues:	1-413 <COL>
A	Cross-references:	GB:Z838860; GB:AL123456; NID:93251681; PIDN:CA06157.1; PID:91
A	Experimental source:	strain H37RV
C	Genetics:	
C	Superfamily:	Phaseolus glycine-rich cell wall protein 1.8
Query Match	4.2%	Score 102.5; DB 2; Length 413;
Best Local Similarity	25.5%	Pred. No. 5;
Matches	51;	Conservative
QY	287	ASSGCGPPSGGAL-----GPRALFASRVRCQRYVVAERDGDRLLPAAVHSVTI 337
DB	28	ANAAAAPTPAVGLAGGDDVSAGIAALFHDRL-----FVQI 79
QY	338	SEEAGAYAPLTAQSTLINVLASCYAVIEHWSWAHAFAPPRLAHALLAALAPARTDR 397

Db 80 LOEQAAYAANAL----PLQKAQGVYSELAQDRT-- 113
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-481 <WIL>
 A;Cross-references: EMBL:279605; PIDN: CAB01902.1; GSPDB: GN00028; CESP: ZK678.5
 A;Experimental source: Clone ZK678.5
 A;Gene: CESP-ZK678.5
 A;Map position: X
 A;Introns: 33/3; 99/3; 131/2; 211/1; 324/3; 342/1; 381/3; 436/3
 Db 398 GDSGGEDRGCGGGRVLTAACTAACADPGRAGATAGTHWYDOLLYQIGTWWILDSEALHHP--- 454
 Qy 114 GTGTGGSRSRAGG----FFGVGQAGKKGWDGGTIGNGQVGEQHAGQLGSTDGNGYA 167
 Qy 455 ---LGNVAKVSKXSRSRGAGGA 471
 Db 168 GAHGSGSVASHGSGATGAA 187

RESULT 45
 hypothetical protein Rv0341 - Mycobacterium tuberculosis (strain H37RV)
 C;Species: Mycobacterium tuberculosis
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C;Accession: F70573
 R;Cole, S.T.; Broscb, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 527-544, 1998
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitchurch, S.; Barrell, B.G.
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A;Reference number: A70500; MUID: 98295987; PMID: 9634230
 A;Accession: F70573
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-479 <COL>
 A;Cross-references: GB:Z93224; GB:AU123456; NID:93261760; PIDN: CAB08573.1; PMID:92094820
 A;Experimental source: strain H37RV
 C;Genetics:

C;Gene: Rv0341
 C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8
 C;Homologs: Deinococcus radiodurans (strain R1)

Query Match 4.2%; Score 102.5; DB 2; Length 479;
 Best Local Similarity 24.6%; Pred. No. 6.1; Indels 91; Gaps 13;
 Matches 77; Conservative 30; Mismatches 115; Indels 115;

Qy 237 DFLTPLDRDGAKKVFYVETPRERLLITAHILLFVAPNHSATGE---PEASSGSCP 293
 Db 6 DYIISLFREDDAARSFVAPGR----AMTSAGLIDIAHQISSYAAANTVPGLNIGAGD 59
 Qy 294 PSSGALGPAPLFAASRVRPGQRVTVVAEEDGDRLLPAVHSVTLSPEAGAYAPLTA--- 350
 Db 60 PMSGL----RQAVAAHRHFQADVANVGFAGD---AGRAVASVTTDVGAAGSLGAGEL 112
 Qy 351 -QGTI----LINEVVLASCVAVIEBSWAHRAFAPFRD----AHALLAAL 390
 Db 113 GQGGLALAASSGGPGQVLAQVGLGFTAVAEVGA-QVAGGLGIGTGGLGAQGMGFG 171
 Qy 391 APARTDRGGDSGG-----GDRGGGGRRVALTAPGAAADAPGAGATAGIHWS 436
 Db 172 GGVGIGLGQAGGVGGAGGAGAAGVGGAGQAV--GAGYAGVGGQAA 228
 Qy 437 QLXQIG----TWLIDSE--AHLPLGHAVKKS 462
 Db 229 GIASQIGVSAAGGGGGAGAAGVGGAGLJASEGAALNAAAMPHLSG 288

Qy 463 XSRGAGGGAREGA 475
 Db 289 PLAGYGVGGGAGA 301

RESULT 46
 hypothetical protein ZK678.5 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C;Accession: T27975
 R;Kershaw, J.
 Submitted to the ENBL Data Library, August 1996
 A;Reference number: Z20449
 A;Accession: T27975

Db	787	-VARAAAGTGTAT-----VTP-----	Qy	GGAPVSASTGTVSAPTSILN	827	Qy	448	DSEAHPLGM-AVKSSXSGAGGGAR	472
313	QRTYVAERGDRRLPPA-----VHSVTLSEEAGAYAPLTAQGTI---	354	Db	828 VAVTRVG-DGSAKLTSAATPVEVDIINPNDSLVTLSPLSTSNSNPLLASCTTASE	885	Db	1043 RSEGDAVNRRGGCGERDKSEGPARR	1068	
Qy	355 -LINRVLASCYAVIEHSMWAHRAFPLLAHALAAPARTDREG-----DGGGG	404	Qy	886 GMLTSDADHLYLVLTGYA-ASVGLANVKAADSATTPRVICRLDSACTVDTTTLPDAYSQ	944	Qy	887 NDTSAASTGDRSFYTTGNSGVRLYALGSSGLISSAA-----SNLRQLGIF---GD	995	
Db	405 DR-----GGGRVRAVLTAPGAQDAPGANGATGIIHWYSQLQIGMILDSE	450	Db	945 DNTSAASTGDRSFYTTGNSGVRLYALGSSGLISSAA-----SNLRQLGIF---GD	995	Db	946 QLY-----VSSGSGNGTK	1008	
Qy	451 ALHPLGMVAKSSXSRGAGGGAR	472	Qy	947 A; Status: translated from GB/EMBL/DBJ		Qy	948 A; Status: Homo sapiens (man) sequence revision 01-Feb-1999 #text_change 21-Jul-2000		
Db	996 QLY-----VSSGSGNGTK	1008	Db	A; Accession: T00373		Db	C; Species: Homo sapiens (man)		
Qy	10373	hypothetical protein KIAA0649 - human	Qy	10373		Qy	C; Date: 01-Feb-1999 #text_change 21-Jul-2000		
Db			Db			Db	C; Title: Prediction of the coding sequences of unidentified human genes. X. The complete		
Qy	R; Iishikawa, K.; Nagase, T., Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.		Qy	A; Reference number: 214142; MUID: 9734811		Qy	A; Title: Preliminary		
Db	DNA Res. 5, 169-176, 1998		Db	A; Accession: T00373		Db	A; Molecule type: DNA		
Qy	A; Status: Homo sapiens (man) sequence revision 01-Feb-1999 #text_change 21-Jul-2000		Qy	A; Cross-references: EMBL:AB014549; NID:93327111; PID:93327112		Qy	A; Cross-references: GB:AE004437; NID:910581323; PID:AG20078.1; GSPDB:GN00138		
Db	C; Accession: T00373		Db	A; Accession: T00373		Db	C; Genetics:		
Qy	A; Status: translated from GB/EMBL/DBJ		Qy	A; Status: mRNA		Qy	A; Genetics:		
Db	A; Molecule type: mRNA		Db	A; Cross-references: EMBL:AB014549; NID:93327111; PID:93327112		Db	A; Reference number: 214142; MUID: 9734811		
Qy	A; Experimental source: brain		Qy	A; Experimental source: brain		Qy	A; Reference number: KIAA0649		
Db	C; Genetics:		Db	C; Genetics:		Db	C; Genetics:		
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			Best Local Similarity	20.9%	Pred. No. 22;				
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			Conservative	52;	Mismatches	220;			
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			Matches	82;	Mismatches	127;	Indels	115;	
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A;Accession: C70584

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-664 <COL>

A;Cross-references: GB:Z95209; GB:AU123456; NID:93261750; PIDN:CA08487.1; PID:92078052

A;Experimental source: strain H37Rv

C;Genetics:

A;Gene: PknD

F;14-277/Domain: protein kinase homology <KIN>

Query Match Score 4.1%; Score 101.5; DB 2; Length 664;
Best Local Similarity 20.4%; Pred. No. 11; Matches 113; Conservative 60; Mismatches 175; Gaps 26;Matches 113; Conservative 60; Mismatches 175; Gaps 26;
Qy 41 PLAYKQFPNVAKTIGASGR--YEGKISNSNE--RFKEFLTPNNDPFDIYKDEENTGAD 95
Db 6 PQVGSQFGPYQQLRLIGGMGEVYEADTRKRVVALKLSPQYSDNAFRMREAD 65

Qy 96 -----RIMTQRCDEKDUNALALISVNQWPGV 120

Db 66 TAGRLTEPHIVPHDYBINGQPFVENNMIDTSILRAIKYQGYLTPARAVAIYRQIAA 125

Qy 121 KLRVTEGWWDGHSEESLHYEGRADITTSDDRS---KYGMLARIAYEVAGF----- 170

Db 126 L-----DAHANGTTTHRDVKPENITVTSDFAYLVDFG-TAAASDQGLQTGTAV 175

Qy 171 -----DWVYCESKAHTHCSYKAE-----NSV-----AAKSG 196

Db 176 GTNYMAPPRFTGGEVTRADITYLACVYIGECUTGAPPYRADSVERLIAHMDPAPQPS 235

Qy 197 GCFPGSATVHLQGGTK-LVKD----LSPGDRVLAADDQGRLLYSD--FLTFELDRDDG 247

Db 236 QLRGRVPALDQVTAKGNAKNAKPAAERFNSAGDIAAHHD--ALTTSQHQATTIURGDN 293

Qy 248 AKKVYVITREPRERLITTAHLFVARHNDSATGEPF--ASSGGSPGSGALGPRL 304

Db 294 A-----TLLATPA-----DTGLSQSESGTAGAGTGPPTIG----- 323

Qy 305 FASVRPGRVYVVAERDDDR-----LIPAV-----HSVYLSEAAAGAYAP 347

Db 324 -AARWSPGDSATVAGPLAADSQRGNGNWPSTGHSPPAVPNLAQSLGHAVPAGNKRKWA 382

Qy 348 LTAQQTILNRVLAQCYAVTAWHRAFA-----PFLLAHALAALAPARTDR 397

Db 383 VGAIAIVLVAIAVALAGYLVRP-SWSPTQASGQTVLPEFTGIDFRLSESGVAV----- 433

Qy 398 GGDSCGG--DRGGGGGRVALTAPGAADAPGAGATAGIHWSQOLLYQITGWLDSSEALH- 453

Db 434 --DSAGNVTYTSEGMYGRVYKLATGST-----GTTVLPFNGLYQ 470

Qy 454 PLGMVAKSXSRGAG 468

Db 471 PQGLAVD----GAG 480

Search completed: March 29, 2004, 18:34:07
Job time : 28 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 29, 2004, 18:24:49 ; Search time 17 Seconds

(without alignments)
1454.901 Million cell updates/sec

Title: US-09-883-848a-15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listings First 150 summaries

Database : SwissProt_42.4

Pred. No. is the number of results Predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	24.07	SHH_HUMAN	462	1	SHH_MOUSE	Q15465	homo sapien
2	20.68	SHH_MOUSE	437	1	SHH_MOUSE	Q62246	mus musculus
3	20.60	SHH_RAT	437	1	SHH_RAT	Q63673	rattus norvegicus
4	18.07	SHH_CHICK	425	1	SHH_CHICK	Q91035	Gallus gallus
5	15.94	SHH_CYNP	432	1	SHH_CYNP	Q93435	Cynops pyrrhodon
6	15.95	SHH_BRARE	61.0	1	SHH_BRARE	Q92048	Brachydanio tristis
7	14.98	SHH_XENIA	418	1	SHH_XENIA	Q92000	Xenopus laevis
8	14.32	TWHH_BRARE	58.0	1	TWHH_BRARE	Q90419	Brachydanio tristis
9	12.85	SHH_HUMAN	51.9	1	SHH_HUMAN	Q98318	Gallus gallus
10	12.71	SHH_HUMAN	51.5	1	SHH_HUMAN	Q14623	homo sapien
11	12.62	SHH_MOUSE	51.1	1	SHH_MOUSE	P97812	mus musculus
12	12.48	SHH_XENLA	50.5	1	SHH_XENLA	Q91512	Xenopus laevis
13	12.13	SHH_BRARE	49.1	1	SHH_BRARE	Q98862	Brachydanio tristis
14	11.83	DHH_MOUSE	47.9	1	DHH_MOUSE	Q61485	mus musculus
15	11.77	SHH_HUMAN	47.7	1	SHH_HUMAN	Q43323	homo sapien
16	10.93	SHH_XENLA	43.7	1	SHH_XENLA	Q91610	Xenopus laevis
17	10.77	SHH_MOUSE	43.6	1	SHH_MOUSE	P97812	mus musculus
18	8.90	SHH_XENLA	36.0	1	SHH_XENLA	Q02935	Xenopus laevis
19	8.54	SHH_BRARE	34.6	1	SHH_BRARE	P56674	drosophila melanogaster
20	6.02	SHH_RASSEL	24.4	1	SHH_RASSEL	P79858	rasbora elegans
21	5.99	SHH_DANZA	24.3	1	SHH_DANZA	P79691	carassius auratus
22	5.99	SHH_PUNTE	24.3	1	SHH_PUNTE	P79850	puntius tetrazona
23	5.98	SHH_RASSE	24.2	1	SHH_RASSE	P79864	rasbora heteromorpha
24	5.98	SHH_DROME	24.2	1	SHH_DROME	P79869	rasbora parva
25	5.97	SHH_TANAL	24.2	1	SHH_TANAL	P79915	tanichthys tanichthys
26	5.95	SHH_AMBER	24.1	1	SHH_AMBER	P79682	amblypharynx amboinensis
27	5.94	SHH_DANZA	24.1	1	SHH_DANZA	O13235	danio affinis
28	5.94	SHH_DANZE	24.1	1	SHH_DANZE	O13234	danio aequipinnatus
29	5.94	SHH_DANAT	24.1	1	SHH_DANAT	O13238	danio affinis
30	5.94	SHH_DANPR	24.1	1	SHH_DANPR	O13245	danio franklini
31	5.94	SHH_DANCE	24.1	1	SHH_DANCE	P79709	danio kerri
32	5.94	SHH_DANPU	24.1	1	SHH_DANPU	P20264	danio pulchellus
33	5.94	SHH_DEVDE	24.1	1	SHH_DEVDE	P16818	human cytomel

Result No.	Score	Query	Match	Length	DB	ID	Description
1	594	SHH_DEVNA	24.1	1	SHH_DEVPA	O13247	devario malabaricus
2	594	SHH_DEVPA	24.1	1	SHH_PUNCO	O13250	devario pattoni
3	590	SHH_BRARE	23.9	1	SHH_BRARE	P79938	puntius canthoides
4	37	SHH_BRARE	16.0	1	SHH_BRARE	P79729	brachydanio rerio
5	37	SHH_CARAU	11.9	1	SHH_CARAU	P79693	carassius auratus
6	38	SHH_DANAT	11.9	1	SHH_DANAT	O13240	danio affinis
7	39	SHH_DANAT	11.9	1	SHH_DANAT	P79711	danio kerri
8	40	SHH_DANKE	11.9	1	SHH_DANKE	O13243	danio pulchellus
9	41	SHH_DANPE	11.9	1	SHH_DANPE	P79952	puntius tetrazonatus
10	42	SHH_DANPE	11.9	1	SHH_PSPR	P79839	pseudorabora parva
11	42	SHH_PSPR	11.9	1	SHH_PSPR	P79837	pseudorabora parva
12	43	SHH_PSPR	11.9	1	SHH_PSPR	P79860	rasbora elephas
13	43	SHH_PSPR	11.9	1	SHH_PSPR	P79861	rasbora rasbora
14	44	SHH_PSPR	11.7	1	SHH_PSPR	P79862	devario malabaricus
15	45	SHH_PSPR	11.7	1	SHH_PSPR	P79863	devario devarensis
16	46	SHH_PSPR	11.7	1	SHH_PSPR	P79864	devario devarensis
17	47	SHH_PSPR	11.7	1	SHH_PSPR	P79865	devario devarensis
18	47	SHH_PSPR	11.7	1	SHH_PSPR	P79866	devario devarensis
19	48	SHH_PSPR	11.7	1	SHH_PSPR	P79867	devario devarensis
20	48	SHH_PSPR	11.7	1	SHH_PSPR	P79868	devario devarensis
21	48	SHH_PSPR	11.7	1	SHH_PSPR	P79869	devario devarensis
22	49	SHH_PSPR	11.7	1	SHH_PSPR	P79870	devario devarensis
23	50	SHH_PSPR	11.7	1	SHH_PSPR	P79871	devario devarensis
24	51	SHH_PSPR	11.7	1	SHH_PSPR	P79872	devario devarensis
25	52	SHH_PSPR	11.7	1	SHH_PSPR	P79873	devario devarensis
26	53	SHH_PSPR	11.7	1	SHH_PSPR	P79874	devario devarensis
27	54	SHH_PSPR	11.7	1	SHH_PSPR	P79875	devario devarensis
28	55	SHH_PSPR	11.7	1	SHH_PSPR	P79876	devario devarensis
29	56	SHH_PSPR	11.7	1	SHH_PSPR	P79877	devario devarensis
30	57	SHH_PSPR	11.7	1	SHH_PSPR	P79878	devario devarensis
31	58	SHH_PSPR	11.7	1	SHH_PSPR	P79879	devario devarensis
32	59	SHH_PSPR	11.7	1	SHH_PSPR	P79880	devario devarensis
33	59	SHH_PSPR	11.7	1	SHH_PSPR	P79881	devario devarensis
34	59	SHH_PSPR	11.7	1	SHH_PSPR	P79882	devario devarensis
35	59	SHH_PSPR	11.7	1	SHH_PSPR	P79883	devario devarensis
36	59	SHH_PSPR	11.7	1	SHH_PSPR	P79884	devario devarensis
37	59	SHH_PSPR	11.7	1	SHH_PSPR	P79885	devario devarensis
38	59	SHH_PSPR	11.7	1	SHH_PSPR	P79886	devario devarensis
39	59	SHH_PSPR	11.7	1	SHH_PSPR	P79887	devario devarensis
40	59	SHH_PSPR	11.7	1	SHH_PSPR	P79888	devario devarensis
41	59	SHH_PSPR	11.7	1	SHH_PSPR	P79889	devario devarensis
42	59	SHH_PSPR	11.7	1	SHH_PSPR	P79890	devario devarensis
43	59	SHH_PSPR	11.7	1	SHH_PSPR	P79891	devario devarensis
44	59	SHH_PSPR	11.7	1	SHH_PSPR	P79892	devario devarensis
45	59	SHH_PSPR	11.7	1	SHH_PSPR	P79893	devario devarensis
46	59	SHH_PSPR	11.7	1	SHH_PSPR	P79894	devario devarensis
47	59	SHH_PSPR	11.7	1	SHH_PSPR	P79895	devario devarensis
48	59	SHH_PSPR	11.7	1	SHH_PSPR	P79896	devario devarensis
49	59	SHH_PSPR	11.7	1	SHH_PSPR	P79897	devario devarensis
50	59	SHH_PSPR	11.7	1	SHH_PSPR	P79898	devario devarensis
51	59	SHH_PSPR	11.7	1	SHH_PSPR	P79899	devario devarensis
52	59	SHH_PSPR	11.7	1	SHH_PSPR	P79900	devario devarensis
53	59	SHH_PSPR	11.7	1	SHH_PSPR	P79901	devario devarensis
54	59	SHH_PSPR	11.7	1	SHH_PSPR	P79902	devario devarensis
55	59	SHH_PSPR	11.7	1	SHH_PSPR	P79903	devario devarensis
56	59	SHH_PSPR	11.7	1	SHH_PSPR	P79904	devario devarensis
57	59	SHH_PSPR	11.7	1	SHH_PSPR	P79905	devario devarensis
58	59	SHH_PSPR	11.7	1	SHH_PSPR	P79906	devario devarensis
59	59	SHH_PSPR	11.7	1	SHH_PSPR	P79907	devario devarensis
60	59	SHH_PSPR	11.7	1	SHH_PSPR	P79908	devario devarensis
61	59	SHH_PSPR	11.7	1	SHH_PSPR	P79909	devario devarensis
62	59	SHH_PSPR	11.7	1	SHH_PSPR	P79910	devario devarensis
63	59	SHH_PSPR	11.7	1	SHH_PSPR	P79911	devario devarensis
64	59	SHH_PSPR	11.7	1	SHH_PSPR	P79912	devario devarensis
65	59	SHH_PSPR	11.7	1	SHH_PSPR	P79913	devario devarensis
66	59	SHH_PSPR	11.7	1	SHH_PSPR	P79914	devario devarensis
67	59	SHH_PSPR	11.7	1	SHH_PSPR	P79915	devario devarensis
68	59	SHH_PSPR	11.7	1	SHH_PSPR	P79916	devario devarensis
69	59	SHH_PSPR	11.7	1	SHH_PSPR	P79917	devario devarensis
70	59	SHH_PSPR	11.7	1	SHH_PSPR	P79918	devario devarensis
71	59	SHH_PSPR	11.7	1	SHH_PSPR	P79919	devario devarensis
72	59	SHH_PSPR	11.7	1	SHH_PSPR	P79920	devario devarensis
73	59	SHH_PSPR	11.7	1	SHH_PSPR	P79921	devario devarensis
74	59	SHH_PSPR	11.7	1	SHH_PSPR	P79922	devario devarensis
75	59	SHH_PSPR	11.7	1	SHH_PSPR	P79923	devario devarensis
76	59	SHH_PSPR	11.7	1	SHH_PSPR	P79924	devario devarensis
77	59	SHH_PSPR	11.7	1	SHH_PSPR	P79925	devario devarensis
78	59	SHH_PSPR	11.7	1	SHH_PSPR	P79926	devario devarensis
79	59	SHH_PSPR	11.7	1	SHH_PSPR	P79927	devario devarensis
80	59	SHH_PSPR	11.7	1	SHH_PSPR	P79928	devario devarensis
81	59	SHH_PSPR	11.7	1	SHH_PSPR	P79929	devario devarensis
82	59	SHH_PSPR	11.7	1	SHH_PSPR	P79930	devario devarensis
83	59	SHH_PSPR	11.7	1	SHH_PSPR	P79931	devario devarensis
84	59	SHH_PSPR	11.7	1	SHH_PSPR	P79932	devario devarensis
85	59	SHH_PSPR	11.7	1	SHH_PSPR	P79933	devario devarensis
86	59	SHH_PSPR	11.7	1	SHH_PSPR	P79934	devario devarensis
87	59	SHH_PSPR	11.7	1	SHH_PSPR	P79935	devario devarensis
88	59	SHH_PSPR	11.7	1	SHH_PSPR	P79936	devario devarensis
89	59	SHH_PSPR	11.7	1	SHH_PSPR	P79937	devario devarensis
90	59	SHH_PSPR	11.7	1	SHH_PSPR	P79938	devario devarensis
91	59	SHH_PSPR	11.7	1	SHH_PSPR	P79939	devario devarensis
92	59	SHH_PSPR	11.7	1	SHH_PSPR	P79940	devario devarensis
93	59	SHH_PSPR	11.7	1	SHH_PSPR	P79941	devario devarensis
94	59	SHH_PSPR	11.7	1	SHH_PSPR	P79942	devario devarensis
95	59	SHH_PSPR	11.7	1	SHH_PSPR	P79943	devario devarensis
96	59	SHH_PSPR	11.7	1	SHH_PSPR	P79944	devario devarensis
97	59	SHH_PSPR	11.7	1	SHH_PSPR	P79945	devario devarensis
98	59	SHH_PSPR	11.7	1	SHH_PSPR	P79946	devario devarensis
99	59	SHH_PSPR	11.7	1	SHH_PSPR	P79947	devario devarensis
100	59	SHH_PSPR	11.7	1	SHH_PSPR	P79948	devario devarensis
101	59	SHH_PSPR	11.7	1	SHH_PSPR	P79949	devario devarensis
102	59	SHH_PSPR	11.7	1	SHH_PSPR	P79950	devario devarensis
103	59	SHH_PSPR	11.7	1	SHH_PSPR	P79951	devario devarensis
104	59	SHH_PSPR	11.7	1	SHH_PSPR	P79952	devario devarensis
105	59	SHH_PSPR	11.7	1	SHH_PSPR	P79953	devario devarensis
106	59	SHH_PSPR	11.7	1	SHH_PSPR	P79954	devario devarensis

CC CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS
CC 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY
CC SIMILARITY).

CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
CC cell, while the N-terminal peptide remains associated with the
CC cell surface. It is also secreted in either cleaved or uncleaved form
CC to mediate signaling to other cells (By similarity).

CC -!- TISSUE SPECIFICITY: Expressed in fetal intestine, liver, lung, and
CC kidney. Not expressed in adult tissues.

CC -!- PTM: The C-terminal domain displays an autoproteolysis activity
CC and a cholesterol transferase activity. Both activities result in
CC the cleavage of the full-length protein and covalent attachment of
CC a cholesterol moiety to the C-terminal of the newly generated N-
CC terminal fragment (N-product). This covalent modification appears
CC to play an essential role in restricting the spatial distribution
CC of the protein activity to the cell surface. The N-product is the
CC active species in both local and long-range signaling, whereas the
CC C-product has no signaling activity (By similarity).

CC -!- DISEASE: Defects in SHH are the cause of holoprosencephaly 3
(HPB3) [MIM:129495]. HPB3 is a clinically variable and genetically
CC heterogeneous malformation in which the developing forebrain fails
CC to correctly separate into right and left hemispheres. HPB3 is
CC associated with several distinct facies and phenotypic
CC variability. In the most extreme cases, anophthalmia or cyclopia
CC is evident along with congenital absence of the mature nose. The
CC less severe form features facial dysmorphia characterized by
CC ocular hypertelorism, defects of the upper lip and/or nose, and
CC absence of the olfactory nerves or corpus callosum. The majority
CC of HPB3 cases are apparently sporadic, although clear examples of
CC autosomal dominant inheritance have been described. Interestingly,
CC up to 30% of obligate carriers of the HPB3 gene in autosomal dominant
CC pedigrees are clinically unaffected.

CC -!- SIMILARITY: Belongs to the hedgehog family.

CC -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haemacol.;
CC WWW=<http://www.infobiogen.fr/services/chromcancer/Genes/SHHTD378.html>".

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or send an email to license@isb-sib.ch).

CC EMBL; 138518; AAA62179_1; -.
CC EMBL; AA02484; AAB67604_1; -.
CC HSSP; Q62226; 1VHH.
CC MEROPS; CA6_002; -.
CC Genew; HGNC:10848; SHH.
CC MIM; 600725; -.
CC MIM; 142945; -.
CC GO; GO:000500; Pinesoderm cell fate determination; TAS.
CC GO; GO:0007418; P:ventral midline development; TAS.
CC Interpro; IPR009045; Hedgehog/DD pept.
CC Interpro; IPR003587; Hedgehog_hnt_N.
CC Interpro; IPR003586; Hedgehog_hnt_C.
CC Interpro; IPR000320; HH_Signal.
CC InterPro; IPR006141; Interin_S.
CC InterPro; IPR001767; PepT-C46_hnt.
CC Pfam; PF01085; HH_Signal; 1.
CC PRINTS; PRO0632; SONIC_HHOG.
CC ProdDom; PDD030412; HH_Signal; 1.
CC SMART; SM00305; Hnt_C; 1.
CC SM00306; Hnt_N; 1.
CC PROSITE; PS00817; INDEIN_NTER; 1.
CC Developmental_protein; AutoCatalytic cleavage; Hydrolase; Protease;
CC KW Signal; Lipoprotein; Palmitate; Disease mutation; Holoprosencephaly
CC SIGNAL; 1; 23; POTENTIAL.
CC FT CHAIN; 24; 462; SONIC_HEDGEHOG PROTIN.
CC FT CHAIN; 24; 197; SONIC_HEDGEHOG PROTIN_N-PRODUCT.
CC FT CHAIN; 198; 462; SONIC_HEDGEHOG PROTIN_C-PRODUCT.

	FT DOMAIN SITE	407	411	POLY-GLY. (AUTO-) CLEAVAGE (BY SIMILARITY).
	FT PT SITE	197	198	INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY).
	FT PT SITE	243	243	INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
	FT PT ACT_SITE	267	267	ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
	FT PT LIPID	270	270	N-Palmitoyl cysteine ester (By similarity).
	FT PT LIPID	24	24	Cholesterol glycine ester (By similarity).
	FT PT VARIANT	197	197	G->R (in HPB3).
	FT PT VARIANT	31	31	/FTId=VAR 003619.
	FT PT VARIANT	88	88	D->V (in HPB3; familial).
	FT PT VARIANT	100	100	/FTId=VAR 009163.
	FT PT VARIANT	115	115	Q->H (in HPB3; sporadic).
	FT PT VARIANT	117	117	N->K (in HPB3; familial).
	FT PT VARIANT	117	117	/FTId=VAR 009165.
	FT PT VARIANT	117	117	W->G (in HPB3).
	FT PT VARIANT	117	117	/FTId=VAR 003620.
	FT PT VARIANT	117	117	W->R (in HPB3).
	FT PT VARIANT	188	188	/FTId=VAR 003621.
	FT PT VARIANT	222	222	B->Q (in HPB3; familial).
	FT PT VARIANT	224	224	/FTId=VAR 009166.
	FT PT VARIANT	226	226	D->N (in HPB3; familial).
	FT PT VARIANT	236	236	/FTId=VAR 009167.
	FT PT VARIANT	236	236	V->E (in HPB3).
	FT PT VARIANT	236	236	/FTId=VAR 009168.
	FT PT VARIANT	236	236	A->T (in HPB3; familial).
	FT PT VARIANT	236	236	/FTId=VAR 009169.
	FT PT VARIANT	236	236	S->R (in HPB3; familial).
	FT PT VARIANT	236	236	Score 2407; DB 1; Length 462;
	FT PT VARIANT	236	236	Query Match 97.5%; Score 2407; DB 1; Length 462;
	FT PT VARIANT	236	236	Best Local Similarity 100.0%; Pred. No. 2.1e-166; Mismatches 0; Indels 0; Gaps 0;
	FT PT VARIANT	236	236	Matches 462; Conservative 0; N mismatches 0;
Qy	1 MILLARCLLVVLSLLIVVSCGLACGPGRGFGRKRRPKLTPLAYKFQTIPNVAKTKLGASG	60		
Db	1 MILLARCLLVVLSLLIVVSCGLACGPGRGFGRKRRPKLTPLAYKFQTIPNVAKTKLGASG	60		
Qy	61 RYEGKISRSNSRFKEITPNPDIFKDDENTGADRMTORCKDKLNALAISVNMQWPGV	120		
Db	61 RYEGKISRSNSRFKEITPNPDIFKDDENTGADRMTORCKDKLNALAISVNMQWPGV	120		
Qy	121 KLRVTCWDEGHHSSES1AYEGRADITTSDRDSKYGMALARVEAGFDWVYYESKAH	180		
Db	121 KLRVTCWDEGHHSSES1HYEGRADITTSDRDSKYGMALARVEAGFDWVYYESKAH	180		
Qy	181 IHCSVKQENSYAAKSGCCPPSATAYLEQGSTKLVKDISPDRVLAADDGGRILYSDELT	240		
Db	181 IHCSVKQENSYAAKSGCCPPSATAYLEQGSTKLVKDISPDRVLAADDGGRILYSDELT	240		
Qy	241 FLDRDGAKKVYYVTEPREPLLTAAHLLFVAEHNDSATGEPEASSSSGGPGGALG	300		
Db	241 FLDRDGAKKVYYVTEPREPLLTAAHLLFVAEHNDSATGEPEASSSSGGPGGALG	300		
Qy	301 PRALFASRVPRVQRYVVAERGDRIILPAAVHSTVSEAGAYAPLTTQGTILINRVL	360		
Db	301 PRALFASRVPRVQRYVVAERGDRIILPAAVHSTVSEAGAYAPLTTQGTILINRVL	360		
Qy	361 ASCYATEEHSVAHRAFAPFLAHALLAALAPARTDRGDRILLPAAVHSTVSEAGAYAPLTTQGTILINRVL	420		
Db	361 ASCYATEEHSVAHRAFAPFLAHALLAALAPARTDRGDRILLPAAVHSTVSEAGAYAPLTTQGTILINRVL	420		
Qy	421 ADAPGAGATAGIHWYSOILYQIGTWLIDSEAHPLGMVAKSS	462		
Db	421 ADAPGAGATAGIHWYSOILYQIGTWLIDSEAHPLGMVAKSS	462		
RESULT 2				
SSH_MOUSE				
ID_SSH_MOUSE				
PRT;				
437 AA.				

AC Q62226; 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 42, Last annotation update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Sonic hedgehog protein precursor (SHH) (HHG-1).
 GS SHH OR HHG1.
 OS *Mus musculus* (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murines; Mus;
 OX NCBI_TaxID=10090;
 RN [1] SEQUENCE FROM N.A., STRAIN=C57BL/6J; TISSUE=Embryo;
 RP STRAIN=C57BL/6J; TISSUE=Embryo;
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=940594334; Published=7916661;
 PA Bechard Y., Epstein D.J., St. Jacques B., Shen L., Mohler J., McMahon J.A., McMahon A.P.;
 RA "Sonic hedgehog, a member of a family of putative signaling molecules, is involved in the regulation of CNS polarity.";
 RT Call 751417-1430(1993).
 RL [2] REVISION TO 122.
 RP SPAIN=C57BL/6J;
 RA McMahon A.P.;
 RA Subunit (Nov-1997) to the EMBL/GenBank/DDBJ databases.
 RN [3] SEQUENCE FROM N.A., AND AUTOPROTEOLYTIC CLEAVAGE.
 RX MEDLINE=95236997; Published=7720571;
 RP FUNCTION, AND AUTOPROTEOLYTIC CLEAVAGE.
 RA Chang D.T., Lopez A., von Kessler D.P., Chiang C., Simandl B.K., Zhao R., Seidin M.F., Fallon J.P., Beachy P.A., "Products, genetic linkage and limb patterning activity of a murine hedgehog gene.", RT Development 120:3339-3353 (1994).
 RN FUNCTION, AND AUTOPROTEOLYTIC CLEAVAGE.
 RX MEDLINE=95254654; Published=7736596;
 RA Roelink H., Porter J.A., Chiang C., Tanabe Y., Chang D.T., Beachy P.A., Jessell T.M.; RT Floor plate and motor neuron induction by different concentrations of the amino-terminal cleavage product of sonic hedgehog development 121:445-455 (1995).
 RL [5] X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 34-195.
 RX MEDLINE=1606944; Published=7477329;
 RA Hall T.M.T., Porter J.A., Beachy P.A., Leith D.J.; RT "A potential catalytic site revealed by the 1.7-A crystal structure of the amino-terminal signalling domain of sonic hedgehog.", Nature 378:212-216 (1995).
 CC -!- FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTc REGULATES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT; SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB. BUD DISPLAYS BOTH FLOOR PLATE- AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. Is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN A NUMBER OF EMBRYONIC TISSUES INCLUDING THE NOTOCHORD, VENTRAL NEURAL TUBE, FLOOR PLATE, LUNG, BUD, ZONE OF POLARIZING ACTIVITY AND POSTERIOR DISTAL MESENCHIME OF LIMBS. IN THE ADULT, EXPRESSED IN LONG AND NEURAL RETINA.
 CC -!- DEVELOPMENTAL STAGE: FIRST DETECTABLE DURING GASTRULATION.
 CC -!- INDUCTION: By retinoic acid.
 CC -!- PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transferase activity. Both activities result in

the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity.

-!- SIMILARITY: Belongs to the hedgehog family.

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CC EMBL; X76290; CA453922.1; -.
 DR PDB; 1VRF; 29-JAN-96.
 DR MEROPS; C46_002; -.
 DR MGDB; MG1_98297; Shh.
 DR GO; GO:0007411; P:axon guidance; IDA.
 DR GO; GO:0001708; P:cell fate specification; IMP.
 DR GO; GO:0007417; P:central nervous system development; IMP.
 DR GO; GO:0001747; P:eye morphogenesis; IDA.
 DR GO; GO:0001654; P:eye morphogenesis; IMP.
 DR GO; GO:0030539; P:male genital morphogenesis; IMP.
 DR GO; GO:0007389; P:pattern specification; IMP.
 DR GO; GO:0042127; P:regulation of cell proliferation; IDA.
 DR InterPro; IPR009045; Hedgehog/PP Pept.
 DR InterPro; IPR03587; Hedgehog_hnt_N.
 DR InterPro; IPR03586; Hedgehog_hntC.
 DR InterPro; IPR00320; HH signal.
 DR InterPro; IPR006141; Interdis.
 DR InterPro; IPK01767; Pept_C76_hnt.
 DR InterPro; IPR001657; PeptIdse_C46.
 DR Pfam; PF01085; HH signal; 1.
 DR Pfam; PF01079; Hnt; 1.
 DR PRINTS; PR00632; SONICHHOG.
 DR ProdDom; PD003042; HH signal; 1.
 DR SMART; SM00305; HntC; 1.
 DR SMART; SM00306; HntN; 1.
 DR PROSITE; FS50817; INTEIN_N_TER; 1.
 KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
 KW Signal; Lipoprotein; Palmitate; 3D-structure.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 437 SONIC HEDGEHOG PROTEIN.
 FT CHAIN 25 198 SONIC HEDGEHOG PROTEIN N-PRODUCT.
 FT CHAIN 159 437 SONIC HEDGEHOG PROTEIN C-PRODUCT.
 FT DOMAIN 383 387 POLY-GLY.
 FT SITE 198 199 CLEAVAGE (AUTO-) (BY SIMILARITY).
 FT SITE 244 244 INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY).
 FT SITE 268 268 INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
 FT ACT_SITE 271 271 ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
 FT LIPID 25 25 N-palmitoyl cysteine (By similarity).
 FT LIPID 198 198 Cholesterol glycine ester (By similarity).

PT	TURN	119	120	
PT	STRAND	123	127	
PT	TURN	137	138	
PT	HELIX	140	143	
PT	TURN	144	144	
PT	STRAND	146	151	
PT	TURN	152	153	
PT	HELIX	156	158	
PT	HELIX	159	168	
PT	TURN	169	170	
PT	STRAND	173	178	
PT	TURN	179	180	
PT	STRAND	181	185	
PT	HELIX	189	192	
PT	TURN	193	193	MW: 47773 MW: DOEB7F08E7860EF CRC64:
SQ	SEQUENCE	437 AA:	47773 MW:	DOEB7F08E7860EF CRC64:
Query Match		83.8%	Score 2068; DB 1;	Length 437;
Best Local Similarity		87.4%	Pred. No. 5.9e-14;	
Matches 404; Conservative		8;	Mismatches 24;	Indels 25; Gaps 3;
Qy	1	MILLARCLLIVLVLVSSLLVSGLAGPGRGGFGRHRPKKLTPAKYQFPVNAEAKTLGASG	60	
Db	2	LILLARCFLVLLAVSLLYLPGLAGPGRGGFGRHRPKKLTPAKYQFPVNAEAKTLGASG	61	
Qy	62	RYEKGKISRNSERPERKELTPNPDIIKDPEENTGADRUMTQRCKDKLNALAISWMNQPGV	120	
Db	62	RYEKGKISRNSERPERKELTPNPDIIKDPEENTGADRUMTQRCKDKLNALAISWMNQPGV	121	
Qy	121	KLRVTEGWDDEGHSEESSHYEGRAVDITTSDRSKYQMLARLAVEAGFDWVYYESKAH	180	
Db	122	KLRVTEGWDDEGHSEESSHYEGRAVDITTSDRSKYQMLARLAVEAGFDWVYYESKAH	181	
Qy	181	IHCSYKAENSAVAKGCGFGSATVHLEGGTQLVKDLSPGDVLAAQDGRLYSDLT	240	
Db	182	IHCSYKAENSAVAKGCGFGSATVHLEGGTQLVKDLSPGDVLAAQDGRLYSDLT	241	
Qy	241	FLDRDDGAKKVYYVETREPRERLILTAHLLFYAPHDNSATGEPEASSGSGPPSGGALG	300	
Db	242	FLDRDDGAKKVYYVETREPRERLILTAHLLFYAPHDNSATGEPEASSGSGPPSGGALG	306	
Qy	301	PRALFASRVPGQTYVVAERDGDPRRLLAAVHVSYTSESEAAGAYAPTAQGTILINRLV	360	
Db	287	PSALFASRVPGQTYVVAERGDDRLLPAVHVSYTSESEAAGAYAPTAQGTILINRLV	346	
Qy	361	ASCYATEERSWAHAFAPRFLAHLLAAPARTDRGDSGGDRGGCGRVALTARG	420	
Db	347	ASCYATEERSWAHAFAPRFLAHLLAAPARTD-----GGCGGSI-AAAOSA	395	
Qy	421	ADAPGAGATAGHWSQLYQIGTMWLDSEALHPGMVAKS 462		
Db	396	TEARGAEPATIHWMSQLHIGTMWLDSEALHPGMVAKS 437		
RESULT 3				
SHH_RAT	ID	SHH_RAT STANDARD; SHH_RAT PRT; SHH_RAT PRT;	437 AA.	
AC	Q6373;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-OCT-2003 (Rel. 42, Last sequence update)			
DB	Sonic hedgehog protein precursor (SHH).			
GN	SHH OR VHH-1.			
OS	Battus norvegicus (Battus).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID1011;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN_Sprague-Dawley; TISSUE=Embryonic floor plate;			
RX	MEDLINE=9417037; PubMed=8124744;			
RA	Roellink H., Augsburger A., Heenskerk J., Korzh V., Norlin S., Jesseil T.M., Ruiz i Altaba A., Tanabe Y., Placzek M., Edlund T., Jesseil T.N.,			
FT	ACT_SITE 271	271		

RA Dodd J.; "Floor plate and motor neuron induction by vhh-1, a vertebrate homolog of hedgehog expressed by the notochord.", Cell 76:761-775 (1994).
 RT RT of hedgehog expressed by the notochord.
 RL Cell 76:761-775 (1994).
 CC -; FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER TARGET, THE GJ11 ONCOGENE, INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE-AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. Is also secreted in either cleaved or uncleaved form (By similarity).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE NODE, NOTOCHORD, FLOOR PLATE, AND POSTERIOR LIMB BUD MESENCHYME.
 CC -!- PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transfer activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity).
 CC -!- SIMILARITY: Belongs to the hedgehog family.
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 CC EMBL; I27340; AAA20999.1; -.
 DR PIR; B53193; B53193.
 DR HSSP; Q62226; 1VHH.
 DR MEROPS; C46.002/-.
 DR InterPro; IPR00045; Hedgehog/DD_Dept.
 DR InterPro; IPR00587; Hedgehog_hint_N.
 DR InterPro; IPR003586; Hedgehog_hint_C.
 DR InterPro; IPR00320; HH_Signal.
 DR InterPro; IPR00641; Intein_S.
 DR InterPro; IPR00167; Pept_C46_hint.
 DR InterPro; IPR001657; Pept_Ddase_C46.
 DR Pfam; PF01055; HH_signal_1.
 DR SMART; SM00306; HintC_1.
 DR PRINTS; PR00632; SONIC_HEDGEHOG.
 DR PDD03042; SONIC_HEDGEHOG.
 DR SMART; SM00305; HintC_1.
 DR PROSITE; P855017; INTB1_N_TER_1.
 KW Developmental Protein; Autocatalytic cleavage; Hydrolase; Protease; Signal; Lipoprotein; Palmitate.
 KW SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 SONIC_HEDGEHOG PROTEIN.
 FT CHAIN 25 SONIC_HEDGEHOG PROTEIN N-PRODUCT.
 FT DOMAIN 199 437 SONIC_HEDGEHOG PROTEIN C-PRODUCT.
 FT SITE 383 387 POLY-GLY.
 FT SITE 198 199 CLEAVAGE (AUTO-).
 FT SITE 244 244 INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY).
 FT SITE 268 268 INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
 FT ACT_SITE 271 271 ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).

FT	LIPID	25	25	SIMILARITY N-palmitoyl cysteine (By similarity).
FT	LIPID	198	198	Cholesterol Glycine ester (By similarity).
PT	SEQUENCE	437 AA;	47630 MW;	ODBFC19FD01662A0 CRC64;
Query Match	Best Local Similarity	83.4%;	Score 2060;	DB 1; Length 437;
Matches	405; Conservative	87.5%;	Pred. No. 2, 2e-141;	Indels 28; Gaps 4;
Qy	1	MILLIARCLLIVVSSLLVSGLAGCPGRGFGKRRHPKPKLPLAYKFIPIVPAEKTIGASG 60		
Db	2	ILLIARCPVALSSLVCPGLACGPGRGFGKRRHPKPKLPLAYKFIPIVPAEKTIGASG 61		
Qy	61	RVECKISNSRERKELTDPYNNPDLIKYDENGADRMTQCRDKUNALSAVSNQWPGV 120		
Db	62	RVECKITNSRERKELTNYNPDLIFDENGADRMTQCRDKUNALSAVSNQWPGV 121		
Qy	121	KLRVTEGWDDEGHSEEEHYGRADITTSDRDSKYGMLARLAVERAGFDWVYYESKAH 180		
Db	122	KLRVTEGWDDEGHSEEEHYGRADITTSDRDSKYGMLARLAVERAGFDWVYYESKAH 181		
Qy	181	IHC SVKAENSVAAKSGGCPGSATVHLLEQGGTKLVKDLSPGVRVLAADDQGRLLSDFLT 240		
Db	182	IHC SVKAENSVAAKSDDGCPGSATVHLLEQGGTKLVKDLSPGVRVLAADDQGRLLSDFLT 241		
Qy	241	FLD RDGAYKVFVYIETRPRERILLTAHLLLEVAPHDNATGEPEASSGSCPPSGGALG 300		
Db	242	FLD RDEGAKKVVFVYIETRPRERILLTAHLLFVAPND-----SQTPEG 286		
Qy	301	PRL FAS RTRP QGR VVYVAERGDPRRLIPLA VHSVTLSEA QAY APLTA CCTT ILINRV L 360		
Db	287	PSPL FAS RTRP QGR VVYVAERGDPRRLIPLA VHSVTLRE A QAY APLTA DGT T ILINRV L 346		
Qy	361	ASCYAVIEBHSHWAHRAFA PERLA HALLA LAPARTD QRG DSGGG DRG GGR VAL TAP G 419		
Db	347	ASCYAVIEBHSHWAHRAFA PERLA HALLA LAPARTD-----GGGGG -SIPAPQS 394		
Qy	420	AAD A D P G A G ATAGTHW YSOL YQ IGT W L DSE ALH P LGM K V K S S 462		
Db	395	V A E R G A G P A G I H W Y S Q L Y H I G T W L D S E T D H P L G M K V K S S 437		
<hr/>				
RESULT 4	SHH_CHICK	STANDARD;	PRT;	425 AA..
ID	Q91015;			
AC	15-JUL-1999	(Rel. 38, Created)		
DT	15-JUL-1999	(Rel. 38, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE		Sonic hedgehog protein precursor (SHH).		
GN	SHH.			
OS	Gallus gallus (Chicken).			
OC	Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI-TaxID=9031;			
RN	[1]	SEQUENCE FROM N.A.		
RP	FUNCTION, AND AUTOPOTEOLYTIC CLEAVAGE.			
RC	TISSUE=Limb bud;			
RX	MEDLINE=91094333; PubMed=8269518;			
RA	Riddle R.D., Johnson R.L., Laufer E., Tabin C.;			
RT	"Sonic hedgehog mediates the polarizing activity of the ZPA."			
RL	Cell 75:101-116 (1993).			
RN	[2]	FUNCTION, AND AUTOPOTEOLYTIC CLEAVAGE.		
RP	MEDLINE=95254654; PubMed=736596;			
RA	Beachy P.A., Porter J.A., Chiang C., Tanabe Y., Chang D.T.,			
RA	Jessel T.M.;			
RT	"Floor Plate and motor neuron induction by different concentrations of the amino-terminal cleavage product of sonic hedgehog autoptotoclysis";			
RT	Cell 81:445-455 (1995).			
RL				

CC	-1- FUNCTION: BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSES THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO. ALSO REGULATES ANOTHER TARGET, THE GLI ONCOGENE. INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT: SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES VENTRAL CELL FATE IN THE NEURAL TUBE AND SOMITES, AND THE POLARIZING SIGNAL FOR PATTERNING OF THE ANTERIOR-POSTERIOR AXIS OF THE DEVELOPING LIMB BUD. DISPLAYS BOTH FLOOR PLATE AND MOTOR NEURON-INDUCING ACTIVITY. THE THRESHOLD CONCENTRATION OF N-PRODUCT REQUIRED FOR MOTOR NEURON INDUCTION IS 5-FOLD LOWER THAN THAT REQUIRED FOR FLOOR PLATE INDUCTION.
CC	-1- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. It is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (BY SIMILARITY).
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN THE POSTERIOR LIMB BUD, MESENCHYM, THE HENSEN'S NODE, THE NOTOCHORD, AND THE FLOOR PLATE.
CC	-1- DEVELOPMENTAL STAGE: FIRST DETECTABLE AT STAGE 17 DURING THE INITIATION OF LIMB BUD FORMATION. FROM THAT POINT ONWARDS, THE EXPRESSION PATTERN EXACTLY MATCHES THE LOCATION OF THE ZONE OF POLARIZING ACTIVITY (ZPA).
CC	-1- INDUCTION: By retinoic acid.
CC	-1- PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity.
CC	-1- SIMILARITY: Belongs to the hedgehog family.
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CC	DR EMBL: L28099; AAA7428.1; -
DR	HSSP: Q62226; 1VHH.
DR	MEROPS: C46_0001; -
DR	InterPro: IPR009045; Hedgehog/DD_dept.
DR	InterPro: IPR003587; Hedgehog_hint_C_N.
DR	InterPro: IPR003586; Hedgehog_hint_C.
DR	InterPro: IPR003220; HH_signal.
DR	InterPro: IPR006141; InterIn_S.
DR	InterPro: IPR01767; Pept_C46_hint.
DR	InterPro: IPR01657; Pept_Idase_C46.
DR	Pfam: PF01015; HH_signal_1.
DR	Pfam: PF01079; Hint_1.
DR	PRINTS: PRO0632; SONICHHCG.
DR	Prodrom: P003042; HH_signal_1.
DR	SMART: SM00305; HintC_1.
DR	SMART: SM00306; HintN_1.
DR	PROSITE: PS500817; INTEIN_N_TER; 1.
KW	Developmental Protein; Autocatalytic cleavage; Hydrolase; Protease; Signal; Lipoprotein; Palmitate.
PT	POTENTIAL.
PT	CHAIN 1 26 POTENTIAL.
PT	CHAIN 27 425 SONIC HEDGEHOG PROTEIN.
PT	CHAIN 200 200 SONIC HEDGEHOG PROTEIN N-PRODUCT.
PT	CHAIN 201 425 SONIC HEDGEHOG PROTEIN C-PRODUCT.
PT	DOMAIN 390 393 POLY-THR.
PT	SITE 200 201 CLEAVAGE (AUTO-) (PROBABLE).
PT	SITE 246 246 INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY).
PT	SITE 270 270 INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).

				ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
PT	ACT_SITE	273	273	
PT	LIPID	27	27	N-palmitoyl cysteine (By similarity).
PT	LIPID	200	200	Cholesterol glycine ester (By similarity).
PT	SEQUENCE	425 AA;	46474 MW;	DR9627443DAA0173 CRC44;
Query Match		73.2%; Score 1807; DB 1; Length 425;		
Best Local Similarity		77.8%; Pred. No 3; Se-123; Indels 44; Gaps 6;		
Matches 361; Conservative 22; Mismatches 3; Indels 44; Gaps 6;				
Db	1	MILLARCILIVLSSLLIVCSGLAGPGRGFGKGRHPKQLTPLAYQFIPVAEKTIGASG 60		
Db	4	MLLTRILIVGFLICLIVSGLTGPGRIGKGRHPKQLTPLAYQFIPVAEKTIGASG 63		
Qy	61	RVEGKISRNSERFKELTTPNPDIFKDENTGADRIMTQRCKDKLNALAISYMNQPGV 120		
Db	64	RYEGKRITRNSERFKELTTPNPDIFKDENTGADRIMTQRCKDKLNALAISYMNQPGV 123		
Qy	121	KLRVTEGWDGDGHISBESEHLYEGRAVDITTSDRRSKYGMLARLAVEANGFDWVYYESKAH 180		
Db	124	XLRVTEGWDGDGHISBESEHLYEGRAVDITTSDRRSKYGMLARLAVEANGFDWVYYESKAH 183		
Qy	181	IHCSTYKAENSVAAKSGGGFFGSATVHLEGGTGTKLVKDLSPGDRVLAADQGRLLYSDFLT 240		
Db	184	IHCSTYKAENSVAAKSGGGFFGSATVHLEGGTGTKLVKDLSPGDRVLAADQGRLLYSDFLT 243		
Qy	241	FLDRDGAKKVVYTFETREPERELLTAAHLLFTAP-ENDS-ATGEPPASSGAGPPCGA 298		
Db	244	FLDRDSSRFLFVYBTRQRARLLTAAHLLFTAPQHNSQEAHG----STSG----- 292		
Qy	299	LGPRLAFASRVPRGQRVYTYAERDGDRRLPAAYHSVTLSEEAGAYAPLTAQGTILINR 358		
Db	293	---QALFASTYKPGQRVYVGE-GGQQQLPASTHSVSRLREEASGAYAPLTAQGTILINR 347		
Qy	359	VLASCYAVTEBHSWAHRAFPLAHALLALAPARTDEGGDGGDRGGSRVALTAP 418		
Db	348	VLASCYAVTEBHSWAHWAFAPLAQLAAL-----CP 381		
Qy	419	GAADPAGAATAGIHWISQYLQITGWLLDSEALHPLGNAKSS 462		
Db	382	DGAIFTAATTTGTHWYSLLYRIGSWVLDGDALHPLGNVAPAS 425		
				RESULT 5
SHH_CYNFY	ID	SHH_CYNFY	STANDARD:	PRT; 432 AA.
AC	090385;			
DT	15-JUL-1999	(Rel. 38; Created)		
DT	15-JUL-1999	(Rel. 38; Last sequence update)		
DT	20-OCT-2003	(Rel. 42; Last annotation update)		
DE	Sonic hedgehog protein precursor (SHH).			
GN	SHH.			
OS	Cynops pyrrhogaster	(Japanese common newt).		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
CC	Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.			
OX	NCBI_TaxID=8330; [1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Embryo;			
RX	Medline=96136334; PubMed=8573168;			
RA	Takabatake T.; Takahashi T.C.; Inoue K.; Ogawa M.; Takeshima K.;			
"Activation of two Cynops genes, fork head and sonic hedgehog, in animal cap explants";				
RT	Biochem. Biophys. Res. Commun. 218: 395-401 (1996).			
RL	- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT AND METAMORPHOSIS. INVOLVED IN LIMB FORMATION, PATTERNING OF THE CENTRAL NERVOUS SYSTEM AND VENTRAL SOMITE DIFFERENTIATION. INDUCES ECTOPIC CEMENT GLAND FORMATION IN EMBRYOS. BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH TRANSCRIPTION IN ASSOCIATION WITH SMOOTHENED (SMO), TO ACTIVATE THE CC TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SHH, PTC REPRESSIONS THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (By			
Qy	1	MILLARCILIVLSSLLIVCSGLAGPGRGFGKGRHPKQLTPLAYQFIPVAEKTIGASG 60	Query Match	62.4%; Score 1539.5; DB 1; Length 432;
DB	4	MILLRVLVLAGFLICLIVSGLAGPGRGFGKGRHPKQLTPLAYQFIPVAEKTIGASG 63	Best Local Similarity	67.7%; Pred. No. 8.1e-104;
Qy	61	RYEGKISRNSERFKELTTPNPDIFKDENTGADRIMTQRCKDKLNALAISYMNQPGV 120	Matches 3:5; Conservative	36; Mismatches 36; Index 39; Gaps 8;
DB	64	RYEGKISRNSERFKELTTPNPDIFKDENTGADRIMTQRCKDKLNALAISYMNQPGV 123		
Qy	121	KLRVTEGWDGHSSSESLHYEGRAVDITTSDRDRSKYGMALARLAVEAGEDPWVYYESKAH 180		

Db 124 KLRVTEGNDEDGHFFERSLHYGRAVDITTSDRSKYGMRLAAEAGFDWVYFESKAH 183
Qy 181 IHSVKAINSYAKSGGGFPGSATVHLEGGTRKLYKDLSPEDRVLAADDGRLLYSDFLR 240
Db 184 IHCVKAINSYAKSGCCPGSATVALEGVIPVDRPLPDRVLAADGLKLYSDFL 243
Qy 241 FLDRDGAKKVYVETREPRLLLTAHHLFVVA--PHNSATGEPEASSGSPGSG 297
Db 244 FMRKEETTRKVFIET-SRERVLTAHHLFVQHNGND---SGGDRFSVFG 293
Qy 298 ALGRALPAVRPGORYVVAERDGRRLPPAVHSVTLSSEAAAGAYAPLITAQGTILIN 357
Db 294 SAGERSMSSVPAQRHTLV-DREG-RGLRATVERVYL-BEATAYAPTAHQTVVID 350
Qy 358 RVLASCYAVIEPHSWAHAFAPRLHALAALAPARTDRGSDGGDRGGGRVALTA 417
Db 351 RVLASCYAVIEPHSWAHAFAPRLVGILSFSR--QDYSHS----- 392
Qy 418 PGAADAPAGATAGTGHWYSQLYQIGTMILDSEALHPGMAYKSS 462
Db 393 -----PPAPSQSCDVHYYEITRIGWVQBDTHLGWAKSS 432

RESULT 6

SHH_BRAE STANDARD; PRT; 418 AA.
 ID Q92008; O13170; O13171;
 AC Q92008; O13170; O13171;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Sonic hedgehog protein precursor (SHH) (YTHH-1).
 GN SHH CR YTHH1.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 RN [1] SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 MEDLINE=94170375; PubMed=8124714;
 RX Roelink H, Augsburg A., Heemskerk J., Korzh V., Norlin S.,
 MEDLINE=96014264; PubMed=753153;
 RA Rödiger U., Altaba A., Tanabe Y., Placzek M., Edlund T., Jessell T.M.,
 RA Dodd J.;
 RT "Floor plate and motor neuron induction by vhh-1, a vertebrate homolog
 of hedgehog expressed by the notochord.";
 RL 76:761-775 (1994).
 RN [2] SEQUENCE FROM N.A. AND AUTOPROTEOLYTIC CLEAVAGE.
 RP SEQUENCE FROM N.A. AND AUTOPROTEOLYTIC CLEAVAGE.
 RX Fiercz M.J., Concordet J.-P., Barrosa R., Johnson R., Krauss S.,
 MEDLINE=92225458; PubMed=10207136;
 RA Muller F., Chang B., Albert S., Fischer N., Tora L., Strahle U.,
 RA McManam A.P., Tabin C., Ingham P.W.;
 RT "The hedgehog gene family in Drosophila and vertebrate development."
 RL Development Suppl. 43:51(1994).
 RN [3] SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A. PubMed=7579523;
 RX Fiercz M.J., Concordet J.-P., Barrosa R., Johnson R., Krauss S.,
 MEDLINE=92225458; PubMed=10207136;
 RA Muller F., Chang B., Albert S., Fischer N., Tora L., Strahle U.,
 RA "Intrinsic enhancers control expression of zebrafish sonic hedgehog in
 floor plate and notochord.";
 RL Development 126:2103-2116 (1999).
 RN [4] SEQUENCE FROM N.A.
 RP SEQUENCE OF 30-92 AND 113-170 FROM N.A.
 RX TISSUE=Muscle;
 MEDLINE=97075114; PubMed=8917540;

Db RA Zardoya R., Abouheif E., Meyer A.; Meyer A.;
 RT "Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species
 closely related to the zebrafish";
 RT Proc. Natl. Acad. Sci. U.S.A. 93:1336-1341 (1996).
 RL -!
 CC -!
 CC FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
 CC PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE
 CC NOTOCHORD THAT INDUCES SOMITE PATTERNING, ORSO-VENTRAL PATTERNING
 CC OF THE BRAIN AND EARLY PATTERNING OF THE DEVELOPING EYES. DISPLAYS
 CC FLOOR PLATE-INDUCING ACTIVITY. BINDS TO THE PATCHED (PTC)
 CC RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
 CC ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IN THE ABSENCE OF SMO,
 CC PTC REPRESSIONS THE CONSTITUTIVE SIGNALING ACTIVITY OF SMO (BY
 CC SIMILARITY).
 CC -!
 CC SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
 CC cell, while the N-terminal peptide remains associated with the
 CC cell surface. Is also secreted in either cleaved or uncleaved form
 CC to mediate signaling to other cells (By similarity).
 CC -!
 CC TISSUE SPECIFICITY: EXPRESSED IN THE VENTRAL MIDLINE OF THE NEURAL
 CC TUBE AND BRAIN. ALSO FOUND IN THE NOTOCHORD AND IN DEVELOPING FIN
 CC BUD. IN THE DEVELOPING BRAIN, EXPRESSION OCCURS IN DOMAINS THAT
 CC INCLUDE A DISCRETE REGION IN THE FLOOR OF THE DIENCEPHALON.
 CC -!
 CC DEVELOPMENTAL STAGE: FIRST DETECTABLE IN THE INNER CELL LAYER OF
 CC THE EMBRYONIC SHIELD DURING GASTRULATION. BY 9.5 HRS OF
 CC DEVELOPMENT, EXPRESSED IN A CONTINUOUS BAND THAT EXTENDS FROM THE
 CC POSITIONED IN THE CENTER OF THE ANIMAL POLE ANTERIOR TO THE
 CC PRESUMPTIVE MIDBRAIN.
 CC -!
 CC PTM: The C-terminal domain displays an autoproteolytic activity in
 CC and a cholesterol transferase activity. Both activities result in
 CC the cleavage of the full-length protein and covalent attachment of the
 CC a cholesterol moiety to the C-terminal of the newly generated N-
 CC terminal fragment (N-product). This covalent modification appears
 CC to play an essential role in restricting the spatial distribution
 CC of the protein activity to the cell surface. The N-product is the
 CC active species in both local and long-range signaling, whereas the
 CC C-product has no signaling activity (By similarity).
 CC -!
 CC SIMILARITY: Belongs to the hedgehog family.
 CC -!
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 CC -!
 CC EMBL: L27585; AAA20998; 1; -
 DR EMBL: U30711; AAC59742; -;
 DR EMBL: Z35669; CAA84738; 1; -
 DR EMBL: AF1243382; AAD47913; 1; -
 DR EMBL: U51351; AAB35551; -;
 DR EMBL: U51370; AAB35593; 1; -
 PIR: A53193; A53193.
 DR HSSP: Q6226; 1VHH.
 DR MERO: C46_000; -;
 DR ZFIN: ZDB-GENE_980326-166; shh.
 DR InterPro: IPR03586; Hedgehog/DD_dept.
 DR InterPro: IPR03586; Hedgehog_hntC.
 DR InterPro: IPR00320; HH_signal.
 DR InterPro: IPR00141; Integrin_S.
 DR InterPro: IPR01767; Pept_C46_hint.
 DR InterPro: IPR01657; Pept_Idase_C46.
 DR pfam: PF01085; HH_signal; 1.
 DR Pfam: PF01079; Hint; 1.
 DR PRINTS: PR00632; SONICHHOG.
 DR PRODOM: PB003042; HH_signal; 1.
 DR SMART: SM00305; HintC; 1.
 DR PROSITE: PS50817; INTEIN_N_TER; 1.
 KW Developmental Protein; Autocatalytic cleavage; Hydrolase; Protease;
 KW Signal; Lipoprotein; Palmitate.
 FT SIGNAL 1 23 POTENTIAL.

				SONIC HEDGEHOG PROTEIN.
	CHAIN	24	418	SONIC HEDGEHOG PROTEIN N-PRODUCT.
	CHAIN	24	197	SONIC HEDGEHOG PROTEIN C-PRODUCT.
	SITE	198	418	CLEAVAGE (AUTO-).
	SITE	197	198	INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY).
	SITE	243	243	INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
	ACT_SITE	267	267	ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
	LIPID	24	24	N-palmitoyl cysteine (By similarity).
	LIPID	197	197	Cholesterol glycone ester (By similarity).
SEQUENCE	418 AA;	46402 MW;	CFC00AAFFED2F5795 CRC64;	
Query Match		61.0%	Score 1506; DB 1; Length 418;	
Best Local Similarity		64.5%	Pred. No. 10-101; Mismatches 47; MisMatches 68; Index 50; Gaps 5;	
Matches 300; Conservative				
Dy	1	MILLIARCLLIVLVLSSGLACSGPGRGFKRRIIFKLTPLAKCQFIPVNAEKTGASG 60		
Db	1	MRLLITRVLVLSSLLTISLIVSGLACSGPGRGFKRRIIFKLTPLAKCQFIPVNAEKTGASG 60		
Dy	61	RYEGKISIRNSERFKELTPTNYPNDI1FKDEENTGADRMLTORCKDKLNALAI SVWNCMPGV 120		
Db	61	RYEGKTRISERFKELTPTNYPNDI1FKDEENTGADRMLTORCKDKLNALAI SVWNCMPGV 120		
Dy	121	KLRVTEGWDGDGHHSSESTLYHEGRAVDITTSDRDRSKYGMARLAVEAGFDWVYYSKSH 180		
Db	121	KLRVTEGWDGDGHHSPESTLYHEGRAVDITTSDRDRSKYGTLSRSLAVEAGFDWVYYSKSH 180		
Dy	181	IHCSTKAENSAAKGGCFEGSATVLEQEGTKLVDLSPCDRVLAADDQGRLYLDFLT 240		
Db	181	IHCSTKAENSAAKGGCFEPASALVLQDGQKAVDLDNPDKVLLADSAGNLVDFDFM 240		
Qy	241	FLDRDDGAKYKVYIETREPERLLITAHHILPVAPINDSATGEPASSGSGPPGGALG 300		
Db	241	FTDRDSTTRVVFYIETQEPVEKITTAHHILFVL--DNSTEDEDIHTMT----- 286		
Qy	301	PRAIFASRVPFGQRVYVVAEFDGDRLELPAAVHSVTLSSEEAGAYAPLTAQDTILNRLV 360		
Db	287	-AAYASSVRAQGKVN--DDSSQLSKSVIVORYTEEQRSQFAPVTAQITIVVDRIL 340		
Qy	361	ASCYVATEENSWAHRAFAFPFLAHAAATAPARTDGGDSCEGGDRGGGGVALTAPGA 420		
Db	341	ASCYVATEDQGLAHAFAPALLYYYSELFQONS----- 375		
Qy	421	ADAPRGAT--AGIHWYSQULLQYQIGNWLLSDBALHPGLMAYKSS 462		
Db	377	CONVENTIONAL CONFORMITY SP1YQOMTTT11NNMM1KDLGCMSTSS 419		

RESULT 7
SH_XENIA
) SHH_XENLA
STANDARD; PRT; 444 AA.

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EMBL; U26313; AAC12227.1;
EMBL; U26314; AAA85162.1;
EMBL; L2558; AAA49981.1.;
PIR; S56765; S56765.
HSSP; Q62226; 1VHH.
MEROPS; C46_002/-
DR InterPro; IPR019045; Hedgehog/DD_Pept.
DR InterPro; IPR003587; Hedgehog hint_N.
DR InterPro; IPR003586; Hedgehog hint_C.
DR InterPro; IPR003220; HH_SIGNAL.
DR InterPro; IPR006141; Intein_S.
DR InterPro; IPR01767; Pept_C46_hint.
DR InterPro; IPR001657; Pept_Tdase_C46.

Query Match Score 1498; DB 1; Length 44;
Best Local Similarity 6.1%; Pred. No. 8.e-10; Indels 46; Gaps 7;
Matches 305; Conservative 38; Mismatches 87.

Qy 1 MILLARCLIV-LYSSLIVCGSLACGPGRGFKRHPKLTPLAYKQFIPNVAEKTLGAS 59
(IN REF. 3).
Db 1 MLVATQSLLISFLCTLYTPPGLCPGRGIGRKHRPKLTPLAYKQFIPNVAEKTLGAS 60
SEQUENCE 444 AA: 432 MW: 7348E932FA2BFF2 CRC64;

Qy 60 GRYEGKISNSERKEFTLPNYPDILIFKDEENTCADRLMTQRCKDKUNALAISVNQWPG 119
Db 61 GRYEKITRNSDCFKELTPNYPDLMKFBESTDADRLMTQRCKDKUNALAISVNQWPG 120
Qy 120 VKLRTVEGWDGHSSESHYEGRADITTSDRSKYGMARLAVAFDVYYESKA 179
Db 121 VKLRTVEGWDGHSSESHYEGRADITTSDRSKYGMGRLAETAFDVYYESKA 180
Qy 180 HIHCSVKANSAKSGCCGPGSATVHLFQGTTKLVKDLSPGDRVLAAADDQGRLLYDEL 239
Db 181 HIHCSVKANSAKSGCCGPGAPAGRMVTFGGTAKVDRPGRDVLSSDPQGNLLISDEL 240
Qy 240 TFLDRDGAKKFVYIETTREPRLLTAAHLIFVAPINDSATGEPEANSGSPPSGAL 299
Db 241 MFIDQRDVKLFVYIETSO--RCIRLTAHLLIPEAQ-----TKYNGTR 282
Qy 300 GPRALFASRYRPQGRVYVVAERDGDPRLLPAAVSVTLSSEAAGAYAALTAQSTILINRV 359
Db 283 SFKSYFASNFQPGDIYTADPK-TMTLIAVKVKVLD EEDTGYAATLTAHGTVVIDQV 339
Qy 360 LASCYAVIEEESWAHRAAPFRLLAHALLALAPARTDRGDGGDGGDRGGGG----- 411
Db 340 LASCYAVIEEETWAILAFLREFGMNSLSSYYIYPR-----DSSPPSGLQPHHQVD 388
Qy 412 -----RVALTAGAADAQGAGATGTHWSQQLQIQLPMKSS 462
Db 389 LQSHHQQVDSLQSHHQVDSLQSHHQLEGITHWSQQLQIQLPMATKSS 444

RESULT 8
TWHH-BRAKE STANDARD PRT: 416 AA.
AC Q90419;

DR Pfam; PF01085; HH signal; 1.
DR Pfam; PF01079; H1t2; 1.
DR PRINTS; PR00302; SONICRHOG.
DR PROBMM; PD003042; HH signal; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR PROSITE; PS00017; INTEIN_N-TER; 1.
DR Developmental Protein; Autocatalytic cleavage; Hydrolase; Protease;
KW Signal; Lipoprotein; Palmitate; Peptidase; Repeat.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 444 SONIC HEDGEHOG PROTEIN N-PRODUCT.
FT CHAIN 25 198 SONIC HEDGEHOG PROTEIN C-PRODUCT.
FT DOMAIN 199 444 SONIC HEDGEHOG PROTEIN C-PRODUCT.
FT DOMAIN 386 409 3 X 8 AA TANDEM REPEATS OF Q-V-D-L-Q-S-H-H.
FT REPEAT 386 393 1.
FT REPEAT 394 401 2.
FT REPEAT 403 409 3.
FT SITE 198 199 CLEAVAGE (AUTO-) (BY SIMILARITY).
FT SITE 266 266 INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
FT ACT_SITE 269 269 ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
FT LIPID 25 25 N-palmitoyl cysteine (By similarity).
FT LIPID 198 198 Cholesterol glycine ester (By similarity).
FT CONFLICT 5 9 TQSII--> NSNLICW (IN REF. 3).
FT CONFLICT 302 319 DPKMTLAKVKEVKDLE --> ESQDHDLERGKWRLLR
FT CONFLICT 432 432 N-> S (IN REF. 3).
SQ SEQUENCE 444 AA: 49453 MW: 7348E932FA2BFF2 CRC64;

DR Pfam; PF01085; HH signal; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR PRINTS; PR00302; SONICRHOG.
DR PRODOM; PD003042; HH signal; 1.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR Devellopmental protein; Autocatalytic cleavage; Hydrolase; Protease;
KW Signal; Lipoprotein; Palmitate; POTENTIAL.

FT SIGNAL 1 26 TIGGY-WINKLE HEDGEHOG PROTEIN.
FT CHAIN 27 416 TIGGY-WINKLE HEDGEHOG PROTEIN N-PRODUCT.
FT CHAIN 27 200 TIGGY-WINKLE HEDGEHOG PROTEIN C-PRODUCT.
FT SITE 201 416 CLEAVAGE (AUTO-).

RESULT 10
 ID _IH_HUMAN STANDARD; PRT; 411 AA.
 AC Q14623; Q43322; Q8N4B9;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Indian hedgehog protein precursor (IHH) (HHG-2).
 RN 1
 OS Homo sapiens (Human).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarzhini; Hominidae; Homo.
 OC -
 RN 1
 SEQUENCE FROM N.A.
 RA "Expression of Sonic hedgehog and its receptor Patched/Smoothened in
 RA human cancer cell lines and embryonic organs.";
 J. Biochem. Mol. Biol. Biophys. 4:27-34 (2000).
 [2]
 RP SEQUENCE OF 95-411 FROM N.A.
 RX MEDLINE=22389257; PubMed=12447932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.M., Wagner L., Shuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Shaeffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Maxx S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Matsunaga A., Farmer A.A., Rubin G.M., Hong L.,
 RA Strelton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S., Loqueline N.A., Peters G.J., Abramson R.D., Mulahay S.J.,
 RA Bosak S.A., McEwan P.J., McErlean K.J., Malek J.A., Gunnarate P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heitton E., Keitman M., Madan A., Marra M.A., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
 RA Butterfield Y.S.N., Krywinski M.I., Skalaka U., Smilus D.E.,
 RA Schnier A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 SEQUENCE OF 100-411 FROM N.A.
 RP
 RC TISSUE=Fetal lung;
 RX MEDLINE=26070431; PubMed=7590746;
 RA Marigó V., Robert D.J., Lee S.M.K., Tsukurov O., Levi T., Copeland N.G., Seidman C.E.,
 RA Gaster J.M., Epstein D.J., Gilbert D.J., Tabin C., Jenkins N.A., Seidman J.G., McMahon A.P., Tabin C.,
 RA

RT "Cloning, expression, and chromosomal location of SHH and IHH: two
 human homologues of the *Drosophila* segment polarity gene hedgehog.";
 RL Genomics 28:44-51 (1995).
 RN [4]
 SEQUENCE OF 124-172 FROM N.A.
 RP MEDLINE=95236997; PubMed=7720571;
 RA Chang D.T., Lopez A., von Kesseler D.P., Chiang C., Simardl B.K.,
 RA Zhao R., Selain M.F., Fallon J.F., Beachy P.A.;
 RA "Products, genetic linkage and limb patterning activity of a murine
 hedgehog gene.";
 RT Development 120:3339-3353 (1994).
 RL RN [5]
 RP VARIANTS BDA1 LYS-95; GLU-100 AND LYS-131.
 RX MEDLINE=1317448; PubMed=11455389;
 RA Gao B., Guo J., She C., Shu A., Yang M., Tan Z., Yang X., Guo S.,
 RA Feng G., He L.;
 RA "Mutations in IHH, encoding Indian hedgehog, cause brachydactyly type
 A-1.";
 RT Nat. Genet. 28:386-388 (2001).
 RL RN [6]
 RP VARIANT BDA1 ASN-100.
 RX MEDLINE=22271632; PubMed=12384778;
 RA McCready M.E., Sweeney E., Fryer A.E., Donnai D., Baig A., Racacho L.,
 RA Warman M.L., Hunter A.G.W., Bulman D.E.;
 RA "A novel mutation in the IHH gene causes brachydactyly type A1: a
 95-year-old mystery resolved.";
 RT Hum. Genet. 111:363-375 (2002).
 RL RN [7]
 RP VARIANTS ACFD LEU-46 AND ALA-190.
 RX MEDLINE=22534978; PubMed=12632327;
 RA Hellermans J., Coucke P.J., De Pepe A., Kramer P.,
 RA Beemer F., Mortier G.R.;
 RA "Homozygous mutations in IHH cause acrocapitofemoral dysplasia, an
 autosomal recessive disorder with cone-shaped epiphyses in hands and
 hips";
 RT Am. J. Hum. Genet. 72:1040-1046 (2003).
 RL RN [8]
 RP INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF
 CC PATTERNING EVENTS DURING DEVELOPMENT. BINDS TO THE PATCHED (PTC)
 CC RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SMO), TO
 CC ACTIVATE THE TRANSCRIPTION OF TARGET GENES. IMPLICATED IN
 CC ENDOCHONDRAL OSSIFICATION: MAY REGULATE THE BALANCE BETWEEN GROWTH
 CC AND OSSIFICATION. INDUCES THE EXPRESSION
 CC OF PARATHYROID HORMONE-RELATED PROTEIN (PTHRP) (BY SIMILARITY).
 CC -|- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the
 CC cell, while the N-terminal peptide remains associated with the
 CC cell surface. Is also secreted in either cleaved or uncleaved form
 CC to mediate signaling to other cells (By similarity).
 CC -|- TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC LUNG, AND IN ADULT
 CC KIDNEY AND LIVER.
 CC -|- PTM: The C-terminal domain displays an autoproteolysis activity
 CC and a cholesterol transferase activity. Both activities result in
 CC the cleavage of the full-length protein and covalent attachment of
 CC a cholesterol moiety to the C-terminal of the newly generated N-
 CC terminal Fragment (N-product). This covalent modification appears
 CC to play an essential role in restricting the spatial distribution
 CC of the protein activity to the cell surface. The N-product is the
 CC active species in both local and long-range signaling, whereas the
 CC C-product has no signaling activity (By similarity).
 CC -|- DISEASE: Defects in IHH are the cause of brachydactyly type A1
 CC (BDA1) [MIM:112500]. BDA1 is an autosomal dominant disorder
 CC characterized by middle phalanges of all the digits rudimentary or
 CC fused with the terminal phalanges. The proximal phalanges of the
 CC thumbs and big toes are short.
 CC -|- DISEASE: Defects in IHH are a cause of acrocapitofemoral
 CC dysplasia (ACFD) [MIM:607781]. ACD is a disorder characterized by
 CC short stature of variable severity with postnatal onset. The most
 CC constant radiographic abnormalities are observed in the tubular
 CC bones of the hands and in the proximal part of the femur. Cone-
 CC shaped epiphyses or a similar epiphyseal configuration with
 CC premature epiphyseal fusion result in shortening of the
 CC skeletal components involved. Cone-shaped epiphyses were also
 CC present to a variable extent at the shoulders, knees, and ankles.
 CC -|- SIMILARITY: Belongs to the hedgehog family.

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BAA33523.2; JOINED.
EMBL; AB010922; BAA33523.2; JOINED.
EMBL; AB018076; BAA33523.2; JOINED.
EMBL; BC034757; BAA33523.2; JOINED.
EMBL; L38517; AAH34757.1; ALT_INIT.
HSSP; Q62226; IVEH.
MEROPS; C46.003; -.
DDR Generew; HGNC:5956; INH.
MIM; 600726; -.
DDR MIM; 112500; -.
DDR MIM; 607778; -.
DDR GO; GO:005576; C:extracellular; NAS.
DDR GO; GO:000513; P:cholesterol binding; NAS.
DDR GO; GO:0027867; P:cell-cell signaling; NAS.
InterPro; IPR003587; Hedgehog_hnt_N.
InterPro; IPR003586; Hedgehog_hnt_C.
InterPro; IPR003520; HH signal.
InterPro; IPR006141; Intein_S.
InterPro; IPR001676; Pept_C46_hnt.
InterPro; IPR001657; Pept_Drase_C46.
Pfam; PF01079; Hint_1; -.
PRINTS; PRO00632; SONIC_HOG.
ProDom; PD003042; HH signal; 1.
SMART; SM00305; Hint_C; 1.
SMART; SM00306; Hint_N; 1.
PROSITE; PS00817; INTRIN_N_TER; 1.
Developmental_protein; Autocatalytic cleavage; Hydrolase; Protease;
Signal; Lipoprotein; Palmitate; Disease mutation.
SIGNAL; SIGNAL; 27
SIGNALLING; 27
CHAIN 28 411
CHAIN 28 202
CHAIN 203 411
SITE 202 203
SITE 248 248
SITE 272 272
ACT_SITE 275 275
LIPID 28 28
LIPID 202 202
VARIANT 46 46
VARIANT 95 95
VARIANT 100 100
VARIANT 100 100
VARIANT 131 131
VARIANT 190 190
CONFLICT 100 100
CONFLICT 246 246
CONFLICT 309 309
SEQUENCE 411 AA; 45250 MW; 4DA90C83F5ABF758 CRC64;

Query Match 51.5%; Score 1271; DB 1; Length 411;
Best Local Similarity 57.7%; Prec No. 1.BE-84;
Matches 267; Conservative 45; Mismatches 85; Indels 66; Gaps 10

```

QY	7	CLLIVLVSSLVCGGACCPGRGEG-KRHPKLTPLAYKQFIPNVAEKTLLGASRYEGK	65
Db	13	CLVLIL--LIVVPAWGCGPGRVYGSRRREPRLVPLAYKQFSNVPERKLVLGASRYEGK	70
QY	66	TSRSERFKELTPNYPDIFKDENTGADRMLTQCRDKLNLAISVNQWPQGMQLRVT	125
Db	71	IARSERFELTPNYPDIFKDENTGADRMLTQCRDLNSLAISVNQWPQGMQLRVT	130
QY	126	EGWDEGDGHSEESLHYEGRADITTSDRSKYGMARLAVEAGFDWVITYESKAIIHCSV	185
Db	131	EGWDGDGHSEESLHYEGRADITTSDRDANKYGLARLAVEAGFDWVITYESKAIIHCSV	190
QY	186	KAEVSAAATSGGGCPEGSATVHLBECGTTKLVKDLSEGDRLAADDGGRLLYSDFTEFLDLD	245
Db	191	KSEHSAAATGGCFPAGAQVRLESARVALSAVEGDRVIAMGBCSPSPSDVLFLDRE	250
QY	246	DGAKKVVFYVLTREPRLLTAAHLYFAVPHNDSATGPEAASSGGPPSGGALGPRAFLP	305
Db	251	PHRLRAFOVETOPPRRLATPAHLLFTA---DHT-BPAFARF-----RATF	294
QY	306	ASRYPGQRQYVYTAERDGERDLPAHVSYTLSEAAAGAYAPLTAQGTILINRVLASCYA	365
Db	295	ASHYQPQGYVLLVA---GVPGLQPARVAAVS-THVALGAYAPL-TKGTLVVEDVYASCFC	349
QY	366	VIEEWSWAHAFAPRLALAALAPARTDGGSGGGGRVALTAQGADADP	425
Db	350	AVADHHLAQAFWPRLFLS-----	-----
QY	426	AGATAGIHWYSCQLYQIGTWLDSBALHPLGMAVYSSXSBRGAG	468
Db	379	---EGVHWIPQLLIRGLLLEFGSFPLGMS-----GAG	410
RESULT 11			
IH _H MOUSE STANDARD			
ID	IHH MOUSE	PRT,	411 AA.
AC	P977612; 0611724;		
DT	15-JUL-1999 (Rel. 38, Created)		
DT	15-JUL-1999 (Rel. 38, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DB	Indian hedgehog protein precursor (IHH) (IHG-2).		
GN	IHH.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX			
DB	TAXID=10990;		
RN	[1]		
RP	SEQUENCE FROM N.A., AND AUTOPROTEOLYTIC CLEAVAGE.		
RC	STRAIN=CD-1; TISSUE=Kidney;		
RX	MEDLINE=97236302; PubMed=9075674;		
RA	Valentini R.P.; Brookhiser W.T.; Park J.; Yang T.; Briggs J.;		
RA	Dressler G.; Holzman L.;		
RT	"Post-translational processing and renal expression of mouse Indian hedgehog."		
RT	J. Biol. Chem. 272:8466-8473(1997).		
RL	[2]		
RN	SEQUENCE OF 76-411 FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Embryo;		
RX	MEDLINE=9409434; PubMed=7916661;		
RA	Echeland Y.; Epstein D.J.; St Jacques B.; Shen L.; Mohler J.;		
RA	McMahon J.A.; McMahon A.P.;		
RT	"Sonic hedgehog," a member of a family of putative signaling molecules, is implicated in the regulation of CNS polarity."		
RT	Cel1 75:1417-1430(1993).		
RN	[3]		
RP	REVISONS.		
RC	STRAIN=C57BL/6J;		
RA	St Jacques B.;		
RL	Submitted (APR-1997) to the EMBL/GenBank/DDJB databases.		
RA	[4]		
RN	SEQUENCE OF 124-172 FROM N.A.		
RP	MEDLINE=93236997; PubMed=7720571;		
RX			

RA	Chang D.T., Lopez A., von Kessier D.P., Chiang C., Simandi B.K., Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.;	ACT SITE	275	275	ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
PA	products, genetic linkage and limb patterning activity of a murine hedgehog gene.";	FT	LIPID	28	N-Palmitoyl cysteine (By similarity).
RT	Development 120:3339-3353 (1994).	FT	LIPID	202	Cholesterol ester (By similarity).
RL	-: FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT, BINDS TO THE PATCHED (PTC) RECEPTOR, WHICH FUNCTIONS IN ASSOCIATION WITH SMOOTHENED (SNO), TO ACTIVATE THE TRANSCRIPTION OF TARGET GENES, IMPLIMENTED IN ENDCHONDRAL OSSIFICATION; MAY REGULATE THE BALANCE BETWEEN GROWTH AND OSSIFICATION OF THE DEVELOPING BONES. INDUCES THE EXPRESSION OF PARATHYROID HORMONE RELATED PROTEIN (PTHrP).	FT	CONFFLICT	383	W -> S (IN REF. 2).
CC	-: SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell surface. Is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).	FT	SEQUENCE	411 AA;	45485 MW; 08BEAD8507C0D9B CRC64;
CC	-: TISSUE SPECIFICITY: DETECTED IN THE EMBRYO, DETECTED IN THE DEVELOPING GUT, THE GROWTH ZONE OF CARTILAGE OF DEVELOPING LONG BONES, EPITHELIUM AND UROGENITAL SINUS. IN THE ADULT KIDNEY, FOUND IN PROXIMAL CONVOLUTED AND PROXIMAL TUBULE.	Query Match	51.1%	Score 1262; DB 1; Length 411;	
CC	-: DEVELOPMENTAL STAGE: Detected at 10 dpc in developing gut, at 14.5 days dpc in the cartilage primordium and in the developing urogenital sinus. Expression increases with gestational age in kidney and duodenum, becoming maximal in adulthood.	Best Local Similarity	56.9%	Pred. No. 8 1e-34;	
CC	-: PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transfer activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity).	Matches 264;	Conservative	46;	Mismatches 86; Indels 68; Gaps 10;
CC	-: SIMILARITY: Belongs to the hedgehog family.	Qy	7	CILIVLYSSLLIVSGLACGPGRGFG-KRRHPEKLTPLAKOFIPIVTAEKTIGASGRYEGK 65	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	Db	13	CLFLILL-LLVAAARGCPGRVGSRRPRPLVPAKQSPNPVEKTLGASGRYEGK 70	
CC	EMBL; U85610; NAB9692_1; ALT_INIT.	Qy	66	ISRNSEERPEKLTNPNNPDIFKDENTGADRINTQRCKDKUNALATVMNONPGVKLVRT 125	
CC	HSSP; Q2226; 1VHH.	Db	71	TARSERPEKLTNPNNPDIFKDENTGADRINTQRCKDRUNSLATVMNONPGVKLVRT 130	
CC	MEROPS; C46_003 ;	Qy	126	EGWDEDDGHSEESLHYEGRADTTTSRSDRSKYGMLARLAVERAGEDWYVYSSKAHICSV 185	
CC	DR	Db	131	EGWDEDDGHSEESLHYEGRADTTTSRDRDNKYLGLLRLAVERAGEDWYVYSSKAHICSV 190	
CC	InterPro; IPR00905; Hedgehog/DD Pept.	Qy	186	XAEENVAAKSGGCCPPGSAVTHLEGGGFLKVLKDISPGRVLAADDQGELLYSDFLTFLDRD 245	
CC	InterPro; IPR003587; Hedgehog_hint_N.	Db	191	KSESAAXTGGCFPAGQVRLENGERVALSAVKPGRVLANGEDGTPTFSVLYFIDRE 250	
CC	InterPro; IPR003588; Hedgehog_hint_C.	Qy	246	DGARKVVFVYETREPERRILLLTAHHLFVAPHRDSDATGEPASSGSSPPSGGALGPALF 305	
CC	InterPro; IPR001767; HH_signal_I.	Db	251	PNRURAFQVLETQDPFRRLALPAHLLFIA--DNTF-EPAHF----RATF 294	
CC	InterPro; IPR01657; PeptCf6_hint.	Qy	306	ASRYRPQGVVYVAERDGDRRLPAAYHSVTLSBAAAGAYAPLTAQGTILINRVLASCYA 365	
CC	Pfam; PF01085; HH_signal_1.	Db	295	ASHYQGQTFLV---SGVPGQLPARIAVS-THVALGYSYLTRHTGLVVVDVVASCPA 349	
CC	PRINTS; PR00632; SONICHHOG.	Qy	366	VIEBHSWAHRAFAFPLAHALL-AAALAPARTDGGDSGGDRGGCGRVVALTAGADAP 424	
CC	SMART; SM00305; HntC.	Db	350	AVADHHLAQAFWPLRFLPPSLANGSWTPSE-----379	
CC	PROSITE; PS50817; INTIN_N_TER; 1.	Qy	425	GAGATAGIHWYQULYQIQTWLDEAHLPLGNAVKSSXSRGAG 468	
CC	Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; Signal; Lipoprotein; Palmitate.	Db	380	-GVHWYQPMLYRLGRLLBESTFHPLGNS-----GAG 410	
CC	Pfam; PF01079; HntC_1.	RESULT 12			
CC	DR	IHH_XENLA	ID	IHH_XENLA	STANDARD;
CC	SMART; SM00306; HntC.	AC	Q91612;	PRT;	409 AA.
CC	SMART; SM00305; HntC.	DR	15-JUL-1999 (Rel. 38, Created)		
CC	PROSITE; PS50817; INTIN_N_TER; 1.	DT	15-JUL-1999 (Rel. 38, Last sequence update)		
CC	Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; Signal; Lipoprotein; Palmitate.	DT	10-OCT-2003 (Rel. 42, Last annotation update)		
CC	Pfam; PF01079; HntC_1.	DR	DB Indian hedgehog protein Precursor (IHH) (Banded hedgehog protein (X-BHH))		
CC	DR	DE	GN IHH OR BH.		
CC	SMART; SM00305; HntC.	DR	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Xenopus laevis (African clawed frog).		
CC	PROSITE; PS50817; INTIN_N_TER; 1.	DR	OS Xenopus laevis; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus.		
CC	Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; Signal; Lipoprotein; Palmitate.	DR	OC NCBI_TaxID:8355;		
CC	Pfam; PF01079; HntC_1.	DR	RN [1] _		
CC	SMART; SM00305; HntC.	DR	RC SEQUENCE FROM N.A.		
CC	PROSITE; PS50817; INTIN_N_TER; 1.	DR	RP TISSUE=Embryo;		
CC	Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; Signal; Lipoprotein; Palmitate.	DR	RX MEDLINE=93401852; PubMed=7671800;		
CC	Pfam; PF01079; HntC_1.	DR	RA Elke S.C., McCraw L.J., Lai C.-J., Lee J.-J., von Kessler D.P., Moon R.T., Beachy P.A.;		
CC	SMART; SM00306; HntC.	DR	RA "Distinct expression and shared activities of members of the hedgehog gene family of <i>Xenopus laevis</i> ";		
CC	PROSITE; PS50817; INTIN_N_TER; 1.	DR	RT Development 12:1337-1347 (1995).		
CC	Developmental protein; Autocatalytic cleavage (AUTO-).	DR	CC - FUNCTION: SIGNAL INVOLVED IN THE EARLY INDUCTION AND PATTERNING OF ANTERODORSAL ECTODERM. NERVOUS SYSTEM AND SOMITES. INDUCES ECTOTIC CEMENT GLAND FORMATION IN EMBRYOS		
CC	Signal; Lipoprotein; Palmitate.	DR	CC - SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE		
CC	Pfam; PF01079; HntC_1.	DR	CC - SIMILARITY: INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).		

CC	CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. HEDGEHOG PROTEIN IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).	Db	123 RVTEGMDDEGHFEESEHYSRGRDITTSDRDRSKYGMMLARLAVAGFDWVYYESKAHH 182
CC	-!- DEVELOPMENTAL STAGE: DETECTABLE WITHIN THE EARLY GASTRULA, AT STAGE 14 NEURULA, HIGH EXPRESSION IN NEUROECTODERM, EXPRESSED THROUGHOUT THE NEURAL PLATE AND SUBSEQUENTLY IN BOTH THE NERVOUS SYSTEM AND IN THE DERMATOME OF SOMITES.	Qy	183 CSVKAEVNSVAAKSGGGPGSATVHLEQGTTKLVRDLSPGDRVLADQCRLLYSDFLFL 242
CC	-!- INDUCTION: BY activation.	Db	183 CSVKSHSAAAKTGGFPGRALATLSEGEKIPVSQSLSPGRVLLANDNSGPYTSDFLSFL 242
CC	-!- PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity).	Qy	243 DRDGAKRKVFVTEBPEBRRLTAHLLLEVPHNDSATGEPEASGSOPPSGGALGPR 302
CC	-!- SIMILARITY: Belongs to the hedgehog family.	Db	243 DHSPKCEEHMFQVKTQDPHRFLFTFAHLFVSDNYSTPASEFQ 286
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	Qy	303 ALFASVRPGORVYVAERDQRRLPAATHSVTLEEAQAYAPLAQCTTILNRVLAS 362
CC	CC	Db	287 AVFASSTRPQYI-LVSNVVG-LIPAKYRSVN-TQTYNGAYAPLQHGTLVVDVVVS 341
CC	CC	Qy	363 CYAVIEEHSHWAFFPFRFHALLAALAPARTDGGDSCEGGDRGGGRVALTAQGAAD 422
CC	CC	Db	342 CFALVKQRLAQIVVPLRVNL-GRIAGTOP 373
CC	CC	Qy	423 APGAGATAGTHWYSQOLYOIGTWLJIDSEALHPGLM 457
CC	CC	Db	374 ---SQQMGIIHWYSKALYHGLRLILIGNEFRPLGI 404
RESULT 13			
CC	DB_IHH_BRAE_BARE_ID	STANDARD; PRT; 412 AA.	
CC	AC Q9862;		
CC	DT 15-JUL-1999 (Rel. 38, Created)		
CC	DT 15-JUL-1999 (Rel. 38, Last sequence update)		
CC	DT 10-OCT-2003 (Rel. 42, Last annotation update)		
CC	DE Indian hedgehog protein precursor (IHh) (Echidna hedgehog protein).		
CC	GN IHh OR EHH.		
CC	OS Brachydanio rerio (Zebrafish) (Danio rerio).		
CC	OC Bularyota; Metacoa; Chorata; Cranata; Vertibrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.		
CC	NCBI_TaxID:7955;		
CC	RN [1]		
CC	RP SEQUENCE FROM N.A.		
CC	RX MEDLINE=9631086; PubMed=8684485;		
CC	RA Currie P.D., Ingham P.W., Meyer A.; Zaridova R., Abouheif E., Meyer A.; Evolutionary analyses of hedgehog and Hoxd-10 genes in fish species closely related to the zebrafish.".		
CC	RT "Induction of a specific muscle cell type by a hedgehog-like protein in zebrafish."		
CC	RT Proc. Natl. Acad. Sci. U.S.A. 93:1036-13041(1996).		
CC	RT Nature 382:452-455(1996).		
CC	RN [2]		
CC	RP SEQUENCE OF 113-170 FROM N.A.		
CC	RC TISSUE-Muscle;		
CC	RX MEDLINE=97075114; PubMed=8917540;		
CC	RA Zardoya R., Abouheif E., Meyer A.;		
CC	RT "Induction of a specific muscle cell type by a hedgehog-like protein during development. Signal produced by the notochord that induces somite patterning and muscle pioneer differentiation.		
CC	RT Proc. Natl. Acad. Sci. U.S.A. 93:1036-13041(1996).		
CC	CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT. SIGNAL PRODUCED BY THE NOTOCHORD THAT INDUCES SOMITE PATTERNING AND MUSCLE PIONEER DIFFERENTIATION.		
CC	CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. Is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).		
CC	CC -!- TISSUE-SPECIFICITY: EXPRESSED EXCLUSIVELY IN THE NOTOCHORD.		
CC	CC -!- DEVELOPMENTAL-STAGE: FIRST DETECTABLE AT THE MID-GASTRULA STAGE.		
CC	CC -!- DISAPPEARS AT THE END OF THE SOMITOGENESIS.		
CC	CC -!- PIM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity).		
Qy	4 LARCLLIVLSSLLVSGL-ACGPNGFGGRHPKLTPLAYKQTPNAAEKTLGASRY 62		
Db	3 LPKVWLLCAALLLSGAVRGCGPGRVGRRRPKLSPVSYKQFSNPVPEKTLGASRY 62		
Qy	63 EGKISRSNSERPEKLTNNPDIFKDENTGADRMLTKDKDNLASIVSNQMPGTYL 122		
Db	63 EGKISRSNSERPEKLTNNPDIFKDENTGADRMLTKDKDNLASIVSNQMPGTYL 122		
Qy	123 RVTEGMDDEGHFEESEHYSRGRDITTSDRDRSKYGMMLARLAVAGFDWVYYESKAHH 182		

-	-	SIMILARITY: Belongs to the hedgehog family.
CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration - between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	DR	EMBL: Y08426; CAA69702.1; -.
CC	DR	HSSP: Q62246; 1VHW.
CC	DR	MEROPS; C46_UPW; -.
CC	DR	ZFIN: ZDB-GENE-080526-135; ehh.
CC	DR	InterPro; IPR00045; Hedgehog/DD_pept.
CC	DR	InterPro; IPR003387; Hedgehog hint_N.
CC	DR	InterPro; IPR003386; Hedgehog hint_C.
CC	DR	InterPro; IPR003320; HH_Signal.
CC	DR	InterPro; IPR006141; Intein_S.
CC	DR	InterPro; IPR001767; Pept_C46_hint.
CC	DR	InterPro; IPR001657; PeptIdase_C46.
CC	DR	Pfam; PF01085; HH_Signal; 1.
CC	DR	Pfam; PF010719; Hint; 1.
CC	DR	PRINTS; PRO0632; SONICHHOG.
CC	DR	Prodrom; PDD03042; HH_Signal; 1.
CC	DR	SMART; SM00305; HintC; 1.
CC	DR	SMART; SM00306; HintN; 1.
CC	DR	PROSITE; P855017; INTEIN_N-TER; 1.
CC	KW	Developmental protein; Autocatalytic cleavage; Hydrolase; Protease;
CC	KW	Signal; Lipoprotein; Palmitate.
FT	FT SIGNAL	POTENTIAL.
FT	FT SIGNAL	INDIAN HEDGEHOG PROTEIN.
FT	FT CHAIN	INDIAN HEDGEHOG PROTEIN N-PRODUCT.
FT	FT CHAIN	INDIAN HEDGEHOG PROTEIN C-PRODUCT.
FT	FT SITE	N-Palmityl cysteine (By similarity).
FT	FT SITE	CLEAVAGE (AUTTO) (BY SIMILARITY).
FT	FT SITE	INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY).
FT	FT SITE	INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
FT	ACT_SITE	ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
FT	FT LIPID	N-Palmityl cysteine (By similarity).
FT	FT LIPID	Cholesterol glycine ester (By similarity).
FT	FT CONFLICT	R → K (IN REF 2).
FT	SEQUENCE	45746 MW; 21D43F152A2'8CA1 CRC64;
SQ	SEQUENCE	412 AA; 412 AA; 45746 MW; 21D43F152A2'8CA1 CRC64;
Query	Match	Score 1213; DB 1; Length 412;
Best	Local Similarity	Score 1213; DB 1; Length 412;
Matches	251; Conservative	Pred. No. 2.3e-80; Mismatches 86; Indels 56; Gaps 7;
Qy	24	CGPGRGKGRHRPKKLTPLAYKOPPNVAEKTIGASGRYEGKISNSRKFELTPNNPND 83
Dp	24	CGPSRGYGRGRTPKPLTPAYKOPPNVAEKTIGASGRYEGKISNSRKFELTPNNPND 83
Qy	84	IIFDEENTGADRMTQCKDKNLAIATSNQNGVKRUTGEDEGHSEELHYEG 143
Db	84	IIFDEENTGADRMTQCKDKNLAIATSNQNGVKRUTGEDEGHSEELHYEG 143
Qy	144	RADITTSDDRSKGIMLARLAVEGGFDWVYESKAHHSVKAENSVAAKSGGGPPGSA 203
Db	144	RADITTSDDRSKVYRMLARLAVEGGFDWVYESKAHHSVKAENSVAAKSGGGPPGSA 203
Qy	204	TVHLQGQTKLVDLSPGDEVLA---ADDGGRLLSDFLTRDGGAKVYYETREP 260
Db	204	LVTMKDSHRQIRDIAQGDLYLVAQSGSDGTDLIITSEVLTFLDRPITQKHFYVIRT-ED 262
Qy	261	RERLIITAHLFLFYVAPHDNTSATGPEAASSGGPPGGALPRAFSYRFGQRYVVAA 320
Db	263	GASVSLTAHLLFMVGNCNRGEKP-----GAV--RTIASDAQVGQCLL--- 308
Qy	321	RDGDRLPRAVHSYTLLSEAAAGAATPLAQGTILINVLASCYVIEEWSWAHAFAPP 380

Db	309	->GKURKRFQITHVGRED-CQLYPPLTAHGTIVVVRDVLTSCAYVNRCQLAHWAFPL	365
Qy	381	RLAHLALLAALAPARTDRGGDSGGDGGGGRRVALATGAAADAPGGATAGTHWSQLY	440
Db	366	RLLYSW-----TGPDQVLRKGTHWSQYLI	390
Qy	441	QIGTWLDSLSPALHPGM	457
Db	391	GLGKLLDLSLFHFLAI	407
RESULT 1.4			
DHH_MOUSE	SEQUENCE FROM N.A.		
ID DHH_MOUSE	STANDARD;	PRT;	396 AA.
AC Q61486;			
DT 15-JUL-1999	(Rel. 38, Created)		
DT 15-JUL-1999	(Rel. 38, Last sequence update)		
DT 10-OCT-2003	(Rel. 42, Last annotation update)		
DE Desert hedgehog protein precursor (DHH) (HMG-3).			
GN DHH.			
OS Mus musculus (Mouse).	Cetacea; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC NCBI_TaxID=10090;			
OX RN			
RP SEQUENCE FROM N.A.			
RC MEDLINE=129_Sv			
RX MEDLINE=901094334; PubMed=7916661;			
RA Echelard Y., Epstein D.J., St Jacques B., Shen L., Mohler J.,			
RA McMahon J.A., McMahon A.P.;			
RT "Sonic hedgehog, a member of a family of putative signaling molecules, is implicated in the regulation of CNS polarity.";			
RL Cell 75:1417-1430(1993).			
RN [2]			
RP SEQUENCE OF 120-168 FROM N.A.			
RX MEDLINE=93236997; PubMed=7720571;			
RA Chang D.T., Lopez M.A., von Kessler D.P., Chiang C., Simmandl B.K.,			
RA Zhao R., Seldin M.F., Fallon J.F., Beachy P.A.;			
RT "Products, generic linkage and limb patterning activity of a murine hedgehog gene.";			
RL Development 120:3339-3353(1994).			
CC -!- FUNCTION: INTERCELLULAR SIGNAL ESSENTIAL FOR A VARIETY OF PATTERNING EVENTS DURING DEVELOPMENT MAY FUNCTION AS A SPERMATOZYTE SURVIVAL FACTOR IN THE TESTES. ESSENTIAL FOR TESTES DEVELOPMENT.			
CC -!- SUBCELLULAR LOCATION: The C-terminal peptide diffuses from the cell, while the N-terminal peptide remains associated with the cell surface. It is also secreted in either cleaved or uncleaved form to mediate signaling to other cells (By similarity).			
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ADULT TESTES. NOT EXPRESSED IN LIMB BUDS.			
CC -!- PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity).			
CC -!- SIMILARITY: Belongs to the hedgehog family.			
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CC DR X76291; CBA53924.1; -			
CC DR PIR: B49425; B49425.			
CC EMBL: 062226; 1vrM			

CC dysgenesis with minifascicular neuropathy 46,XY (PGD) [MIM:607080]. PGD is characterized by the presence of a testis on one side and a streak or an absent gonad at the other, persistence of Mullerian duct structures, and a variable degree of genital ambiguity.

-1- SIMILARITY: Belongs to the hedgehog family.

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DR EBO10994; BAA24866_1; JOINED.
 DR EMBL; ABO10931; BAA24866_1; JOINED.
 DR EMBL; ABO10933; BAA24866_1; JOINED.
 DR EMBL; BCO33507; ABH33507_1; -.
 DR EMBL; US97498; AAB03398_1; -.
 DR PIR; G02735; G02735.
 DR HSSP; Q22226; 1VHH.
 DR MEROPS; C46_004; -.
 DR Genew; HGNC:2865; DHX.
 DR MIM; 603423; -.
 DR MIM; 607080; -.
 DR InterPro; IPR009045; Hedgehog/DD_Pept.
 DR InterPro; IPR003557; Hedgehog_hnt_N.
 DR InterPro; IPR003556; Hedgehog_hnt_C.
 DR InterPro; IPR000320; HH_Signal.
 DR InterPro; IPR001767; Pept_C16_hnt.
 DR InterPro; IPR000167; Pept_Database_C46.
 PFam; PF01085; HH_signal_1.
 PRINTS; PR00612; SONICHHG.
 PRODOM; PD005042; HH_signal_1.
 SMART; SM00305; HintC_1.
 SMART; SM00306; HintN_1.
 DR Signal; Lipoprotein; Autocatalytic cleavage; Hydrolase; Protease; KW Developmental protein; Autocatalytic cleavage; Hydrolase; Protease; KW Signal; Lipoprotein; Palmitate.
 PT SIGNAL 1 22 POTENTIAL.
 PT CHAIN 23 396 DESERT HEDGEHOG PROTEIN_N-PRODUCT.
 PT CHAIN 23 198 DESERT HEDGEHOG PROTEIN_C-PRODUCT.
 PT CHAIN 199 396 DESERT HEDGEHOG PROTEIN_C-PRODUCT.
 PT SITE 198 199 CLEAVAGE (AUTO-) (BY SIMILARITY).
 PT SITE 244 244 INVOLVED IN CHOLESTEROL TRANSFER (BY SIMILARITY).
 PT SITE 268 268 INVOLVED IN AUTO-CLEAVAGE (BY SIMILARITY).
 PT ACT_SITE 271 271 ESSENTIAL FOR AUTO-CLEAVAGE (BY SIMILARITY).
 PT LIPID 23 23 N-Palmitoyl cysteine (By similarity).
 PT LIPID 198 198 Cholesterol glycine ester (By similarity).
 PT CONFLICT 177 177 B->G (IN REF. 3).
 SQ SEQUENCE 396 AA; 43577 MW; FCE4FB21972C3ADS; CRC64;

Query Match 47.7%: Score 1177; DB 1; Length 396;
 Best Local Similarity 54.4%; Pred. No. 1.le-77; Indels 58; Gaps 10;
 Matches 245; Conservative 54; Mismatches 93;

Qy 1 MLLAARCLLIVLVLSSLLVSGLAGCPGRG-FGRRRHPKK-LPDISPLAYQFIPVNAEKTIGA 58
 Db 1 MALLTNLPLCCL-ALLAPAOQSCGPGRCPVGRYYARKQVPLLYKOFVPGYPERTIGA 59
 Qy 59 SGRYEGKISBRNSBREFKELTPNYPDDIFDEENTGADRMLTORCKDLNALATSNQW 118
 Db 60 SGPAQGRVAGSERPDRDLPNNEYDIIIFDEENSGADLMTECKERVALIAVQMW 119
 Qy 119 GVKLRYTEGMDDEGHSEESLHYGRAVDTTSQRDRSKYGMARLAVEAGEDMWYTESK 178
 Db 120 GVRLRVTEGWDEGHQAQDSLHYEGRALDITTSQRDRNKGILLARLAVEAGEDMWYTESR 179

Qy	179 AHHCSCKAENSVAAKSGCCPPGSATVHLBQGCTKLVKDLSPGDRVLAADDGRLLYSDF 238	Db	180 NHVYVSKRADDNLAVRAAGCCPPONATVRLWSERKGRELHGDNVIAADASGRVYTRPV 239
Db	239 LTFLDRDGAKKVYVTEIPEPRLITAHLFVPHNDSATGEBAESSGGP-SGG 297	Qy	240 LLFLDRDLORRASFVAETEMPRLLTPTWHLVEA-----RGPADPG 284
Qy	298 ALGRALFAASRVRPGORYVVAERDGDRLLPAAVHSVTLSEBAAGAYAPLTAQGTILIN 357	Db	285 DFAP--VFARRLRAFGDSVIA---PGGDALRPARVARA-REEAVGTFPLTAHTGTLVN 337
Db	358 RVLASCYAVIEEEFWAHRAFAPPRLAHALLAALAPARTDRGGDSGCGDRGGGGRVALTA 417	Qy	338 DVLASCYAVIEEEFWAHRAFAPPRLAHALLAALAPARTDRGGDSGCGDRGGGGRVALTA 417
Db	DH1_XENLA	DB	DH1_XENLA
AC	ID DH1_XENLA STANDARD;	PRT;	396 AA.
AC	Q91670;	DT	15-JUL-1999 (Ref. 38, Created)
AC		DT	15-JUL-1999 (Ref. 38, Last sequence update)
AC		DT	10-OCT-2003 (Ref. 42, Last annotation update)
DE	Desert hedgehog protein precursor 1 (DHH-1) (Cephalic hedgehog protein) (X-CHH).	GN	Xenopus laevis (African clawed frog).
DE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; Amphibia; Barrochia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus.	OC	Xenopus laevis (African clawed frog).
RN	[1] - TaxID=8355;	RC	SEQUENCE FROM N.A.
RN		RC	TISSUE=Embryo;
RC		RC	MEDLINE=9340852; PubMed=7671800;
RA		RA	Beker, S.C.; McGrew, L.L.; Lai, C.-J.; Lee, J.-J.; von Kessler, D.P., Moon, R.T.; Beachy, P.A.;
RA		RT	"Distinct expression and shared activities of members of the hedgehog gene family of Xenopus laevis";
RA		RL	Development 121:2337-2347 (1995).
CC		CC	-!- FUNCTION: SIGNAL INVOLVED IN THE EARLY INDUCTION AND PATTERNING OF ANTERODORSAL ECTODERM, NERVOUS SYSTEM AND SOMITES. INDUCES ECTOPIC GERMANT GLAND FORMATION IN EMBRYOS.
CC		CC	-!- SUBCELLULAR LOCATION: THE C-TERMINAL PEPTIDE DIFFUSES FROM THE CELL, WHILE THE N-TERMINAL PEPTIDE REMAINS ASSOCIATED WITH THE CELL SURFACE. HEDGEHOG PROTEIN IS ALSO SECRETED IN EITHER CLEAVED OR UNCLEAVED FORM TO MEDIATE SIGNALING TO OTHER CELLS (BY SIMILARITY).
CC		CC	-!- DEVELOPMENTAL STAGE: DETECTABLE WITHIN THE EARLY GASTRULA. IN THE NEURULA EXPRESSION BECOMES RESTRICTED TO ANTERIOR STRUCTURES, ENCOMPASSING BOTH NEURAL PLATE AND ENDODERMAL CELLS.
CC		CC	-!- PTM: The C-terminal domain displays an autoproteolysis activity and a cholesterol transferase activity. Both activities result in the cleavage of the full-length protein and covalent attachment of a cholesterol moiety to the C-terminal of the newly generated N-terminal fragment (N-product). This covalent modification appears to play an essential role in restricting the spatial distribution of the protein activity to the cell surface. The N-product is the active species in both local and long-range signaling, whereas the C-product has no signaling activity (By similarity).
CC		CC	-!- SIMILARITY: Belongs to the hedgehog family.
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